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(54) Title: METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.

METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS.

This application is related to USSN 60/299,234, filed June 18, 2001; USSN 60/315,287, filed August 27, 2001; USSN 60/317,544, filed September 5, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002, each of which is incorporated herein by reference for all purposes.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in ovarian cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of ovarian cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit ovarian cancer.

BACKGROUND OF THE INVENTION

Ovarian cancer is the sixth most common cancer in women, accounting for 6% of all female cancers. It ranks fifth as the cause of cancer death in women. The American Cancer Society predicts that there will be about 23,100 new cases of ovarian cancer in this country in the year 2000 and about 14,000 women will die of the disease. Because many ovarian cancers cannot be detected early in their development, they account for a disproportionate number of fatal cancers, being responsible for almost half the deaths from cancer of the female genital tract; more deaths than any other reproductive organ cancer.

Most patients with epithelial ovarian cancer, the predominant form, are asymptomatic in early-stage disease and usually present with stage III or IV disease. Their five-year survival is less than 25%, with lower survival among African-American women. The minority of patients discovered with early-stage disease have a five-year survival rate of 80%-90%. See, Parker, et. al.. (1997) "Cancer Statistics, 1997" CA Cancer J. Clin. 47:5-27.

In the absence of a family history of ovarian cancer, lifetime risk of ovarian cancer is 1/70. Risk factors include familial cancer syndromes (risk of up to 82% by age 70 in women

with hereditary breast/ovarian syndrome); family history (1.4% lifetime risk with no affected relatives, 5% with one affected relative, 7% with two affected relatives; Kerlikowske, et.al. (1992) Obstet. Gynecol. 80:700-707); nulliparity; advancing age; obesity; personal history of breast, endometrial, or colorectal cancer; fewer pregnancies; or older age (>35 years) at first pregnancy. However, 95% of all ovarian cancers occur in women without risk factors. Use of hormonal contraceptives, oophorectomy, and tubal sterilization reduce risk of ovarian cancer (Kerlikowske, et. al. (1992) Obstet. Gynecol. 80:700-707; Grimes (1992) Am J. Obstet. Gynecol. 166:1950-1954; Hankinson, et. al. (1993) JAMA 270:2813-2818); however, even bilateral oophorectomy may not be completely effective in preventing ovarian cancer.

Treatment of ovarian cancer consists largely of surgical oophorectomy, anti-hormone therapy, and/or chemotherapy. Although many ovarian cancer patients are effectively treated, the current therapies can all induce serious side effects which diminish quality of life. Deciding on a particular course of treatment is typically based on a variety of prognostic parameters and markers (Fitzgibbons, et al. (2000) Arch. Pathol. Lab. Med. 124:966-978; Hamilton and Piccart (2000) Ann. Oncol. 11:647-663), including genetic predisposition markers BRCA-1 and BRCA-2 (Robson (2000) J. Clin. Oncol. 18:113sup-118sup).

The identification of novel therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Recent advances in molecular medicine have increased the interest in tumor-specific cell surface antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated. Examples of such antigens include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

Potential immunotherapeutic targets have been identified for ovarian cancer. One such target is polymorphic epithelial mucin (MUC1). MUC1 is a transmembrane protein, present at the apical surface of glandular epithelial cells. It is often overexpressed in ovarian cancer, and typically exhibits an altered glycosylation pattern, resulting in an antigenically

distinct molecule, and is in early clinical trials as a vaccine target. Gilewski, et al. (2000) Clin. Cancer Res. 6:1693-1701; Scholl, et al. (2000) J. Immunother. 23:570-580. The tumor-expressed protein is often cleaved into the circulation, where it is detectable as the tumor marker, CA 15-3. See, e.g., Bon, et al. (1997) Clin. Chem. 43:585-593. However, many patients have tumors that express neither HER2 nor MUC-1; therefore, it is clear that other targets need to be identified to manage localized and metastatic disease.

Mutations in both BRCA1 and BRCA2 are associated with increased susceptibility to ovarian cancer. Mutations in BRCA1 occur in approximately 5 percent (95 percent confidence interval, 3 to 8 percent) of women in whom ovarian cancer is diagnosed before the age of 70 years. See Stratton, et al. (1997) N.E.J. Med. 336:1125-1130. And, in BRCA1 gene carriers, the risk for developing ovarian cancer is .63. See Easton (1995) Am. J. Hum. Genet. 56:267-xxx; and Elit (2001) Can. Fam. Physician 47:778-84.

Other biochemical markers such as CA125 have been reported to be associated with ovarian cancer, but they are not absolute indicators of disease. Although roughly 85% of women with clinically apparent ovarian cancer have increased levels of CA125, CA125 is also increased during the first trimester of pregnancy, during menstruation, in the presence of non-cancerous illnesses, and in cancers of other sites.

While industry and academia have identified novel gene sequences, there has not been an equal effort exerted to identify the function of these novel sequences. The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in ovarian and other cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of ovarian cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate ovarian cancer.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in ovarian cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate ovarian cancer, such as hormones or antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for many purposes, e.g., early detection of ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment (of primary or metastatic tumors), and early detection of pre-cancerous lesions. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the present invention provides a method of determining the level of an ovarian cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat ovarian cancer. In another embodiment, the patient is suspected of having metastatic ovarian cancer.

In one embodiment, the patient is a human.

In one embodiment, the ovarian cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids

before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of an ovarian cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic ovarian cancer. In a further embodiment, the patient has a drug resistant form of ovarian cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the ovarian cancer-associated transcript to a level of the ovarian cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-26.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting an ovarian cancer cell in a biological sample from a patient, the method comprising contacting the biological

sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to ovarian cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates an ovarian cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with an ovarian cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of an ovarian cancer-associated cell to treat ovarian cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having ovarian cancer or to a cell sample isolated from; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of ovarian cancer.

In one embodiment, the control is a mammal with ovarian cancer or a cell sample that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or is non-malignant tissue.

In one embodiment, the test compound is administered in varying amounts or

concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-26 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

In another aspect, the present invention provides a method for treating a mammal having ovarian cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having ovarian cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in an ovarian cancer. In one embodiment, a gene is selected from Tables 1-26. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the ovarian cancer modulatory protein, or an animal lacking the ovarian cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-26, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with ovarian cancer is

provided. The method comprises determining the expression of a gene of Tables 1-26 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with ovarian cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in ovarian cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of an ovarian cancer modulating protein (ovarian cancer modulatory protein) or a fragment thereof and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining an ovarian cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. The method further includes determining the binding of said ovarian cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits ovarian cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising an ovarian cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises an ovarian cancer modulating protein, preferably encoded by a nucleic acid of Table 1-26 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding an ovarian cancer modulating protein, preferably selected from the nucleic acids of Tables 1-26, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of an ovarian cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

In another aspect of the invention, a method of treating an individual for ovarian cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of an ovarian cancer modulating protein. In another embodiment, the method comprises administering to a patient having ovarian cancer an antibody to an ovarian cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for ovarian cancer (OC), including metastatic ovarian cancer, as well as methods for screening for compositions which modulate ovarian cancer. Also provided are methods for treating ovarian cancer and related conditions, e.g., ovarian carcinoma (e.g., epithelial (including malignant serous tumors, malignant mucinous tumors, and malignant endometrioid tumors), germ cell (including teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, and gonadoblastoma), and stromal carcinomas (e.g., granulosal stromal cell tumors)), fallopian tube carcinoma, and peritoneal carcinoma.

Tables 1-26 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in ovarian cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "ovarian cancer protein" or "ovarian cancer polynucleotide" or "ovarian cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-26; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26. A polynucleotide or polypeptide

sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. An "ovarian cancer polypeptide" and an "ovarian cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" ovarian cancer protein or nucleic acid refers to an ovarian cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type ovarian cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of an ovarian cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of particular interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default

parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990)

J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5887). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells, such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (2001) Molecular Biology of the Cell (4th ed.) Garland Pub.; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β-sheet and α-helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the non-covalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds,

although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986), Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucl. Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Angew. Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature, 365:566-568; Carlsson, et al. (1996) Nature 380:207, each of which is incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs,

et al. (1994) J. Biomolecular NMR 34:17-xx; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (p. 35 June 2, 1997) C&E News. Each of these references is hereby expressly incorporated by reference.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched base pairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic,

photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the ovarian cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945-xxx; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the

stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) <u>Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology)</u> (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target

sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are available, e.g., in Innis, et al. (1990) <u>PCR Protocols: A Guide to Methods and Applications</u> Academic Press, N.Y.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided, e.g., Ausubel, et al. (ed. 1991 and supplements) <u>Current Protocols in Molecular Biology</u> Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that

modulate activity of an ovarian cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the ovarian cancer protein or nucleic acid, e.g., a functional, physical, physiological, or chemical effect, such as the ability to decrease ovarian cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an ovarian cancer protein sequence, e.g., functional, enzymatic, physical, physiological, and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the ovarian cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on ovarian cancer can also be performed using ovarian cancer assays known to those of skill in the art such as an in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. The functional effects can be evaluated by means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for ovarian cancer-associated sequences, measurement of RNA stability, or identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of ovarian cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of ovarian cancer polynucleotide and

polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of ovarian cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate ovarian cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of ovarian cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Assays for inhibitors and activators include, e.g., expressing the ovarian cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of ovarian cancer can also be identified by incubating ovarian cancer cells with the test compound and determining increases or decreases in the expression of one or more ovarian cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more ovarian cancer proteins, such as ovarian cancer proteins encoded by the sequences set out in Tables 1-26.

Samples or assays comprising ovarian cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25% or less. Activation of an ovarian cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., 2-5 fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, e.g., cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, change in contact inhibition or density limitation of growth, loss of growth factor or serum requirements, change in cell morphology, gain or loss of immortalization, gain or loss of tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss.

"Tumor cell" refers to pre-cancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is typically associated with phenotypic changes, such as immortalization of cells, aberrant growth control, non-morphological changes, and/or malignancy. See, Freshney (1994) Culture of Animal Cells.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See, e.g., Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody,

one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al., pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Transgenic mice, or other organisms, e.g., other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of ovarian cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is

characteristic of the state of the cell. That is, normal tissue (e.g., normal ovarian or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the ovarian, or ovarian cancer tissue or metastatic ovarian cancerous tissue can be compared with tissue samples of ovarian and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different ovarian cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in ovarian cancer versus non-ovarian cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate ovarian cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, does existing treatment induce expression of a target. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of ovarian cancer in the tissue or origin of the primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the ovarian cancer expression profile. This may be done by making biochips comprising sets of the important ovarian cancer genes, which can then be used in these screens. These methods can also be based on evaluating protein expression; that is, protein expression levels of the ovarian cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the ovarian cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or RNAi nucleic acids, or the ovarian cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in ovarian cancer relative to normal tissues and/or non-malignant tissues, herein termed "ovarian cancer sequences." As outlined below, ovarian cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in ovarian cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the ovarian cancer sequences are from humans; however, as will be appreciated by those in the art, ovarian cancer sequences from other organisms may be useful

in animal models of disease and drug evaluation; thus, other ovarian cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Ovarian cancer sequences, e.g., counterpart genes, from other organisms may be obtained using the techniques outlined below.

Ovarian cancer sequences can include both nucleic acid and amino acid sequences. Ovarian cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids. Screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the ovarian cancer sequences, are also provided.

An ovarian cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying ovarian cancer-associated sequences, the ovarian cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing ovarian cancer samples with metastatic cancer samples from other cancers, such as lung, ovarian, gastrointestinal cancers, etc. Samples of different stages of ovarian cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal ovarian, but also including, and not limited to, lung, heart, brain, liver, ovarian, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the ovarian cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, expression in non-essential tissues may be tolerated. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side

effects by interaction with target present in other organs.

In a preferred embodiment, ovarian cancer sequences are those that are up-regulated in ovarian cancer; that is, the expression of these genes is higher in the ovarian cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Other embodiments are directed to sequences up regulated in non-malignant conditions relative to normal.

Unigene cluster identification numbers and accession numbers herein refer to the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nucl. Acids Res. 26:1-7; and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, e.g., FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, ovarian cancer sequences are those that are down-regulated in ovarian cancer; that is, the expression of these genes is lower in ovarian cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three-fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in ovarian cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. Expression profiles can be used in diagnostic or prognostic evaluation of patients with ovarian cancer. Subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA) or in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable

exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database, and can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing ovarian cancer, e.g., the identification of ovarian cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, and outcome data, among others. Although data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method

using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

Fundamentals of bioinformatics are provided, e.g., in Mount, et al. (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge Univ. Press; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d ed.) Wiley-Liss; Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for ovarian cancer. In another variation, assay records cross-tabulate one or more of the following parameters for a target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or

characteristic separation coordinate (e.g., electrophoretic or genomic position coordinates); (2) sample source; and (3) absolute and/or relative quantity of target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells)

composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, e.g., which typically comprises one or more of: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by methods of the inventions, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of ovarian cancer-associated proteins

Ovarian cancer proteins of the present invention may be categorized as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the ovarian cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes. See, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins can also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are often involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-

322.

In another preferred embodiment, the ovarian cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their

cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules, or may be processed or shed to the blood stream. In this respect, they can mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Ovarian cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful ovarian markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the ovarian cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to an adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus, secreted molecules often find use in modulating or altering numerous aspects of physiology. Ovarian cancer proteins that are secreted proteins are particularly preferred as good diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be

antibody or small molecule therapeutic targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms, as protein or DNA vaccines.

Use of ovarian cancer nucleic acids

As described above, ovarian cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The ovarian cancer nucleic acid sequences of the invention, e.g., in Table 1-26, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the ovarian cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once the ovarian cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire ovarian cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised as a linear nucleic acid segment, the recombinant ovarian cancer nucleic acid can be further-used as a probe to identify and isolate other ovarian cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant ovarian cancer nucleic acids and proteins.

The ovarian cancer nucleic acids of the present invention are useful in several ways. In a first embodiment, nucleic acid probes to the ovarian cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, the ovarian cancer nucleic acids that include coding regions of ovarian cancer proteins can be put into expression vectors for the expression of ovarian cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to ovarian cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the ovarian cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent

attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See, e.g., WO0055627 Reusable Low Fluorescent Plastic Biochip.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxyl groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using

functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of ovarian cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, an ovarian cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of ovarian cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are available. See, e.g., Innis, et al.(1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be

extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR; see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1980; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of ovarian cancer proteins from nucleic acids

In a preferred embodiment, ovarian cancer nucleic acids, e.g., encoding ovarian cancer proteins are used to make a variety of expression vectors to express ovarian cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known and are used to express proteins. See, e.g., Ausubel, supra; and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the ovarian cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a pre-protein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; and two sequences may be operably linked when they are physically part of the same polymer. Generally,

"operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the ovarian cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences typically encode constitutive or inducible promoters. The promoters may be naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, supra.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The ovarian cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an ovarian cancer protein, under the appropriate conditions to induce or cause expression of the ovarian cancer protein. Conditions appropriate for ovarian cancer protein expression will vary with

the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculovirus systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the ovarian cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. See, e.g., Fernandez and Hoeffler, supra. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, ovarian cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters

are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the ovarian cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others. See Fernandez and Hoeffler, supra. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, ovarian cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, an ovarian cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The ovarian cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the ovarian cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the ovarian cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the ovarian cancer protein is an ovarian cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the ovarian cancer protein is purified or isolated after expression. Ovarian cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the ovarian cancer protein may be purified using a standard anti-ovarian cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the ovarian cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the ovarian cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of ovarian cancer proteins

In one embodiment, the ovarian cancer proteins are derivative or variant ovarian cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative ovarian cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most any residue within the ovarian cancer peptide.

Also included within one embodiment of ovarian cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the ovarian cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant ovarian cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the ovarian cancer protein amino acid sequence. The variants typically exhibit the same

qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed ovarian cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of ovarian cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the ovarian cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the ovarian cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the ovarian cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine,

valine, or alanine; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Covalent modifications of ovarian cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an ovarian cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an ovarian cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking ovarian cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-ovarian cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutamine and asparagine residues to the corresponding glutamic and aspartic acid residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine, or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1983) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the ovarian cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence ovarian cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence ovarian cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express ovarian cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to ovarian cancer polypeptides may also be

accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence ovarian cancer polypeptide (for O-linked glycosylation sites). The ovarian cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the ovarian cancer polypeptide at pre-selected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the ovarian cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem. CRC Press.

Removal of carbohydrate moieties present on the ovarian cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol., 138:350-359.

Another type of covalent modification of ovarian cancer comprises linking the ovarian cancer polypeptide to one of a variety of non-proteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylene. See, e.g., U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Ovarian cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules, e.g., comprising an ovarian cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an ovarian cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the ovarian cancer polypeptide. The presence of such epitope-tagged forms of an ovarian cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the ovarian cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an ovarian cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of

the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; His6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Mol. Cell. Biol. 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include, e.g., the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other ovarian cancer proteins of the ovarian cancer family, and ovarian cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related ovarian cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the ovarian cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to ovarian cancer proteins

In a preferred embodiment, when the ovarian cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the ovarian cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller ovarian cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a

mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at

least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Table 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to ovarian cancer protein are capable of reducing or eliminating a biological function of an ovarian cancer protein, as is described below. That is, the addition of anti-ovarian cancer protein antibodies (either polyclonal or preferably monoclonal) to ovarian cancer tissue (or cells containing ovarian cancer) may reduce or eliminate the ovarian cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the ovarian cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Humanization can be essentially performed following the method of Winter and co-workers, e.g., by substituting rodent CDRs or CDR sequences for the

corresponding sequences of a human antibody. See, e.g., Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; Presta (1992) Curr. Op. Struct. Biol. 2:593-596; and Verhoeyen, et al. (1988) Science 239:1534-1536). Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (see, e.g., Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; and Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (see, e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. See, e.g., U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016; Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of ovarian cancer, e.g., with an antibody raised against ovarian cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the ovarian cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby

inactivating the secreted ovarian cancer protein.

In another preferred embodiment, the ovarian cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the ovarian cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane ovarian cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the ovarian cancer protein. The antibody is also an antagonist of the ovarian cancer protein. Further, the antibody prevents activation of the transmembrane ovarian cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the ovarian cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, ovarian cancer is treated by administering to a patient antibodies directed against the transmembrane ovarian cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the ovarian cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the ovarian cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with ovarian cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to ovarian cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with ovarian cancer. Cytotoxic agents are numerous and varied and include, but are not limited to,

cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against ovarian cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane ovarian cancer proteins not only serves to increase the local concentration of therapeutic moiety in the ovarian cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the ovarian cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the ovarian cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The ovarian cancer antibodies of the invention specifically bind to ovarian cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μM, preferably at least about 0.1 μM or better, and most preferably, 0.01 μM or better. Selectivity of binding is also important.

Detection of ovarian cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the ovarian cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing ovarian cancer) and in ovarian cancer tissue (and in some cases, for varying severities of ovarian cancer that relate to prognosis, as outlined below, or in non-malignant disease are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states,

information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus ovarian cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is modulated, either up-regulated, resulting in an increased amount of transcript, or down-regulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, e.g., Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., up-regulation or down-regulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the ovarian cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to ovarian cancer genes, e.g., those identified as being important in an ovarian cancer or disease phenotype, can be evaluated in an ovarian disease diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed, or on an individual basis.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular sample. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the ovarian cancer protein are detected. Although DNA or RNA encoding the ovarian cancer protein may be detected, of particular interest are methods wherein an mRNA encoding an ovarian cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an ovarian cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, ovarian cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as prognostic or diagnostic markers of ovarian disease. Detection of these proteins in putative ovarian cancer tissue allows for detection, diagnosis, or prognosis of ovarian disease, and for selection of therapeutic strategy. In one

embodiment, antibodies are used to detect ovarian cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the ovarian cancer protein is detected, e.g., by immunoblotting with antibodies raised against the ovarian cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the ovarian cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai (ed. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. Cells are contacted with from one to many antibodies to the ovarian cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the ovarian cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of ovarian cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing ovarian cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of ovarian cancer proteins. Antibodies can be used to detect an ovarian cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology, and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous ovarian cancer protein.

In a preferred embodiment, in situ hybridization of labeled ovarian cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including ovarian cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It

is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to ovarian cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of a plurality of genes being preferred. As above, ovarian cancer probes may be attached to biochips for the detection and quantification of ovarian cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified ovarian cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the ovarian cancer phenotype or an identified physiological function of an ovarian cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in ovarian cancer, test

compounds can be screened for the ability to modulate gene expression or for binding to the ovarian cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing ovarian cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in ovarian cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in ovarian cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the ovarian cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more ovarian cancer-associated sequences, e.g., a polynucleotide sequence set out inTables 1-26. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate ovarian cancer, modulate ovarian cancer proteins, bind to an ovarian cancer protein, or interfere with the binding of an ovarian cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the ovarian cancer phenotype or the expression of an ovarian cancer sequence,

e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses an ovarian cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced an ovarian cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of an ovarian cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to an ovarian cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that

display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka (1991) Pept. Prot. Res. 37:487-493; and Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), non-peptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-305), and/or peptidyl phosphonates (Campbell, et al.(1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al.(1996) Nature Biotechnology 14:309-314; and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522; and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33, Baum (Jan. 18, 1993) C&E News; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available.

See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J.; Asinex, Moscow, RU; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD; etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of ovarian cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide

detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of ovarian cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids.

For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702; 5,597,909; 5,545,730; 5,594,117; 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124,246; and 5,681,697, each of which is hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step

parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the ovarian cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress an ovarian cancer expression pattern leading to a normal expression pattern, or to modulate a single ovarian cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated ovarian cancer tissue reveals genes that are not expressed in normal tissue

or ovarian cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for ovarian cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated ovarian cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of ovarian cancer cells, that have an associated ovarian cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., ovarian cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the ovarian cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on ovarian cancer activity. By defining such a signature for the ovarian cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins" or a "ovarian cancer modulatory protein". The ovarian cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the ovarian cancer modulatory protein is a fragment. In a preferred embodiment, the ovarian cancer amino acid sequence which is used to determine

sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the ovarian cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In another embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine. Or, the ovarian cancer proteins are conjugated to an immunogenic agent, e.g., to BSA.

Measurements of ovarian cancer polypeptide activity, or of ovarian cancer or the ovarian cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the ovarian cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of ovarian cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian ovarian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, an ovarian cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the ovarian cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the ovarian cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or

enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the ovarian cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β-gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins." The ovarian cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the ovarian cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an ovarian cancer protein and a candidate compound, and determining the binding of the compound to the ovarian cancer protein. Preferred embodiments utilize the human ovarian cancer protein, although other mammalian proteins, e.g., counterparts, may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative ovarian cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the ovarian cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is non-diffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the ovarian cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the ovarian cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the ovarian cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the ovarian cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one

component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., an ovarian cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically 4-40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hr will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the ovarian cancer protein and thus is capable of binding to, and potentially modulating, the activity of the ovarian cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the ovarian cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the ovarian cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the ovarian cancer proteins. In this embodiment, the methods comprise combining an ovarian cancer protein and a competitor in a first sample. A second sample comprises a test compound, an ovarian cancer protein, and a

competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the ovarian cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the ovarian cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native ovarian cancer protein, but cannot bind to modified ovarian cancer proteins. The structure of the ovarian cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of an ovarian cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of an ovarian cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising ovarian cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an ovarian cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including

chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate ovarian cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the ovarian cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting ovarian cancer cell division is provided. The method comprises administration of an ovarian cancer inhibitor. In another embodiment, a method of inhibiting ovarian cancer is provided. The method comprises administration of an ovarian cancer inhibitor. In a further embodiment, methods of treating cells or individuals with ovarian cancer are provided. The method comprises administration of an ovarian cancer inhibitor.

In one embodiment, an ovarian cancer inhibitor is an antibody as discussed above. In another embodiment, the ovarian cancer inhibitor is an antisense or RNAi molecule.

A variety of cell viability, growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of ovarian cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^{3}H)-thymidine at saturation density can be used to measure density limitation of growth. See, e.g., Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^{3}H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with an ovarian cancer-associated sequence and are grown for 24 hr at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^{3}H)-thymidine is determined autoradiographically. See, e.g., Freshney (1994), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts. See, e.g., Temin (1966) J. Nat'l Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879; and Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly,

tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate ovarian cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Alternatively, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by pre-labeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of ovarian cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the ovarian cancer gene is disrupted or in which an ovarian cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous ovarian cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous ovarian cancer gene with a mutated version of the ovarian cancer gene, or by mutating the endogenous ovarian cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing an ovarian cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of ovarian cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of an ovarian cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., an ovarian cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-

sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the ovarian cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for ovarian cancer molecules. A preferred antisense molecule is for an ovarian cancer sequences in Tables 1-26, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. An antisense or a sense oligonucleotide can be developed based upon a cDNA sequence encoding a given protein. See, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to down-regulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of ovarian cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. Pharmacol. 25: 289-

317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known to those of skill in the art. See, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Hum. Gene Ther. 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Hum. Gene Ther. 5:1151-120; and Yamada, et al. (1994) Virology 205:121-126.

Polynucleotide modulators of ovarian cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of ovarian cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating ovarian cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-ovarian cancer antibody that reduces or eliminates the biological activity of an endogenous ovarian cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding an ovarian cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the ovarian cancer sequence is down-regulated in ovarian cancer, such state may be reversed by increasing the amount of ovarian cancer gene product in the cell. This can be accomplished, e.g., by over-expressing the endogenous ovarian cancer gene or administering a gene encoding the ovarian cancer sequence, using known gene-therapy techniques, e.g.. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when

the ovarian cancer sequence is up-regulated in ovarian cancer, the activity of the endogenous ovarian cancer gene is decreased, e.g., by the administration of an ovarian cancer antisense or RNAi nucleic acid.

In one embodiment, the ovarian cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to ovarian cancer proteins. Similarly, the ovarian cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify ovarian cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to an ovarian cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The ovarian cancer antibodies may be coupled to standard affinity chromatography columns and used to purify ovarian cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the ovarian cancer protein.

Methods of identifying variant ovarian cancer-associated sequences

Without being bound by theory, expression of various ovarian cancer sequences is correlated with ovarian cancer. Accordingly, disorders based on mutant or variant ovarian cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant ovarian cancer genes, e.g., determining all or part of the sequence of at least one endogenous ovarian cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the ovarian cancer genotype of an individual, e.g., determining all or part of the sequence of at least one ovarian cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced ovarian cancer gene to a known ovarian cancer gene, e.g., a wild-type gene.

The sequence of all or part of the ovarian cancer gene can then be compared to the sequence of a known ovarian cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the ovarian cancer gene of the patient and the known ovarian cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the ovarian cancer genes are used as probes to determine the number of copies of the ovarian cancer gene in the genome.

In another preferred embodiment, the ovarian cancer genes are used as probes to determine the chromosomal localization of the ovarian cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the ovarian cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of an ovarian cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Systems Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceutical Assn.; and Pickar (1999) Dosage Calculations Thomson. Adjustments for ovarian cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in ovarian cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the ovarian cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intra-nasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the ovarian cancer

proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise an ovarian cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules, and lozenges. It is recognized that ovarian cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise an ovarian cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs. See, e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gillman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill. Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions are readily available.

The compositions containing modulators of ovarian cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and/or its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic

treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, e.g., in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present ovarian cancer protein-modulating compounds can be administered alone or in combination with additional ovarian cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of ovarian cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, ovarian cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, ovarian cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the ovarian cancer coding regions) can be administered in a gene therapy application. These ovarian cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Ovarian cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-

349), peptide compositions encapsulated in poly(D,L-lactide-co-glycolide, "PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS; see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243), multiple antigen peptide systems (MAPs; see, e.g., Tam (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) AIDS Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Ann. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al.(1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p. 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Ann. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be

used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. See, e.g., Wolff et. al. (1990) Science 247:1465-1468; U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode ovarian cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like, will be apparent. See, e.g., Shata, et al. (2000) Mol. Med. Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; and Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing an ovarian cancer gene or portion of an ovarian cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in an ovarian cancer patient. The ovarian cancer gene used for DNA vaccines can encode full-length ovarian cancer proteins, but more preferably encodes portions of the ovarian cancer proteins including peptides derived from the ovarian cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an ovarian cancer gene. For example, ovarian cancer-associated genes or sequence encoding subfragments of an ovarian cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the ovarian cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment ovarian cancer genes find use in generating animal models of ovarian cancer. When the ovarian cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the ovarian cancer gene will also diminish or repress expression of the gene. Animal models of ovarian cancer find use in screening for modulators of an ovarian cancer-associated sequence or modulators of ovarian cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the ovarian cancer protein. When desired, tissue-specific expression or knockout of the ovarian cancer protein may be necessary.

It is also possible that the ovarian cancer protein is overexpressed in ovarian cancer. As such, transgenic animals can be generated that overexpress the ovarian cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of ovarian cancer and are additionally useful in screening for modulators to treat ovarian cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, ovarian cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, siRNA or antisense polynucleotides, ribozymes, dominant negative ovarian cancer polypeptides or polynucleotides, small molecules inhibitors of ovarian cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium

capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of ovarian cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: an ovarian cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing ovarian cancer-associated activity. Optionally, the kit contains biologically active ovarian cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

TABLE 1A lists about 1119 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59000 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 80th percentile value amongst various ovarian cancers. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues.

TABLE 1A: ABOUT 1119 UP-REGULATED OVARIAN CANCER GENES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
ratio: ratio tumor vs normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	65.7
423017	AW178761	Hs.227948	"serine (or cysteine) proteinase inhibitor, clade B(ovalbumi	63.6
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	58.3
445810	AW265700	Hs.155660	ESTs	35.9
431938	AA938471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
407112	AA070801	Hs.51615	"ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAM	31.3
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	30.0
402075			predicted exon	27.9
400301	X03635	Hs.1657	estrogen receptor 1	26.4

402639			predicted exon	25.3
421948	L42583	Hs.111758	keratin 6A	24.7
414540	BE379050		"gb:601236655F1 NIH_MGC_44 Homo sapiens cDNA clon	24.6
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	24.5
401575			predicted exon	23.6
457024	AA397546	Hs.119151	ESTs	23.2
440684	AI253123	Hs.127356	"ESTs, Highly similar to NEST_HUMAN NESTI [H.sapien	23.1
459006	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
400964			predicted exon	22.5
402421			predicted exon	20.9
437329	AA811977	Hs.291761	ESTs	20.8
414605	BE390440		"gb:601283601F1 NIH_MGC_44 Homo sapiens cDNA clon	20.7
411004	AW813242		"gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapiens	20.4
401283			predicted exon	20.3
440633	AI140686	Hs.263320	ESTs	19.9
445603	H08345	Hs.106234	ESTs	19.7
403786			predicted exon	19.7
436508	AW604381	Hs.121121	ESTs	19.6
459390	BE385725		"gb:601276347F1 NIH_MGC_20 Homo sapiens cDNA clon	19.2
421823	N40850	Hs.28625	ESTs	19.0
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	18.9
422525	AA758797	Hs.192807	ESTs	18.5
458121	S42416	Hs.74647	Human T-cell receptor active alpha-chain mRNA from JM c	18.3
430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	18.1
450192	AA263143	Hs.24596	RAD51-interacting protein	18.0
416839	H94900	Hs.17882	ESTs	17.9
440788	AI806594	Hs.128577	ESTs	17.9
451072	AA013451	Hs.117929	ESTs	17.7
402203			predicted exon	17.3
417611	AW993983		"gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapiens	17.3
438658	AI222068	Hs.123571	ESTs	17.3
403747			predicted exon	17.2
444958	AW292643	Hs.167047	ESTs	17.2
404097			predicted exon	17.1
459375	BE251770		"gb:601112470F1 NIH_MGC_16 Homo sapiens cDNA clon	16.9
443198	AI039813		gb:ox49d06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapi	16.9
441557	AW452647	Hs.270482	ESTs	16.9
433871	W02410	Hs.205555	ESTs	16.8
429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cD	16.7
443406	AI056238	Hs.143316	ESTs	16.7
400613			predicted exon	16.6
448372	AW445166	Hs.170802	ESTs	16.5
410929	H47233	Hs.30643	ESTs	16.5
445887	AI263105	Hs.145597	ESTs	16.1
422036	AA302647	Hs.271891	ESTs	16.0
404767			predicted exon	15.9
420831	AA280824	Hs.190035	ESTs	15.8
405196			predicted exon	15.8
452947	AW130413		"gb:xf50f04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clo	15.8
429538	BE182592	Hs.139322	small proline-rich protein 3	15.8
435313	AI769400	Hs.189729	ESTs	15.7
449635	AI989942	Hs.232150	ESTs	15.6
424098	AF077374	Hs.139322	small proline-rich protein 3	15.4
411660	AW855718		"gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens c	15.4
442653	BE269247	Hs.170226	Homo sapiens clone 23579 mRNA sequence	15.4
443534	AI076123		gb:oy92e04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	15.4
458012	AI424899	Hs.188211	ESTs	15.3
441018	AI809587	Hs.148782	ESTs	15.1
425972	BE391563	Hs.165433	"ESTs, Highly similar to T17342 hypothetical protein DKFZ	15.1
418092	R45154	Hs.106604	ESTs	15.1
410909	AW898161	Hs.53112	"ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	15.1
458234	BE551408	Hs.127196	ESTs	15.0
434208	T92641	Hs.127648	hypothetical protein PRO2176	15.0
403177			predicted exon	15.0
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	14.9
425090	AA350552		"gb:EST57886 Infant brain Homo sapiens cDNA 5' end, mR	14.7
409723	AW885757	Hs.257862	ESTs	14.6
423735	AA330259		"gb:EST33963 Embryo, 12 week II Homo sapiens cDNA 5'	14.6
444266	AI424984	Hs.125465	ESTs	14.5
443341	AW631480	Hs.8688	ESTs	14.4
457336	AW969657	Hs.291029	ESTs	14.4
440500	AA972165	Hs.150308	ESTs	14.4
446292	AF081497	Hs.279682	Rh type C glycoprotein	14.3
438086	AA336519	Hs.301167	"Homo sapiens cDNA: FLJ21545 fis, clone COL06195"	14.3
434715	BE005346	Hs.116410	ESTs	14.2
409387	AW384900	Hs.123526	ESTs	14.2
409272	AB014569	Hs.52526	KIAA0669 gene product	14.2
454913	AW841462		"gb:RC6-CN0014-080300-012-B09 CN0014 Homo sapiens	14.0
439846	T63959	Hs.228320	"Homo sapiens cDNA: FLJ23537 fis, clone LNG07690"	14.0
409695	AA296961		"gb:EST112514 Adrenal gland tumor Homo sapiens cDNA	13.9
422897	AA679784	Hs.4290	ESTs	13.9
404664			predicted exon	13.9
458829	AI557388		"gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3', mRNA	13.8
407327	AA487182	Hs.269414	ESTs	13.8

455435	AW939445		"gb:QV1-DT0072-310100-056-b07 DT0072 Homo sapiens	13.7
449327	AI638743	Hs.224672	ESTs	13.7
411693	AW857271		"gb:CM0-CT0307-210100-158-g09 CT0307 Homo sapiens	13.7
407463	AJ272034		gb:Homo sapiens mRNA for putative capacitative calcium c	13.6
446767	AI380107	Hs.158954	ESTs	13.6
433040	H70423	Hs.300511	ESTs	13.5
435209	AW027809	Hs.187698	"ESTs, Highly similar to cytomegalovirus partial fusion rece	13.5
441459	AI919142	Hs.214233	ESTs	13.5
401269			predicted exon	13.4
438663	AI199575	Hs.153070	ESTs	13.4
426698	AA394104	Hs.97489	ESTs	13.4
423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (from clon	13.2
448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clon	13.2
456714	AW897265		"gb:CM0-NN0057-150400-335-a04 NN0057 Homo sapiens	13.2
458356	AI024855	Hs.131575	ESTs	13.2
431822	AA516049		"gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clo	13.1
454822	AW833793		"gb:QV4-TT0008-130100-080-a06 TT0008 Homo sapiens c	13.1
453358	AI990738	Hs.240066	ESTs	13.1
435542	AA687376	Hs.269533	ESTs	13.1
421286	AA806584	Hs.187895	ESTs	13.0
452799	AI948829	Hs.213786	ESTs	13.0
444355	BE383686	Hs.191621	ESTs	13.0
444271	AW452569	Hs.149804	ESTs	12.9
443860	AW866632		"gb:QV4-SN0024-210400-181-g04 SN0024 Homo sapiens	12.9
428719	AA358193	Hs.193128	hypothetical protein FLJ10805	12.9
418282	AA215535	Hs.98133	ESTs	12.8
437308	AA749417	Hs.292353	ESTs	12.7
400584			predicted exon	12.7
426306	AA447310	Hs.164059	"Homo sapiens cDNA FLJ13338 fis, clone OVARC100188	12.7
448466	AI522109	Hs.171066	ESTs	12.7
402738			predicted exon	12.7
451531	AA018311	Hs.114762	ESTs	12.6
435243	AW292886	Hs.261373	adenosine A2b receptor pseudogene	12.6
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	12.6
425108	AI000489	Hs.96967	ESTs	12.5
422330	D30783	Hs.115263	epiregulin	12.5
432949	AA570749	Hs.298866	ESTs	12.5
417009	AA191719	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA	12.4
456378	AA843387	Hs.87279	ESTs	12.4
432966	AA650114		"gb:ns92h09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clon	12.4
440571	AA904461	Hs.130798	ESTs	12.3
411178	AW820852		"gb:RC2-ST0301-120200-011-f12 ST0301 Homo sapiens c	12.3
445934	AF131737	Hs.13475	hypothetical protein	12.3
433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D15 on chrom	12.2
402018			predicted exon	12.2
424101	AA335394		"gb:EST39787 Epididymus Homo sapiens cDNA 5' end, mR	12.2
448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	12.1
458154	AW816379		"gb:QV4-ST0234-181199-035-g01 ST0234 Homo sapiens c	12.1
440919	AW291274	Hs.262826	ESTs	12.0
415747	AA381209		"gb:EST94257 Activated T-cells I Homo sapiens cDNA 5' e	12.0
411748	AW859920		"gb:QV1-CT0364-260100-052-g05 CT0364 Homo sapiens	12.0
452975	M85521	Hs.69469	dendritic cell protein	12.0
427276	AA400269	Hs.49598	ESTs	12.0
454315	AW373564	Hs.251928	nuclear pore complex interacting protein	12.0
450786	H86632	Hs.33654	ESTs	12.0
402578			predicted exon	11.9
459591	AL037185		gb:DKFZp564A1169_r1 564 (synonym: hfbr2) Homo sapie	11.9
433449	AW772282		"gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA c	11.9
429108	AA890521	Hs.126035	ESTs	11.8
454556	AW807073		"gb:MR4-ST0062-031199-018-d06 ST0062 Homo sapiens	11.7
443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapiens cDNA c	11.7
400385	NM_020389	Hs.283104	putative capacitative calcium channel	11.6
411725	AW858396		"gb:CM0-CT0341-181299-130-c06 CT0341 Homo sapiens	11.5
455174	AI694575	Hs.147801	ESTs	11.5
412402	AW984788		"gb:RC1-HN0015-120400-021-c07 HN0015 Homo sapiens	11.5
434205	AF119861	Hs.283032	hypothetical protein PRO2015	11.5
450496	AW449251	Hs.257131	ESTs	11.5
411149	N68715	Hs.269128	ESTs	11.5
414210	BE383592		"gb:601297871F1 NIH_MGC_19 Homo sapiens cDNA clon	11.4
409994	D86864	Hs.57735	acetyl LDL receptor; SREC	11.3
453845	AL157568		gb:DKFZp761F0816_r1 761 (synonym: hamy2) Homo sapi	11.3
404849			predicted exon	11.3
442824	BE178065	Hs.144081	ESTs	11.3
428548	AA430058	Hs.98649	EST	11.3
434804	AA649530		"gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clo	11.3
430486	BE062109	Hs.241551	"chloride channel, calcium activated, family member 2"	11.3
400174			predicted exon	11.2
424324	AA346316		"gb:EST52440 Greater omentum tumor Homo sapiens cDN	11.2
447724	AW298375	Hs.24477	ESTs	11.2
457028	AW449838	Hs.97562	ESTs	11.2
429900	AA460421	Hs.30875	ESTs	11.2
452240	AI591147	Hs.61232	ESTs	11.2
458067	AA393603	Hs.36752	"Homo sapiens cDNA: FLJ22834 fis, clone KAIA4314"	11.1
402222			predicted exon	11.1

446745	AW118189	Hs.156400	ESTs	11.1
453060	AW294092	Hs.21594	ESTs	11.1
443482	AW188093	Hs.250385	ESTs	11.1
436843	AA824588		"gb:oc83d02.s1 NCI_CGAP_GC81 Homo sapiens cDNA c	11.0
416320	H47867	Hs.34024	ESTs	11.0
435772	AA700019	Hs.132992	"ATP-binding cassette, sub-family G (WHITE), member 5 (	11.0
451542	AA018365	Hs.32713	ESTs	11.0
408522	AI541214	Hs.46320	"Small proline-rich protein SPRK [human, odontogenic kera	11.0
414712	N88858.comp	Hs.77039	ribosomal protein S3A	10.9
411940	AW876686		"gb:CM4-PT0031-180200-507-e05 PT0031 Homo sapiens c	10.9
408733	AW264812	Hs.254290	ESTs	10.9
452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from clon	10.9
458175	AW296024	Hs.150434	ESTs	10.9
400612			predicted exon	10.9
440159	AI637599	Hs.126127	ESTs	10.8
429443	AB028967	Hs.202687	"potassium voltage-gated channel, Shal-related subfamily, m	10.8
416319	AI815601	Hs.79197	"CD83 antigen (activated B lymphocytes, immunoglobulin s	10.8
405783			predicted exon	10.7
405708			predicted exon	10.7
433266	AI863224	Hs.288677	"Homo sapiens cDNA FLJ13872 fis, clone THYRO100132	10.6
456900	AA355442	Hs.169054	ESTs	10.6
432408	N39127	Hs.76391	"myxovirus (influenza) resistance 1, homolog of murine (int	10.6
451702	AW665452	Hs.246503	ESTs	10.6
418179	X51630	Hs.1145	Wilms tumor 1	10.6
408987	H85615		gb:yt03f11.r1 Soares retina N2b5HR Homo sapiens cDNA	10.6
405285			predicted exon	10.5
419276	BE165909	Hs.134682	"Homo sapiens cDNA: FLJ23161 fis, clone LNG09730"	10.5
407287	AI678812	Hs.201658	"ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	10.5
403065			predicted exon	10.5
414195	BE263293		"gb:601144881F2 NIH_MGC_19 Homo sapiens cDNA clon	10.4
454258	AI457286	Hs.143979	"ESTs, Weakly similar to KIAA1276 protein [H.sapiens]"	10.4
412951	BE018611	Hs.251946	"Homo sapiens cDNA: FLJ23107 fis, clone LNG07738"	10.4
428888	AA437010	Hs.266584	ESTs	10.4
440834	AA907027	Hs.128606	ESTs	10.4
437096	AA744406		"gb:ny51h02.s1 NCI_CGAP_Pr18 Homo sapiens cDNA clo	10.4
400135			predicted exon	10.4
447849	AI538147	Hs.164277	ESTs	10.3
400593			predicted exon	10.3
427469	AA403084	Hs.269347	ESTs	10.3
402794			predicted exon	10.2
452743	AW965082	Hs.61455	ESTs	10.2
448983	AI611654	Hs.224908	ESTs	10.2
422696	AF242524	Hs.26323	hypothetical nuclear factor SBBI22	10.2
428949	AA442153	Hs.104744	"ESTs, Weakly similar to AF208855 1 BM-013 [H.sapiens]	10.2
409191	AW818390		"gb:RC1-ST0278-160200-014-d10 ST0278 Homo sapiens c	10.2
428493	AK001745	Hs.184628	hypothetical protein FLJ10883	10.2
406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from clone	10.2
410626	BE407727		"gb:601299771F1 NIH_MGC_21 Homo sapiens cDNA clon	10.1
445835	AW290999	Hs.145534	chromosome 21 open reading frame 23	10.1
452507	AI904646		"gb:QV-BT065-020399-103 BT065 Homo sapiens cDNA, m	10.1
433297	AV658581	Hs.282633	ESTs	10.1
426724	AA383623	Hs.293616	ESTs	10.0
436659	AI217900	Hs.144464	ESTs	10.0
405675			predicted exon	10.0
413466	BE141737	Hs.254105	"enolase 1, (alpha)"	10.0
447198	D61523	Hs.283435	ESTs	10.0
403306	NM_006825	Hs.74368	"transmembrane protein (63kD), endoplasmic reticulum/Go	10.0
413544	BE147225		"gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapiens	9.9
437094	AW103746	Hs.136907	ESTs	9.9
401497			predicted exon	9.9
416203	H27794	Hs.269055	ESTs	9.9
426882	AA393108	Hs.97365	ESTs	9.9
454874	AW836407		"gb:PM3-LT0031-301299-002-b09 LT0031 Homo sapiens	9.9
406702	Z20656	Hs.278432	"myosin, heavy polypeptide 6, cardiac muscle, alpha (cardio	9.9
404952			predicted exon	9.9
430691	C14187	Hs.103538	ESTs	9.9
444518	AI160278	Hs.146884	ESTs	9.8
416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen 1NFLS Homo sapie	9.8
438691	AA906288	Hs.212184	ESTs	9.8
405636			predicted exon	9.8
437242	AA747538	Hs.187942	ESTs	9.8
425627	AF019612	Hs.297007	ESTs	9.8
452226	AA024898	Hs.296002	ESTs	9.8
418986	AI123555	Hs.81796	ESTs	9.8
441139	AW449009	Hs.126647	ESTs	9.7
427244	AA402400	Hs.178045	ESTs	9.7
423756	AA828125		"gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clo	9.7
457940	AL360159	Hs.30445	Homo sapiens mRNA full length insert cDNA clone EURO	9.6
443526	AW792804	Hs.134002	ESTs	9.6
440576	AW449775	Hs.126008	ESTs	9.6
419088	AI538323	Hs.77496	small nuclear ribonucleoprotein polypeptide G	9.6
454707	AW814989		"gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapiens	9.6
446252	AI283125	Hs.150009	ESTs	9.6
434374	AA631439		"gb:np85d02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA cl	9.6

403093			predicted exon	9.6
454633	AW811380		"gb:IL3-ST0143-290999-019-D05 ST0143 Homo sapiens c	9.6
407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo sapiens cDNA	9.5
455203	AW865450		"gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapiens	9.5
403647			predicted exon	9.5
401530			predicted exon	9.5
414281	BE269751	Hs.288995	hypothetical protein FLJ20813	9.5
411057	AW815098		"gb:QV4-ST0212-091199-023-f10 ST0212 Homo sapiens c	9.5
415953	H14425	Hs.27947	ESTs	9.5
450174	T82121	Hs.177285	ESTs	9.5
422949	AA319435		"gb:EST21657 Adrenal gland tumor Homo sapiens cDNA 5	9.5
402112	R58624	Hs.2186	eukaryotic translation elongation factor 1 gamma	9.5
457886	AA742279	Hs.293346	ESTs	9.4
458145	AI239457	Hs.130794	ESTs	9.4
452332	AW014859	Hs.101657	ESTs	9.4
434950	AW974892		"gb:EST386997 MAGE resequences, MAGN Homo sapien	9.3
409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	9.3
419968	X04430	Hs.93913	"interleukin 6 (interferon, beta 2)"	9.3
436211	AK001581	Hs.80961	"polymerase (DNA directed), gamma"	9.3
428412	AA428240	Hs.126083	ESTs	9.3
449441	AI656040	Hs.196532	ESTs	9.3
458771	AW295151	Hs.163612	ESTs	9.3
458543	AA213403	Hs.257542	ESTs	9.3
414257	AI828600	Hs.21124	"ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	9.3
442826	AI018777	Hs.131241	ESTs	9.3
446740	AI611635	Hs.192605	ESTs	9.2
408938	AA059013	Hs.22607	ESTs	9.2
434157	AI538316	Hs.158451	ESTs	9.2
408774	AW270899	Hs.254569	ESTs	9.2
424268	AA397653	Hs.144339	Human DNA sequence from clone 495O10 on chromosome	9.2
415715	F30364		"gb:HSPD20786 HM3 Homo sapiens cDNA clone s400009	9.1
405277			predicted exon	9.1
412167	AW897230		"gb:CM0-NN0057-150400-335-a11 NN0057 Homo sapiens	9.1
442771	AW409808	Hs.101550	ESTs	9.1
404898			predicted exon	9.1
401230			predicted exon	9.1
400623			predicted exon	9.1
418808	AI821836	Hs.10359	ESTs	9.1
436396	AI683487	Hs.299112	"Homo sapiens cDNA FLJ11441 fis, clone HEMBA100132	9.1
440466	AA885871	Hs.135727	ESTs	9.0
437568	AI954795	Hs.156135	ESTs	9.0
405382			predicted exon	9.0
435673	AF202961	Hs.284200	"Homo sapiens uncharacterized gastric protein ZG12P mRN	9.0
405848			predicted exon	9.0
437229	AW976005		"gb:EST388114 MAGE resequences, MAGN Homo sapien	9.0
417728	AW138437	Hs.24790	KIAA1573 protein	9.0
454597	AW809648		"gb:MR4-ST0124-261099-015-d01 ST0124 Homo sapiens	9.0
427093	AA398118	Hs.97579	ESTs	9.0
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	9.0
440556	AW206958	Hs.125968	ESTs	9.0
400163			predicted exon	8.9
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-like 1	8.9
417549	AA203651		gb:zx58f10.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	8.9
406163			predicted exon	8.9
437918	AI761449	Hs.121629	ESTs	8.9
449419	R34910	Hs.119172	ESTs	8.9
434683	AW298724	Hs.202639	ESTs	8.9
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	8.9
454590	AW809762	Hs.222056	"Homo sapiens cDNA FLJ11572 fis, clone HEMBA100337	8.8
454574	AW809109		"gb:MR4-ST0117-070100-027-a04 ST0117 Homo sapiens c	8.8
441433	AA933809	Hs.42746	ESTs	8.8
416858	AW979294	Hs.85634	ESTs	8.8
421978	AJ243662	Hs.110196	NICE-1 protein	8.8
451528	AA018297	Hs.35493	ESTs	8.8
408751	N91553	Hs.258343	ESTs	8.7
401862			predicted exon	8.7
417344	AW997313		"gb:RC2-BN0048-250400-018-f12 BN0048 Homo sapiens	8.7
454455	AW752710		"gb:IL3-CT0219-281099-024-A03 CT0219 Homo sapiens c	8.7
455592	BE008002		"gb:QV0-BN0147-290400-214-h04 BN0147 Homo sapiens	8.7
417650	T05870	Hs.100640	ESTs	8.7
456309	AA225423		"gb:nc24a12.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clon	8.7
432030	AI908400	Hs.143789	ESTs	8.7
421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
402576			predicted exon	8.7
426874	N67325	Hs.247132	ESTs	8.7
403334			predicted exon	8.7
408562	AI436323	Hs.31141	"Homo sapiens mRNA for KIAA1568 protein, partial cds"	8.7
439443	AF086261	Hs.127892	ESTs	8.7
428600	AW863261	Hs.15036	"ESTs, Highly similar to AF161358 1 HSPC095 [H.sapiens	8.7
414539	BE379046		"gb:601236646F1 NIH_MGC_44 Homo sapiens cDNA clon	8.6
432527	AW975028	Hs.102754	ESTs	8.6
403273			predicted exon	8.6
452077	BE144949		"gb:RC2-HT0187-041099-011-d12 HT0187 Homo sapiens	8.6
444598	AI288830	Hs.149924	ESTs	8.6

434066	AF116649	Hs.283944	"Homo sapiens PRO0566 mRNA, complete cds"	8.6
429643	AA455889	Hs.187548	ESTs	8.6
432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens cDNA clon	8.6
446142	AI754693	Hs.145968	ESTs	8.6
417412	X16896	Hs.82112	"interleukin 1 receptor, type I"	8.6
416913	AW934714		"gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapiens	8.5
451318	AA029888	Hs.95071	ESTs	8.5
405547			predicted exon	8.5
423843	AA332652		"gb:EST36627 Embryo, 8 week I Homo sapiens cDNA 5' en	8.5
454145	AA046872	Hs.62798	ESTs	8.4
401200			predicted exon	8.4
404166			predicted exon	8.4
412761	AW995092		"gb:QV0-BN0041-030300-145-a10 BN0041 Homo sapiens	8.4
412333	AW937485		"gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapiens	8.4
455092	BE152428		"gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapiens	8.4
419281	H96452	Hs.42189	ESTs	8.4
446171	AI374927		gb:ta66c04.x1 Soares_total_fetus_Nb2HF8_9w Homo sapie	8.3
437362	AL359561	Hs.16493	hypothetical protein DKFZp762N2316	8.3
402631			predicted exon	8.3
458573	AV653838	Hs.295131	ESTs	8.3
439185	AF087976	Hs.233343	ESTs	8.3
445881	AI263029	Hs.210689	ESTs	8.3
449737	AI668581	Hs.246316	ESTs	8.3
401830	AJ004832	Hs.5038	neuropathy target esterase	8.3
421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
416996	W91892	Hs.59609	ESTs	8.2
443626	AI540644	Hs.138479	"ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	8.2
407471	D55644		gb:Human spleen PABL (pseudoautosomal boundary-like se	8.2
402664			predicted exon	8.2
417682	W69561		gb:zd47a08.r1 Soares_fetal_heart_NbHH19W Homo sapien	8.2
424983	AI742434	Hs.169911	ESTs	8.2
434353	AA630863	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLAS	8.2
453448	AL036710	Hs.209527	ESTs	8.2
455121	BE156459		"gb:QV0-HT0368-040100-082-f06 HT0368 Homo sapiens	8.2
404270			predicted exon	8.1
438297	AW515196	Hs.258238	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	8.1
418122	R42778	Hs.22217	ESTs	8.1
419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.1
400925			predicted exon	8.1
403350			predicted exon	8.1
426116	AA868729	Hs.144694	ESTs	8.1
441518	AW161697	Hs.294150	ESTs	8.1
421888	AA299780	Hs.121036	ESTs	8.1
402745			predicted exon	8.1
402071			predicted exon	8.1
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	8.0
430372	AI206173	Hs.211375	ESTs	8.0
449867	AI672379	Hs.73919	"clathrin, light polypeptide (Lcb)"	8.0
422174	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (from clone	8.0
413382	BE090689		"gb:RC1-BT0720-280300-011-f08 BT0720 Homo sapiens c	8.0
456502	AI798611	Hs.157277	ESTs	8.0
405336			predicted exon	8.0
405917			predicted exon	8.0
436007	AI247716	Hs.232168	ESTs	8.0
439192	AW970536	Hs.105413	ESTs	8.0
437724	AW444828	Hs.184323	ESTs	8.0
452755	AW138937	Hs.213436	ESTs	8.0
401781			predicted exon	7.9
406057			predicted exon	7.9
406289	AW068311	Hs.82582	"integrin, beta-like 1 (with EGF-like repeat domains)"	7.9
421459	AI821539	Hs.97249	ESTs	7.9
448251	BE280486	Hs.84045	"Homo sapiens cDNA FLJ11979 fis, clone HEMBB100128	7.9
429125	AA446854	Hs.271004	ESTs	7.9
440154	BE077129	Hs.126119	"Homo sapiens cDNA FLJ13273 fis, clone OVARC100101	7.9
413233	AW578713	Hs.47534	"ESTs, Weakly similar to ORF YKL201c [S.cerevisiae]"	7.9
438268	AA782163	Hs.293502	ESTs	7.9
452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on chromosome 6	7.9
441194	BE274581		"gb:601120870F1 NIH_MGC_20 Homo sapiens cDNA clon	7.9
425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	7.9
445090	AW205208	Hs.147293	ESTs	7.9
431292	AA370141	Hs.251453	Human DNA sequence from clone 967N21 on chromosome	7.9
414266	BE267834		"gb:601124428F1 NIH_MGC_8 Homo sapiens cDNA clone	7.8
407839	AA045144	Hs.161566	ESTs	7.8
456101	AA159478		gb:zo74d06.s1 Stratagene pancreas (937208) Homo sapiens	7.8
455853	BE147225		"gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapiens	7.8
414995	C18200		gb:C18200 Human placenta cDNA (TFujiwara) Homo sapie	7.8
447247	AW369351	Hs.287955	"Homo sapiens cDNA FLJ13090 fis, clone NT2RP3002142	7.8
416151	T26661		"gb:AB65C7R Infant brain, LLNL array of Dr. M. Soares 1	7.8
446435	AW206737	Hs.253582	ESTs	7.8
403698			predicted exon	7.8
424914	AA348410	Hs.119065	ESTs	7.8
409731	AA125985	Hs.56145	"thymosin, beta, identified in neuroblastoma cells"	7.8
401604			predicted exon	7.8
413025	AA805265	Hs.291646	ESTs	7.8

405896			predicted exon	7.8
454505	AW801365		"gb:IL5-UM0067-240300-050-a01 UM0067 Homo sapiens	7.7
448283	AI340462	Hs.182979	ribosomal protein L12	7.7
434098	AA625499		"gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapiens cDNA	7.7
431673	AW971302	Hs.293233	ESTs	7.7
421029	AW057782	Hs.293053	ESTs	7.7
408391	AW859276		"gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapiens	7.7
422529	AW015128	Hs.256703	ESTs	7.7
454389	AW752571		"gb:IL3-CT0213-170100-055-F02 CT0213 Homo sapiens c	7.7
427821	AA470158	Hs.98202	ESTs	7.7
434657	AA641876	Hs.191840	ESTs	7.7
445628	AI344166	Hs.155743	ESTs	7.7
424872	AA347923		"gb:EST54302 Fetal heart II Homo sapiens cDNA 5' end, m	7.7
439232	N48590	Hs.46693	ESTs	7.7
441417	AI733297	Hs.144474	ESTs	7.7
453596	AA441838	Hs.62905	ESTs	7.7
430440	X52599	Hs.2561	"nerve growth factor, beta polypeptide"	7.7
413306	AW303544	Hs.118654	ESTs	7.7
400968			predicted exon	7.7
446726	AW300144	Hs.209209	"Homo sapiens cDNA FLJ11629 fis, clone HEMBA100424	7.7
427504	AA776743	Hs.191589	ESTs	7.7
405621			predicted exon	7.6
414127	AI431863	Hs.135270	ESTs	7.6
409866	AW502152		gb:UI-HF-BR0p-ajr-f-11-0-UI.r1 NIH_MGC_52 Homo sap	7.6
446232	AI281848	Hs.165547	ESTs	7.6
403568			predicted exon	7.6
451458	AI797558	Hs.270820	ESTs	7.6
439157	AA912737	Hs.20160	ESTs	7.6
401793			predicted exon	7.6
429839	AI190291	Hs.112143	ESTs	7.6
445672	AI907438	Hs.282862	ESTs	7.6
449444	AW818436	Hs.23590	"solute carrier family 16 (monocarboxylic acid transporters)	7.6
447499	AW262580	Hs.147674	KIAA1621 protein	7.6
421773	W69233	Hs.112457	ESTs	7.6
439706	AW872527	Hs.59761	ESTs	7.5
432189	AA527941		"gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clon	7.5
402050			predicted exon	7.5
429687	AI675749	Hs.211608	nucleoporin 153kD	7.5
423193	R07299	Hs.254837	"Homo sapiens cDNA FLJ13502 fis, clone PLACE1004836	7.5
416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen 1NFLS Homo sapien	7.5
443236	AI079496	Hs.134169	ESTs	7.5
436053	AI057224	Hs.15443	ESTs	7.4
437191	NM_006846	Hs.5476	"serine protease inhibitor, Kazal type, 5"	7.4
451829	AW964081	Hs.247377	ESTs	7.4
443151	AI827193	Hs.132714	ESTs	7.4
452055	AI377431	Hs.293772	ESTs	7.4
445265	AI218295	Hs.144942	ESTs	7.4
401032			predicted exon	7.4
448184	BE541249	Hs.109697	ESTs	7.4
414808	T95945		gb:ye42e02.r1 Soares fetal liver spleen 1NFLS Homo sapien	7.4
418540	AI821597	Hs.90877	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.4
410449	AW748954	Hs.18192	Ser/Arg-related nuclear matrix protein (plenty of prolines 1	7.4
435568	AA688048	Hs.294080	ESTs	7.4
459160	AI904723		"gb:CM-BT066-120299-092 BT066 Homo sapiens cDNA,	7.4
419753	N42531		gb:yy11c12.r1 Soares melanocyte 2NbHM Homo sapiens cD	7.4
432383	AK000144	Hs.274449	"Homo sapiens cDNA FLJ20137 fis, clone COL07137"	7.4
404893			predicted exon	7.4
425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5-phosphate epimer	7.4
413864	BE175582		"gb:RC5-HT0580-100500-022-C01 HT0580 Homo sapiens	7.3
426871	AA393041	Hs.216493	ESTs	7.3
415613	R20233		gb:yg18h11.r1 Soares infant brain 1NIB Homo sapiens cDN	7.3
427025	AA397589	Hs.97523	ESTs	7.3
444683	AI375101	Hs.158721	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
447700	AI420183	Hs.171077	"ESTs, Weakly similar to similar to serine/threonine kinase	7.3
412740	AW993984		"gb:RC1-BN0035-130400-013-a05 BN0035 Homo sapiens	7.3
416642	T96118	Hs.226313	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
416506	H59879	Hs.237306	ESTs	7.3
426130	AA853282		gb:NHTBCae04f07r1 Normal Human Trabecular Bone Cell	7.3
407392	AB032369		"gb:Homo sapiens MIST mRNA, partial cds."	7.3
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	7.3
451221	AI949701	Hs.210589	ESTs	7.3
443161	AI038316		gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapi	7.3
418186	BE541042	Hs.23240	"Homo sapiens cDNA FLJ13495 fis, clone PLACE1004471	7.3
439152	H65014		gb:yu66f10.r1 Weizmann Olfactory Epithelium Homo sapie	7.2
459534	BE386808	Hs.147905	ESTs	7.2
443326	BE156494	Hs.188478	ESTs	7.2
417351	T90278	Hs.15049	ESTs	7.2
454182	AW177335		"gb:CM1-CT0129-180899-006-b08 CT0129 Homo sapiens	7.2
402298			predicted exon	7.2
458562	N34128	Hs.145268	ESTs	7.2
407021	U52077		"gb:Human mariner1 transposase gene, complete consensus	7.2
449276	AW241510	Hs.252713	ESTs	7.2
418251	AA832123	Hs.177723	ESTs	7.2
420788	AA937957	Hs.193367	ESTs	7.2

401881			predicted exon	7.2
456436	AA251079	Hs.158386	ESTs	7.2
413425	F20956		"gb:HSPD05390 HM3 Homo sapiens cDNA clone 032-X4-	7.2
448966	AW372914	Hs.287462	"Homo sapiens cDNA FLJ11875 fis, clone HEMBA100707	7.2
429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (from clon	7.2
406053			predicted exon	7.2
405851			predicted exon	7.2
431009	BE149762	Hs.248213	"gap junction protein, beta 6 (connexin 30)"	7.2
426662	AA879474	Hs.122710	ESTs	7.2
408536	AW381532	Hs.135188	ESTs	7.1
455013	BE073250		"gb:MR0-BT0551-060300-102-e05 BT0551 Homo sapiens	7.1
428910	W03667	Hs.193792	ESTs	7.1
424634	NM_003613	Hs.151407	"cartilage intermediate layer protein, nucleotide pyrophosph	7.1
449794	AW444502	Hs.256982	"ESTs, Highly similar to AF116865 1 hedgehog-interacting	7.1
423410	AF058989	Hs.128231	"G antigen, family B, 1 (prostate associated)"	7.1
445460	AI797473	Hs.209468	ESTs	7.1
447285	AI371849	Hs.200696	"ATPase, Class VI, type 11C"	7.1
419750	AL079741	Hs.183114	"Homo sapiens cDNA FLJ14236 fis, clone NT2RP4000515	7.1
438986	AF085888	Hs.269307	ESTs	7.1
420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone receptor; testicular	7.1
432479	AL042844	Hs.275675	katanin p80 (WD40-containing) subunit B 1	7.1
449733	R74546	Hs.29438	"Homo sapiens cDNA FLJ12094 fis, clone HEMBB100260	7.1
437846	AA773866	Hs.244569	ESTs	7.1
454934	AW846080		"gb:MR3-CT0176-081099-002-b09 CT0176 Homo sapiens	7.1
421929	AA300543	Hs.247360	ESTs	7.1
401780			predicted exon	7.0
448106	AI800470	Hs.171941	ESTs	7.0
448835	BE277929	Hs.11081	"ESTs, Weakly similar to S57447 HPBRII-7 protein [H.sap	7.0
400842			predicted exon	7.0
429364	AA451797	Hs.201202	"ESTs, Moderately similar to Pro-Pol-dUTPase polyprotein	7.0
454963	AW847647		"gb:IL3-CT0213-280100-056-A06 CT0213 Homo sapiens c	7.0
423891	AK002042	Hs.134795	"Homo sapiens cDNA FLJ11180 fis, clone PLACE1007452	7.0
407506	U71600		"gb:Human zinc finger protein zfp31 (zf31) mRNA, partial	7.0
413802	AW964490	Hs.32241	ESTs	7.0
440051	BE559980		"gb:601345293F1 NIH_MGC_8 Homo sapiens cDNA clone	7.0
446283	AI948801	Hs.171073	ESTs	7.0
419236	AA330447	Hs.135159	"Homo sapiens cDNA FLJ11481 fis, clone HEMBA100180	7.0
405472			predicted exon	7.0
435024	AI863518	Hs.127743	"ESTs, Weakly similar to V-ATPase G-subunit like protein	7.0
453969	AW090783	Hs.301731	"Homo sapiens cDNA FLJ11738 fis, clone HEMBA100547	7.0
404992			predicted exon	7.0
428129	AI244311	Hs.26912	ESTs	7.0
414315	Z24878		"gb:HSB65D052 STRATAGENE Human skeletal muscle cD	7.0
400491	H25530	Hs.50868	"solute carrier family 22 (organic cation transporter), memb	6.9
459275	AI808913	Hs.118321	ESTs	6.9
450853	AA479629	Hs.44243	ESTs	6.9
457460	AI143312	Hs.164004	ESTs	6.9
434168	AI204525	Hs.116156	ESTs	6.9
445153	AI214671		"gb:qm32d02.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clo	6.9
450028	AI912012	Hs.200737	ESTs	6.9
414954	D81402		gb:HUM162A03B Human fetal brain (TFujiwara) Homo sa	6.9
459478	AW195566	Hs.253182	ESTs	6.9
426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from clon	6.9
401050			predicted exon	6.9
447588	AI394154	Hs.279659	"ESTs, Weakly similar to unknown protein [H.sapiens]"	6.9
449002	AI620018	Hs.117461	ESTs	6.9
452759	AW590773	Hs.258996	ESTs	6.9
443220	R85304	Hs.132032	"Homo sapiens cDNA FLJ11683 fis, clone HEMBA100490	6.9
400749			predicted exon	6.8
406277			predicted exon	6.8
433785	BE044593	Hs.112704	ESTs	6.8
434129	AI807757	Hs.221041	ESTs	6.8
453369	BE551550	Hs.232630	ESTs	6.8
411722	AW875942		"gb:CM1-PT0013-131299-067-b10 PT0013 Homo sapiens	6.8
455152	AW858621		"gb:CM0-CT0342-021299-115-f04 CT0342 Homo sapiens	6.8
412670	AA115456		gb:zk89b05.r1 Soares_pregnant_uterus_NbHPU Homo sapi	6.8
418054	N40340	Hs.191510	"ESTs, Weakly similar to ORF2 [M.musculus]"	6.8
421316	AA287203	Hs.251397	SMA5	6.8
432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone	6.8
458603	AW103046	Hs.6162	KIAA0771 protein	6.8
439527	AW298119	Hs.202536	ESTs	6.8
408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2	6.8
439127	AW978465	Hs.292368	ESTs	6.8
434890	AF161345	Hs.283930	"Homo sapiens HSPC082 mRNA, partial cds"	6.8
429413	NM_014058	Hs.201877	DESC1 protein	6.7
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.7
447252	R90916		gb:yn01e10.r1 Soares adult brain N2b4HB55Y Homo sapien	6.7
455851	BE146879		"gb:QV4-HT0222-261099-014-c11 HT0222 Homo sapiens	6.7
439509	AF086332	Hs.58314	ESTs	6.7
418858	AW961605	Hs.21145	"Homo sapiens cDNA: FLJ22489 fis, clone HRC10951"	6.7
419323	AI092379	Hs.135275	ESTs	6.7
415317	Z43388	Hs.5570	hypothetical protein FLJ10006	6.7
418654	AA226334	Hs.154291	ESTs	6.7
407413	AF067801		"gb:Homo sapiens HDCGC21P mRNA, complete cds."	6.7

439694	AA843915	Hs.54707	ESTs	6.7
451191	N67900	Hs.118446	ESTs	6.7
454006	U12775	Hs.37006	agouti (mouse)-signaling protein	6.7
443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen 1NFLS Homo sapien	6.7
455879	BE153275		"gb:PM0-HT0335-180400-008-e11 HT0335 Homo sapiens	6.7
451368	BE242152	Hs.288417	protein serine threonine kinase Clk4	6.7
453509	AL040021		gb:DKFZp434N1812_r1 434 (synonym: htes3) Homo sapie	6.7
420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	6.7
423372	AI246375	Hs.154458	ESTs	6.7
450316	W84446	Hs.17850	ESTs	6.7
447795	AW295151	Hs.163612	ESTs	6.7
413252	BE074910		"gb:RC5-BT0580-170300-021-F12 BT0580 Homo sapiens	6.7
405771			predicted exon	6.6
411483	AW848115		"gb:IL3-CT0214-301299-048-C09 CT0214 Homo sapiens c	6.6
420271	AI954365	Hs.42892	ESTs	6.6
431948	AA917706	Hs.194616	ESTs	6.6
409629	AW449589	Hs.279724	ESTs	6.6
458841	W28965		gb:54d10 Human retina cDNA randomly primed sublibrary	6.6
416565	AW000960	Hs.44970	ESTs	6.6
409097	AA677927	Hs.144269	ESTs	6.6
441832	AI018249	Hs.128062	ESTs	6.6
457285	AI038858	Hs.228780	"ESTs, Highly similar to AF199597 1 A-type potassium cha	6.6
406504			predicted exon	6.6
414606	BE387771		"gb:601283251F1 NIH_MGC_44 Homo sapiens cDNA clon	6.6
452956	AW003578	Hs.231872	ESTs	6.6
410743	AA089474	Hs.272153	ESTs	6.6
404599			predicted exon	6.6
423575	C18863	Hs.163443	"Homo sapiens cDNA FLJ11576 fis, clone HEMBA100354	6.6
443027	AI027847	Hs.253550	ESTs	6.6
458663	AV658444	Hs.280776	"Homo sapiens cDNA FLJ13684 fis, clone PLACE2000021	6.6
431277	AA501806	Hs.249965	ESTs	6.6
445232	BE294357		"gb:601172878F1 NIH_MGC_17 Homo sapiens cDNA clon	6.6
459170	AI905518		"gb:RC-BT091-210199-098 BT091 Homo sapiens cDNA, m	6.6
437876	AA770151	Hs.126424	ESTs	6.6
406752	AI285598	Hs.217493	annexin A2	6.6
401245			predicted exon	6.6
446102	AW168067	Hs.252956	ESTs	6.5
446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.5
421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (from clone	6.5
458831	H71739	Hs.200227	ESTs	6.5
408914	AW450309		gb:UI-H-BI3-akz-g-08-0-UI.s1 NCI_CGAP_Sub5 Homo sa	6.5
411018	AW813428		"gb:MR3-ST0192-010200-210-c05 ST0192 Homo sapiens c	6.5
436562	H71937	Hs.169756	"complement component 1, s subcomponent"	6.5
457620	AA602711		"gb:np03h06.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clon	6.5
438647	AA813118	Hs.163230	ESTs	6.5
439570	T79925	Hs.269165	ESTs	6.5
419273	BE271180	Hs.293490	ESTs	6.5
443745	AB039670	Hs.9728	ALEX1 protein	6.5
431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q31.1	6.5
458695	AV660159	Hs.282284	ESTs	6.5
410966	AW812088		"gb:RC4-ST0173-191099-032-a07 ST0173 Homo sapiens c	6.4
417135	AA422067	Hs.50547	ESTs	6.4
416441	BE407197		"gb:601301552F1 NIH_MGC_21 Homo sapiens cDNA clon	6.4
413702	BE170313		"gb:QV4-HT0536-040500-193-g02 HT0536 Homo sapiens	6.4
452563	AI907552		"gb:RC-BT147-120499-044 BT147 Homo sapiens cDNA, m	6.4
408956	AK001868	Hs.295306	"ESTs, Highly similar to unnamed protein product [H.sapien	6.4
406349			predicted exon	6.4
425420	BE536911	Hs.234545	"ESTs, Weakly similar to AF155135 1 novel retinal pigmen	6.4
459430	AW662886		gb:hi82h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDN	6.4
425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	6.4
458678	AI306162	Hs.170938	"ESTs, Weakly similar to KIAA0705 protein [H.sapiens]"	6.4
429695	AA835714	Hs.293556	ESTs	6.4
426872	AA410446	Hs.112011	"ESTs, Weakly similar to unknown [H.sapiens]"	6.4
437152	AL050027		gb:Homo sapiens mRNA; cDNA DKFZp566C0324 (from c	6.4
440517	AW139632	Hs.132246	ESTs	6.4
450877	AI799608	Hs.29178	ESTs	6.4
410664	NM_006033	Hs.65370	"lipase, endothelial"	6.4
405793			predicted exon	6.4
418709	AA227394		gb:zr17c10.r1 Stratagene NT2 neuronal precursor 937230 H	6.4
428684	AA431792	Hs.44784	ESTs	6.4
448516	AW898595		"gb:RC1-NN0073-260400-011-g09 NN0073 Homo sapiens	6.4
400983			predicted exon	6.3
422365	AF035537	Hs.115521	"REV3 (yeast homolog)-like, catalytic subunit of DNA poly	6.3
425612	BE004257		"gb:CM0-BN0103-180300-296-c04 BN0103 Homo sapiens	6.3
401521			predicted exon	6.3
430290	AI734110	Hs.136355	ESTs	6.3
414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (from clon	6.3
437939	AW298600	Hs.141840	"ESTs, Weakly similar to S59501 interferon receptor IFNA	6.3
451842	AI820539	Hs.267087	"ESTs, Moderately similar to ALU4_HUMAN ALU SUBF	6.3
405810			predicted exon	6.3
443747	AV646352		"gb:AV646352 GLC Homo sapiens cDNA clone GLCAME	6.3
427287	NM_014903	Hs.174188	KIAA0938 protein	6.3
413521	BE145814		"gb:MR0-HT0208-101299-202-a04 HT0208 Homo sapiens	6.3
429090	AW820278	Hs.99066	ESTs	6.3

451488	H22999	Hs.208846	ESTs	6.3
455713	BE069891		"gb:QV4-BT0401-201299-064-b01 BT0401 Homo sapiens	6.3
452161	R43077	Hs.221747	ESTs	6.3
428647	AA830050	Hs.124344	ESTs	6.3
445063	AI246275	Hs.149196	ESTs	6.3
456671	AB011142	Hs.114293	KIAA0570 gene product	6.3
401508			predicted exon	6.3
412677	AW029608	Hs.17384	ESTs	6.3
441720	AI346487	Hs.28739	ESTs	6.3
418051	AW192535	Hs.19479	ESTs	6.3
438014	N71183	Hs.121806	"Homo sapiens cDNA FLJ11971 fis, clone HEMBB100120	6.3
432101	AI918950	Hs.11092	"Homo sapiens cDNA FLJ14290 fis, clone PLACE1006795	6.3
421032	AW293133	Hs.101340	ESTs	6.3
436532	AA721522		"gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens cDNA clo	6.3
431318	AA502700	Hs.293147	ESTs	6.3
413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Homo sapiens c	6.3
402425			predicted exon	6.3
455993	BE179085		"gb:RC0-HT0613-140300-021-d06 HT0613 Homo sapiens	6.3
400160			predicted exon	6.3
413795	AL040178	Hs.142003	ESTs	6.2
405071			predicted exon	6.2
403741			predicted exon	6.2
432489	AI804855	Hs.207530	ESTs	6.2
402296			predicted exon	6.2
446091	AW022192	Hs.200197	ESTs	6.2
444788	AI871122	Hs.202821	ESTs	6.2
404972			predicted exon	6.2
400227			predicted exon	6.2
433804	AI936561	Hs.112740	ESTs	6.2
448807	AI571940	Hs.7549	ESTs	6.2
404340			predicted exon	6.2
424632	AB014523	Hs.151406	KIAA0623 gene product	6.2
449547	H93543	Hs.117963	ESTs	6.2
406945	K01383	Hs.203967	metallothionein 1A (functional)	6.2
433663	AF083131	Hs.229535	CATX-15 protein	6.2
407809	AW082279	Hs.244106	ESTs	6.2
418342	BE002723	Hs.293504	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.2
438007	AA133008	Hs.158675	ribosomal protein L14	6.2
410536	N39533		gb:yv27d04.s1 Soares fetal liver spleen 1NFLS Homo sapie	6.2
448005	AW207437	Hs.170378	ESTs	6.2
414083	AL121282	Hs.257786	ESTs	6.2
405362			predicted exon	6.2
410102	AW248508	Hs.279727	"Homo sapiens cDNA FLJ14035 fis, clone HEMBA100463	6.2
457868	AW975133		"gb:EST387239 MAGE resequences, MAGN Homo sapien	6.2
407395	AF005082		"gb:Homo sapiens skin-specific protein (xp33) mRNA, part	6.2
443603	BE502601	Hs.134289	"ESTs, Weakly similar to KIAA1063 protein [H.sapiens]"	6.2
430051	AA464611	Hs.52515	transducin (beta)-like 2	6.1
434569	AI311295	Hs.58609	ESTs	6.1
430481	AA479678	Hs.203269	"ESTs, Moderately similar to ALU8_HUMAN ALU SUBF	6.1
402859			predicted exon	6.1
401260			predicted exon	6.1
406544			predicted exon	6.1
428446	AI024600	Hs.98612	ESTs	6.1
412246	AI160873	Hs.69233	"ESTs, Weakly similar to KIAA1064 protein [H.sapiens]"	6.1
400420	AJ277247	Hs.287369	interleukin 22	6.1
455662	BE065387		"gb:RC1-BT0314-030500-016-d03 BT0314 Homo sapiens	6.1
428613	AB037749	Hs.186928	KIAA1328 protein	6.1
443267	AW450630	Hs.133851	ESTs	6.1
433405	AW157566	Hs.156892	ESTs	6.1
416795	AI497778	Hs.168053	"ESTs, Highly similar to AF227948 1 HBV pX associated p	6.1
435706	W31254	Hs.7045	GL004 protein	6.1
450769	AA057418	Hs.33654	ESTs	6.1
427174	AA398848	Hs.97541	ESTs	6.1
425389	AW974499	Hs.192183	ESTs	6.1
416675	H73802	Hs.35381	ESTs	6.1
432749	NM_014438	Hs.278909	Interleukin-1 Superfamily e	6.1
401809			predicted exon	6.1
403041			predicted exon	6.0
408523	AW833259		"gb:RC2-TT0007-131099-011-c01 TT0007 Homo sapiens c	6.0
416515	N91716	Hs.194140	ESTs	6.0
452591	BE173164	Hs.1516	insulin-like growth factor-binding protein 4	6.0
437146	AA730977		"gb:nw55f05.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clo	6.0
450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (from clon	6.0
402529			predicted exon	6.0
430706	NM_003540	Hs.247816	"H4 histone family, member C"	6.0
459186	AI908287		"gb:RC-BT168-020499-035 BT168 Homo sapiens cDNA, m	6.0
452158	AI699120	Hs.61198	ESTs	6.0
411237	AW833676		"gb:QV4-TT0008-181199-038-h04 TT0008 Homo sapiens	6.0
400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	6.0
439398	AA284267	Hs.221504	ESTs	6.0
440862	H39048	Hs.127432	ESTs	6.0
415451	H19415	Hs.268720	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.0
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Homo sapi	6.0
456072	H54381		gb:yq89a03.s1 Soares fetal liver spleen 1NFLS Homo sapie	6.0

409954	AW512770	Hs.266457	ESTs	6.0
443488	AI073495	Hs.133912	"ESTs, Weakly similar to methyl-CpG binding domain-cont	6.0
430825	AI734186	Hs.185105	ESTs	6.0
454466	AA984138	Hs.279895	"Homo sapiens mRNA for KIAA1578 protein, partial cds"	6.0
456506	AA278277	Hs.194212	ESTs	6.0
449228	AJ403107	Hs.148590	"ESTs, Weakly similar to AF208846 1 BM-004 [H.sapiens]	6.0
457727	AW974687		"gb:EST386776 MAGE resequences, MAGM Homo sapien	6.0
442440	BE464435	Hs.146180	"ESTs, Weakly similar to non-receptor protein tyrosine kina	5.9
455110	BE154505		"gb:PM0-HT0343-281299-003-e06 HT0343 Homo sapiens	5.9
402790			predicted exon	5.9
409982	BE005839		"gb:RC2-BN0120-250400-012-f03 BN0120 Homo sapiens	5.9
427635	BE397988	Hs.179982	tumor protein p53-binding protein	5.9
408948	AW296713	Hs.221441	ESTs	5.9
402046			predicted exon	5.9
416438	R89238	Hs.34262	ESTs	5.9
403083			predicted exon	5.9
402481			predicted exon	5.9
409867	AW502161		gb:UI-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_52 Homo sap	5.9
420362	U79734	Hs.97206	huntingtin interacting protein 1	5.9
421375	AA489200	Hs.100595	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.9
437630	AI252782	Hs.153029	ESTs	5.9
443500	AV646388	Hs.137071	ESTs	5.9
448995	AI613276	Hs.5662	"guanine nucleotide binding protein (G protein), beta polyp	5.9
438214	H06076	Hs.26320	TRABID protein	5.9
428046	AW812795	Hs.155381	"ESTs, Moderately similar to I38022 hypothetical protein [H	5.9
431941	AK000106	Hs.272227	"Homo sapiens cDNA FLJ20099 fis, clone COL04544"	5.9
403356			predicted exon	5.9
439031	AF075079		gb:Homo sapiens full length insert cDNA YQ80A08	5.9
430032	AW936136	Hs.99610	ESTs	5.9
423457	F08208	Hs.155606	paired mesoderm homeo box 1	5.9
422158	L10343	Hs.112341	"protease inhibitor 3, skin-derived (SKALP)"	5.9
406592			predicted exon	5.9
418636	AW749855		"gb:QV4-BT0534-281299-053-c05 BT0534 Homo sapiens	5.8
429399	AA452244	Hs.16727	ESTs	5.8
408590	AW238162	Hs.253873	ESTs	5.8
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	5.8
417421	AL138201	Hs.82120	"nuclear receptor subfamily 4, group A, member 2"	5.8
401129			predicted exon	5.8
434745	AW974445	Hs.185155	"ESTs, Weakly similar to HuEMAP [H.sapiens]"	5.8
402800			predicted exon	5.8
436185	AW753380	Hs.49753	"Homo sapiens mRNA for KIAA1561 protein, partial cds"	5.8
419519	AI198719	Hs.176376	ESTs	5.8
452542	AW812256		"gb:RC0-ST0174-191099-031-a07 ST0174 Homo sapiens c	5.8
427166	AA431576	Hs.155658	ESTs	5.8
416168	H23687		gb:yn72d12.r1 Soares adult brain N2b5HB55Y Homo sapie	5.8
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (from clon	5.8
421558	AB011125	Hs.105749	KIAA0553 protein	5.8
458055	AW979121	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLAS	5.8
418345	AJ001696	Hs.241407	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.8
426544	AA492325		gb:ng81b11.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone	5.8
433544	AI793211	Hs.165372	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.8
442007	AA301116	Hs.142838	"Homo sapiens cDNA: FLJ23444 fis, clone HSI01343"	5.8
443422	R10288	Hs.301529	ESTs	5.8
434311	BE543469	Hs.266263	"Homo sapiens cDNA FLJ14115 fis, clone MAMMA10017	5.8
424966	AU077312	Hs.153985	"solute carrier family 7 (cationic amino acid transporter, y+	5.8
441744	AA960922	Hs.200938	ESTs	5.8
413101	BE065215		"gb:RC1-BT0314-310300-015-f01 BT0314 Homo sapiens c	5.7
445687	W80382	Hs.149297	ESTs	5.7
441369	AA931535		gb:oo56a04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clon	5.7
414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associated pr	5.7
431211	M86849	Hs.5566	"gap junction protein, beta 2, 26kD (connexin 26)"	5.7
411541	W03940		gb:za62b02.r1 Soares fetal liver spleen 1NFLS Homo sapien	5.7
448612	AI696363	Hs.171285	ESTs	5.7
419118	AA234223	Hs.139204	ESTs	5.7
406322			predicted exon	5.7
454690	AW854639		"gb:MR1-CT0258-140100-203-d10 CT0258 Homo sapiens	5.7
450313	AI038989	Hs.24809	hypothetical protein FLJ10826	5.7
416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility protein	5.7
449309	AW589823	Hs.224189	ESTs	5.7
408418	AW963897	Hs.44743	KIAA1435 protein	5.7
416100	H18700	Hs.268799	ESTs	5.7
437845	AA769578	Hs.90488	ESTs	5.7
443345	AI052508	Hs.164482	"ESTs, Weakly similar to contains similarity to TPR domain	5.7
418407	AL044818	Hs.84928	"nuclear transcription factor Y, beta"	5.7
434557	AW855466	Hs.271866	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.7
431688	AA513906		"gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clo	5.7
437641	AA811452	Hs.291911	ESTs	5.7
409319	AW752736	Hs.33565	ESTs	5.7
403967	AF030107	Hs.17165	regulator of G-protein signalling 13	5.7
445189	AI936450	Hs.147482	ESTs	5.7
414418	H62943	Hs.154188	ESTs	5.7
446563	BE326588	Hs.141454	ESTs	5.7
446075	AW451457	Hs.279179	ESTs	5.7
428068	AW016437	Hs.233462	ESTs	5.7

438425	AW292922	Hs.293170	ESTs	5.7
415532	R14780	Hs.12826	ESTs	5.7
441442	AL043282	Hs.131824	ESTs	5.7
443380	AI792478	Hs.135377	ESTs	5.7
445527	W39694	Hs.83286	ESTs	5.7
414376	BE393856	Hs.66915	"ESTs, Weakly similar to 16.7Kd protein [H.sapiens]"	5.7
457960	AA771881	Hs.298149	ESTs	5.6
453293	AA382267	Hs.10653	ESTs	5.6
452503	AB000509	Hs.29736	TNF receptor-associated factor 5	5.6
405227			predicted exon	5.6
442257	AW503831		gb:UI-HF-BN0-alb-b-05-0-UI.r1 NIH_MGC_50 Homo sap	5.6
403403			predicted exon	5.6
454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library Hom	5.6
438656	H85310	Hs.209456	"ESTs, Weakly similar to NG22 [H.sapiens]"	5.6
419936	AI792788		"gb:oi91d05.y5 NCI_CGAP_Kid5 Homo sapiens cDNA clo	5.6
437267	AW511443	Hs.258110	ESTs	5.6
430563	AA481269	Hs.178381	ESTs	5.6
444835	AI198994	Hs.158479	ESTs	5.6
444902	AJ132099	Hs.12114	vanin 1	5.6
451800	AW977435	Hs.31890	ESTs	5.6
405465			predicted exon	5.6
403891			predicted exon	5.6
425557	AI694300	Hs.46730	ESTs	5.6
432162	AA584062	Hs.272798	hypothetical protein FLJ20413	5.6
450152	AI138635	Hs.22968	ESTs	5.6
410053	AW579707	Hs.59332	ESTs	5.6
421285	NM_000102	Hs.1363	"cytochrome P450, subfamily XVII (steroid 17-alpha-hydro	5.6
425264	AA353953	Hs.20369	"ESTs, Weakly similar to gonadotropin inducible transcript	5.6
418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	5.6
429616	AI982722	Hs.120845	ESTs	5.6
423528	AB011137	Hs.129740	KIAA0565 gene product	5.6
403089			predicted exon	5.6
414373	AW162907	Hs.75969	proline-rich protein with nuclear targeting signal	5.6
403687			predicted exon	5.6
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	5.5
432501	BE546532	Hs.287329	Fas binding protein 1	5.5
403691			predicted exon	5.5
409545	BE296182		"gb:601177324F1 NIH_MGC_17 Homo sapiens cDNA clon	5.5
435990	AI015862	Hs.131793	ESTs	5.5
444409	AI792140	Hs.49265	ESTs	5.5
435478	AA682622		gb:zj20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	5.5
439981	AI348408	Hs.124675	"ESTs, Weakly similar to unnamed protein product [H.sapie	5.5
433644	AW342028	Hs.256112	ESTs	5.5
441541	AA938663	Hs.199828	ESTs	5.5
400709			predicted exon	5.5
407615	AW753085		"gb:PM1-CT0247-151299-005-a03 CT0247 Homo sapiens	5.5
424153	AA451737	Hs.141496	MAGE-like 2	5.5
452465	AA610211	Hs.34244	ESTs	5.5
406030			predicted exon	5.5
431071	AA491379		"gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA cl	5.5
418086	AA211791	Hs.269666	"Homo sapiens cDNA FLJ13415 fis, clone PLACE1001799	5.5
453034	BE246010	Hs.184109	ribosomal protein L37a	5.5
412953	Z45794	Hs.238809	ESTs	5.5
425351	AI206234	Hs.155924	cAMP responsive element modulator	5.5
406149			predicted exon	5.5
416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	5.5
458378	AI040535	Hs.150524	ESTs	5.5
401213			predicted exon	5.5
405904			predicted exon	5.5
445132	Z44811		gb:HSC29G031 normalized infant brain cDNA Homo sapie	5.5
405138			predicted exon	5.5
442238	AW135374	Hs.270949	ESTs	5.5
416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (from clon	5.5
448691	AA481119	Hs.283558	hypothetical protein PRO1855	5.5
452242	R50956	Hs.59503	"ESTs, Weakly similar to AF157318 1 AD-017 protein [H.s	5.5
456994	AA383623	Hs.293616	ESTs	5.5
440913	AI267491	Hs.160593	ESTs	5.5
435380	AA679001	Hs.192221	ESTs	5.5
450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (meltrin alph	5.5
414035	Y00630	Hs.75716	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.4
459084	H01699	Hs.27289	CGI-125 protein	5.4
405867			predicted exon	5.4
414093	BE544867		"gb:601078872F1 NIH_MGC_12 Homo sapiens cDNA clon	5.4
447306	AI373163	Hs.170333	ESTs	5.4
413083	BE064528		"gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapiens	5.4
404828			predicted exon	5.4
402543			predicted exon	5.4
421988	AW450481	Hs.161333	ESTs	5.4
413404	BE503463	Hs.297431	ESTs	5.4
459043	AI806444	Hs.208113	"ESTs, Weakly similar to N-WASP [H.sapiens]"	5.4
404410			predicted exon	5.4
430264	AA470519		"gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clon	5.4
431499	NM_001514	Hs.258561	general transcription factor IIB	5.4
412566	AW962574		"gb:EST374647 MAGE resequences, MAGG Homo sapien	5.4

454239	BE176420	Hs.8177	ESTs	5.4
458163	AA884304	Hs.131163	ESTs	5.4
446205	AW172662	Hs.149479	ESTs	5.4
455275	AW977806		"gb:EST389810 MAGE resequences, MAGO Homo sapien	5.4
415579	AA165232	Hs.222069	ESTs	5.4
423200	AA323073	Hs.289083	ESTs	5.4
440052	AI633744	Hs.195648	ESTs	5.4
424717	H03754	Hs.152213	"wingless-type MMTV integration site family, member 5A"	5.4
420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clo	5.4
432140	AK000404	Hs.272688	hypothetical protein FLJ20397	5.4
414904	AA157881	Hs.143056	ESTs	5.4
409479	BE163800	Hs.136912	ESTs	5.4
404727			predicted exon	5.4
446011	AI623778	Hs.145809	ESTs	5.4
456083	U46922	Hs.77252	fragile histidine triad gene	5.4
424834	AK001432	Hs.153408	"Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	5.4
425071	NM_013989	Hs.154424	"deiodinase, iodothyronine, type II"	5.4
426065	N32049		gb:yw96g08.s1 Soares_placenta_8to9weeks_2NbHP8to9W	5.4
415602	F12920	Hs.165575	ESTs	5.4
432839	AA579465	Hs.287332	ESTs	5.4
416879	H98899	Hs.42599	ESTs	5.4
456088	BE177320	Hs.156148	"Homo sapiens cDNA: FLJ23082 fis, clone LNG06451"	5.4
423175	W27595	Hs.18653	ESTs	5.4
424585	AA464840		gb:zx43h11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	5.3
452281	T93500	Hs.28792	"Homo sapiens cDNA FLJ11041 fis, clone PLACE1004405	5.3
424323	AA338791	Hs.146763	nascent-polypeptide-associated complex alpha polypeptide	5.3
426701	AI968103	Hs.209461	"Homo sapiens cDNA FLJ12836 fis, clone NT2RP2003206	5.3
447645	AW897321	Hs.159699	ESTs	5.3
402974			predicted exon	5.3
436607	AW661783	Hs.211061	ESTs	5.3
428873	AI701609	Hs.98908	ESTs	5.3
405454			predicted exon	5.3
431867	AA523660	Hs.191727	ESTs	5.3
442768	AL048534	Hs.48458	"ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	5.3
424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	5.3
435098	AF174394	Hs.177461	"Homo sapiens apoptotic-related protein PCAR mRNA, par	5.3
421284	U62435	Hs.103128	"cholinergic receptor, nicotinic, alpha polypeptide 6"	5.3
435711	AF226667	Hs.58553	CTP synthase II	5.3
405292			predicted exon	5.3
410123	T16981	Hs.21963	ESTs	5.3
435435	T89473	Hs.192328	ESTs	5.3
417071	N58820	Hs.275133	ESTs	5.3
438958	H50167	Hs.33113	ESTs	5.3
457405	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202 Homo sapiens	5.3
413642	BE154837		"gb:PM1-HT0345-121199-001-c08 HT0345 Homo sapiens	5.3
433868	AA612960		gb:nq38g06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clo	5.3
444461	R53734	Hs.25978	ESTs	5.3
427088	AA398085	Hs.142390	ESTs	5.3
451307	AW293207	Hs.211516	ESTs	5.3
403831			predicted exon	5.3
402892			predicted exon	5.3
433420	AI674093	Hs.293961	ESTs	5.3
455759	BE080469		"gb:QV1-BT0630-280200-086-d06 BT0630 Homo sapiens	5.3
411379	AI816344	Hs.12554	"ESTs, Weakly similar to Nucleosome Assembly Protein 1-	5.3
428483	AI908539	Hs.184592	KIAA0344 gene product	5.3
429208	AA447990	Hs.190478	ESTs	5.3
447572	AI631546	Hs.159732	ESTs	5.3
434896	AW022054	Hs.136591	ESTs	5.3
417616	R07728	Hs.268668	ESTs	5.3
411805	AW864183		"gb:PM0-SN0014-260400-002-d02 SN0014 Homo sapiens	5.3
419000	T79855	Hs.268592	ESTs	5.3
413488	BE144017	Hs.184693	"transcription elongation factor B (SIII), polypeptide 1 (15k	5.3
400975			predicted exon	5.3
407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein heavy chain (	5.3
430757	AI458623		"gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clo	5.3
417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide B"	5.2
401877	AB011094	Hs.129892	KIAA0522 protein	5.2
457122	AI026157	Hs.33728	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.2
410706	AI732404	Hs.68846	ESTs	5.2
435807	AI033299	Hs.113614	ESTs	5.2
428398	AI249368	Hs.98558	ESTs	5.2
401088			predicted exon	5.2
414501	N43991	Hs.171984	ESTs	5.2
419083	AI479560	Hs.98613	"Homo sapiens cDNA FLJ12292 fis, clone MAMMA10018	5.2
421107	AA283822	Hs.55606	"ESTs, Weakly similar to ZN91_HUMAN ZINC FINGER P	5.2
411489	AW848346		"gb:IL3-CT0214-150200-076-F03 CT0214 Homo sapiens c	5.2
419249	X14767	Hs.89768	"gamma-aminobutyric acid (GABA) A receptor, beta 1"	5.2
430082	AW514083	Hs.190135	ESTs	5.2
425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	5.2
451686	AA059246	Hs.110293	ESTs	5.2
453867	AI929383	Hs.108196	HSPC037 protein	5.2
419985	H66373	Hs.15973	"ESTs, Highly similar to bA393J16.3 [H.sapiens]"	5.2
426650	AA382814		"gb:EST96097 Testis I Homo sapiens cDNA 5' end, mRNA	5.2
424115	AA335497	Hs.293965	ESTs	5.2

405576			predicted exon	5.2
409584	AA076010		gb:zm89f12.s1 Stratagene ovarian cancer (937219) Homo sa	5.2
454423	AW603985	Hs.179662	nucleosome assembly protein 1-like 1	5.2
417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	5.2
439155	H81076	Hs.269001	ESTs	5.2
432267	AK000872	Hs.274227	"Homo sapiens cDNA FLJ10010 fis, clone HEMBA100030	5.2
459024	AA020799	Hs.179825	RAN binding protein 2-like 1	5.2
404088			predicted exon	5.2
403525			predicted exon	5.2
445882	AI948717	Hs.225155	"ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATE	5.2
448257	AW772070	Hs.253146	ESTs	5.2
410500	R09442		gb:yf26c09.r1 Soares fetal liver spleen 1NFLS Homo sapien	5.2
456084	AA155859	Hs.79708	ESTs	5.2
410523	BE143839		"gb:MR0-HT0164-151299-012-d03 HT0164 Homo sapiens	5.2
434623	AB023163	Hs.4014	KIAA0946 protein; Huntingtin interacting protein H	5.2
454484	AW795196	Hs.215857	ring finger protein 14	5.2
402131			predicted exon	5.2
438913	AI380429	Hs.172445	ESTs	5.2
402628			predicted exon	5.1
415973	R24707	Hs.260201	ESTs	5.1
455640	BE064059		"gb:QV3-BT0296-010300-111-e04 BT0296 Homo sapiens	5.1
442750	AI016803	Hs.131096	ESTs	5.1
404638			predicted exon	5.1
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	5.1
428819	AL135623	Hs.193914	KIAA0575 gene product	5.1
439519	AA837118	Hs.118366	ESTs	5.1
427335	AA448542	Hs.251677	G antigen 7B	5.1
416450	AA180467	Hs.142556	ESTs	5.1
440876	AW613524	Hs.279570	ESTs	5.1
414584	BE409585		"gb:601301836F1 NIH_MGC_21 Homo sapiens cDNA clon	5.1
443175	N57863		gb:yv60c02.s1 Soares fetal liver spleen 1NFLS Homo sapie	5.1
408968	AI652236	Hs.49376	hypothetical protein FLJ20644	5.1
415654	AW968363		"gb:EST380439 MAGE resequences, MAGJ Homo sapiens	5.1
440559	AW629054	Hs.125976	"ESTs, Weakly similar to metalloprotease/disintegrin/cystei	5.1
421236	AI287622	Hs.151956	ESTs	5.1
416258	N45661	Hs.275131	ESTs	5.1
405982			predicted exon	5.1
406589			predicted exon	5.1
412458	AW953229	Hs.169142	ESTs	5.1
435693	AI033134	Hs.119887	ESTs	5.1
449182	AW292381	Hs.224150	ESTs	5.1
403963			predicted exon	5.1
440830	AI733112	Hs.176101	ESTs	5.1
415412	F08049	Hs.52132	ESTs	5.1
442832	AW206560	Hs.253569	ESTs	5.1
445359	AI808725	Hs.147783	ESTs	5.1
412088	AI689496	Hs.108932	ESTs	5.1
426785	AI015953	Hs.125265	ESTs	5.1
430163	X66610	Hs.234748	"enolase alpha, lung-specific"	5.1
455441	AW945964		"gb:QV0-ET0001-050500-228-e09 ET0001 Homo sapiens c	5.1
400304	AF005082	Hs.113261	"Homo sapiens skin-specific protein (xp33) mRNA, partial	5.1
403944			predicted exon	5.1
457069	BE159191	Hs.114318	"ESTs, Weakly similar to ORF1 [H.sapiens]"	5.1
414125	BE253197		"gb:601116804F1 NIH_MGC_16 Homo sapiens cDNA clon	5.1
448566	AW291319	Hs.194574	ESTs	5.1
457948	AI498640	Hs.159354	ESTs	5.1
438240	N92638	Hs.124004	ESTs	5.1
404070			predicted exon	5.1
402709			predicted exon	5.1
416425	BE077308		"gb:RC1-BT0606-060200-012-h12 BT0606 Homo sapiens	5.0
407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) Homo sapiens cDN	5.0
452502	AI904296		"gb:PM-BT046-220199-286_1 BT046 Homo sapiens cDNA	5.0
446657	AI335191	Hs.260702	"ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	5.0
459124	AW301478	Hs.299178	ESTs	5.0
409940	BE548143		"gb:601073109F1 NIH_MGC_12 Homo sapiens cDNA clon	5.0
443547	AW271273	Hs.23767	"Homo sapiens cDNA FLJ12666 fis, clone NT2RM400225	5.0
447452	BE618258	Hs.102480	ESTs	5.0
414327	BE408145	Hs.185254	"ESTs, Moderately similar to NAC-1 protein [R.norvegicus]	5.0
416155	AI807264	Hs.205442	"ESTs, Weakly similar to AF117610 1 inner centromere pro	5.0
408081	AW451597	Hs.167409	ESTs	5.0
426834	AI091533	Hs.135167	ESTs	5.0
433368	AW877277		"gb:MR4-PT0051-150200-001-d03 PT0051 Homo sapiens	5.0
433098	AW190593	Hs.151143	ESTs	5.0
439721	W92142	Hs.271963	"ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAM	5.0
441818	AI630451	Hs.7976	KIAA0332 protein	5.0
458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2) Homo sapi	5.0
411905	BE265067		"gb:601193893F1 NIH_MGC_7 Homo sapiens cDNA clone	5.0
434248	AA628151	Hs.187783	ESTs	5.0
423967	AW296756	Hs.11641	"Homo sapiens cDNA: FLJ21432 fis, clone COL04219"	5.0
456212	N51636		gb:yy87b01.s1 Soares_multiple_sclerosis_2NbHMSP Homo	5.0
442914	AW188551	Hs.99519	"Homo sapiens cDNA FLJ14007 fis, clone Y79AA1002407	5.0
436084	AK000185		"gb:Homo sapiens cDNA FLJ20178 fis, clone COL09990"	5.0
449252	AW594482	Hs.253315	ESTs	5.0
454653	AW812227		"gb:RC2-ST0173-201099-011-g09 ST0173 Homo sapiens c	5.0

414699	AI815523	Hs.76930	*synuclein, alpha (non A4 component of amyloid precursor)	5.0
443335	T89697	Hs.16645	ESTs	5.0
448419	AL080072	Hs.21195	Homo sapiens mRNA; cDNA DKFZp564M0616 (from clon	5.0
425574	AA359663		*gb:EST68717 Fetal lung II Homo sapiens cDNA 5' end, mR	5.0
435174	AA687378	Hs.194624	ESTs	5.0
429548	AW138872	Hs.135288	ESTs	5.0
450613	AI702055		*gb:tq20g10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clon	5.0
400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	5.0
421751	AW813731	Hs.159153	ESTs	5.0
405800			predicted exon	5.0
429430	AI381837	Hs.155335	ESTs	5.0
439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W Homo sapien	5.0
430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	5.0
452741	BE392914	Hs.30503	*Homo sapiens cDNA FLJ11344 fis, clone PLACE1010870	5.0
441001	AW137017	Hs.126373	Human DNA sequence from clone RP5-1184F4 on chromos	5.0
438490	AW593272	Hs.26261	ESTs	5.0
408170	AW204516	Hs.31835	ESTs	5.0
449104	R08702		gb:yf24c06.r1 Soares fetal liver spleen 1NFLS Homo sapien	5.0

TABLE 1B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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408523	1063925_1	AW833259 AW833273 AW206846
408914	1089828_-1	AW450309
408987	109306_1	H85615 H86300 H86263 H86282 AA059278 H86304
409191	1107176_1	AW818390 AW818237 AW858911 AW858977 BE072544 W26498
409545	1138823_1	BE296182 AW629821
409584	114165_1	AA076010 AA076009 AI094314
409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
409866	1156522_1	AW502152 H41202 H29772
409867	1156530_1	AW502161 AW502587 AW502345
409940	1160994_1	BE548143 AW511659
409982	1165022_1	BE005839 BE005619 AW516815
410500	1206323_1	R09442 AW846115 AW846108 AW751967 AW846083 AW846087 AW846090
410523	1207041_1	BE143839 AW752787 AW752795 BE143584 N71805
410536	1207322_1	N39533 AW753094 AW753093
410626	1212621_-1	BE407727
410966	1228071_1	AW812088 AW812105 AW812082
411004	1228975_1	AW813242 BE146089 AW813195 AW813173 AW813206 BE145953 BE146212 AW813196 AW854582 AW813241 BE061582
411018	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
411057	1230493_1	AW815098 BE154843 BE154831
411178	1234752_1	AW820852 AW820773 AW821088
411237	1236377_1	AW833676 AW833814 AW833798 AW833677 AW833449 AW833630 AW833626 AW833444 AW833366 AW833791 AW833659 AW833432 AW833534 AW833556 AW833553
411483	1247172_1	AW848115 AW848127 AW887028 AW887117
411489	1247360_1	AW848346 AW848760 AW848340 AW848818 AW849043 AW849061
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411805	1259273_1	AW864183 AW864181 AW864135 AW864198
411905	1265181_1	BE265067 BE264978 AW875420
411940	1266262_1	AW876686 AW876717 AW877215 AW876691 AW876722 AW877218 AW876694 AW876725
412167	1280605_1	AW897230 AW897252 AW897244 AW897231 AW897263
412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
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412740	1324538_1	AW993984 AW994001 AW994002
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413252	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
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413702	1383899_1	BE170313 BE158339 BE158290
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414808	1492624_1	T95945 R98276 BE539541
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415654	154135_1	AW968363 AA465492 R34539 AA165411
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415747	155189_1	AA381209 AA381245 AA167683
416151	1573926_1	T26661 Z44135 H23016
416168	1574545_1	H23687 H46460 H40239
416425	159388_1	BE077308 AL043350 AW962170 AA180251 AA325287
416441	159480_1	BE407197 AA182474 AA180369 BE275628 BE276131
416548	1600181_1	H62953 N76608 N72413
416665	1607797_1	H72974 W28967
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
417344	166827_1	AW997313 AA195805
417549	168700_1	AA203651 R89136
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417682	1692759_1	W69561 R08486 R87183
418636	177402_1	AW749855 AA225995 AW750208 AW750206
418709	178363_1	AA227394 AA641866 AW750732
419753	187763_1	N42531 W25700 AA249574 AA569553
419936	189181_1	AI792788 BE142230 AA252019
420111	190755_1	AA255652 AA280911 AW967920 AA262684
422949	223184_1	AA319435 N56456 AA319377 AW961532 T48452 AA894424
423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
423756	231725_1	AA828125 AA834883 AA330555
423843	232510_1	AA332652 AA331633 AW999369 AW902993 BE170475 AA378845 AW964175 AI475221
424101	235398_1	AA335394 AA335535 AA335244 AW966148
424324	238127_1	AA346316 BE160193 AA338802 AW954536
424585	241151_1	AA464840 AA343628
424872	244505_1	AA347923 AA347928 AW961769
425090	246649_1	AA350552 R21667 AW953258
425574	253317_1	AA359663 AA359654 AW963124
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426650	270283_1	AA382814 AA402411 AA412355
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430757	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
431071	327550_1	AA491379 H86020 AW969148
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431822	338082_1	AA516049 AW004922
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432340	345248_1	AA534222 AA632632 T81234
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432966	356839_1	AA650114 AW974148 AA572946
433368	364276_1	AW877277 AW811294
433449	366532_1	AW772282 AA592974
433868	375629_1	AA612960 AI934769 T12348
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434804	393481_1	AA649530 AA659316 H64973
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436843	427748_1	AA824588 AA732269 AW977146
437096	433006_1	AA744406 AA745347 AA745535
437146	43371_1	AA730977 AI261584 AA334473 Z43283 AW875861 AW938044 BE150701 AW936262 AA306862 BE565575 BE567380 AA728920 AA167612 AI239729 AI251752 AA485791 BE568425 AW962958
437152	43386_1	AL050027 BE089051
437229	434947_1	AW976005 AW419264 AA747275 AA810377
439031	46798_1	AF075079 H48601 H48795
439152	46920_1	H65014 AF086007 H65015
439518	47334_1	W76326 AF086341 W72300
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441194	51193_1	BE274581 BE275382 AA703515 BE166690
441369	515636_1	AA931535 AI458601 Z44913
442257	53699_1	AW503831 AW503317 BE565665
443161	561305_1	AI038316 AI344631 AI261653
443175	561882_1	N57863 AI038952 W90167 N64103
443198	562655_1	AI039813 AI684642 Z40121 AI951414 BE501049
443534	572957_1	AI076123 AI244834 AI695239
443613	575391_1	AI079356 W23287

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443747	57918_1	AV646352 AV652121 AV652008
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445132	63111_1	Z44811 R13709 AV652749 AW814906 AA084016
445153	631644_1	AI214671 Z45244 H24136 R25934
445232	633433_1	BE294357 N36568 AI217006
446171	664826_1	AI374927 AI278380 AI301383
447252	714160_1	R90916 AL120023 R18429 Z42095 AI369730 R90824
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449104	798149_1	R08702 R09864 AI630313
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452563	922265_1	AI907552 C03707 C02870
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454455	1206965_1	AW752710 BE180336 BE180186
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454653	1228081_1	AW812227 AW812294 AW812092
454690	1229106_1	AW854639 AW854719 AW854718 BE145880 AW854692 BE145866 AW816154 AW854698 AW854654 AW813335 AW854699
454707	1230250_1	AW814989 AW814852 AW814808
454822	1236369_1	AW833793 AW833799 AW833346 AW833371 AW833795 AW833562 AW833667 AW833377
454874	1238494_1	AW836407 BE175600 BE175579
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454963	1246752_1	AW847647 AW847659 AW847656 AW847653 AW847717 AW847786
455013	1248899_1	BE073250 BE073378 BE073379 AW850533 AW850529
455092	1252971_1	BE152428 AW855572 AW855607
455110	1253955_1	BE154505 BE154462 BE154454 BE154460 BE154489 BE154496 AW856909 BE154497 BE154565 BE154572 BE154500 BE154472
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455152	1255227_1	AW858621 AW937120
455203	1259973_1	AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390
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455441	1291505_1	AW945964 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039 AW946045 AW946028 AW946036
455592	1335196_1	BE008002 BE007997 BE007998 BE008000
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455662	1349206_1	BE065387 BE065310 BE065391
455713	1352512_1	BE069891 BE158893 BE069898 BE158900
455759	1359316_1	BE080469 BE080474 BE080477 BE080546 BE080545
455851	1375451_1	BE146879 BE146914 BE146918
455853	1375671_1	BE147225 BE147205 BE147234
455879	1380017_1	BE153275 BE153189 BE153329 BE153022 BE153030 BE152974
455993	1398665_1	BE179085 BE179084 BE179086 BE179264
456072	1470256_1	H54381 H54463 BE393262
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456212	1655565_1	N51636 T51874 T51829
456309	177026_1	AA225423 AA225369 BE144153 AW801549
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457405	333127_1	AA504860 AA504911
457620	371514_1	AA602711 BE078290
457727	393566_1	AW974687 AA649656 AA652145
457868	426095_1	AW975133 AA729943 AA805813
458154	491768_1	AW816379 AA888282 AA879046 AA879195
458804	75803_1	AL157625 N72696 BE622492
458829	773443_1	AI557388 BE158936
458841	784186_1	W28965 W28971
459160	920051_1	AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
459170	920646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037
459186	922888_1	AI908287 BE064074 BE068820 BE068823 BE068822 BE068826

TABLE 1C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400584	9887612	Minus	18398-18573
400593	9887642	Minus	25013-25127
400612	9929646	Minus	151513-151662
400613	9864507	Plus	92278-92472
400623	7228177	Plus	74195-74335,74653-74827
400709	7249204	Plus	153075-154680
400749	7331445	Minus	9162-9293
400842	1927148	Plus	90462-90673
400925	7651921	Plus	38183-38391,43900-44086
400964	7139719	Minus	155282-155403
400968	7923967	Plus	19938-20043
400975	7139779	Minus	108473-108847
400983	8081198	Plus	107903-108832
401032	8117525	Minus	68451-68555
401050	8117628	Minus	78449-79425
401088	8492704	Plus	194659-195179
401129	8699792	Minus	62022-62242,62326-62451,62543-62710,63072-63167
401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
401213	9858408	Plus	98243-98380,98489-98619
401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
401245	4827300	Minus	59373-59531
401260	8076883	Minus	86008-86355
401269	8954206	Plus	2259-2591
401283	9800093	Minus	47256-47456
401497	7381770	Plus	92607-92813
401508	7534110	Minus	110779-110983
401521	7705251	Plus	9127-9234
401530	7770649	Plus	41468-42406
401575	7229804	Minus	76253-76364
401604	7689963	Minus	119835-120185
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401793	7263888	Minus	102945-103083
401809	7342191	Minus	107548-108298
401862	7770606	Minus	55839-55993,59145-59293
401881	8122429	Minus	148470-148651,153418-153618,154282-154438
402018	7528100	Plus	168728-168859
402046	8072415	Plus	166394-166556,168167-168395
402050	8076908	Minus	130105-130227
402071	8117361	Plus	85924-86039
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402131	7704961	Minus	33114-33209,33496-33678
402203	8576119	Minus	8124-8285
402222	9958106	Plus	3261-3834,3939-4269
402296	6598824	Plus	22587-23723
402298	6598824	Plus	36758-37953
402421	9796341	Minus	46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924
402425	9796347	Minus	50224-50395
402481	9797406	Plus	87891-88991
402529	7630937	Minus	165-917
402543	9838066	Minus	89684-90893
402576	7230225	Minus	1867-2247
402578	9884928	Plus	66350-66496
402628	9931216	Plus	31753-31966
402631	9931231	Minus	115658-116580
402639	9958129	Minus	20167-22383
402664	8077024	Plus	70318-70846
402709	8901246	Minus	56847-57055
402738	7331557	Minus	8725-8859
402745	9212200	Minus	76516-76690
402790	4835258	Minus	147744-147861
402794	6136940	Minus	131034-131794
402800	6010175	Plus	43921-44049,46181-46273
402859	9588237	Minus	69821-75323
402892	8086844	Minus	194384-194645
402974	9663349	Plus	124035-124321
403041	3171152	Plus	70527-71019
403065	8954197	Minus	71615-71773,73930-74144
403083	8954241	Plus	163070-163351
403089	8954241	Plus	171964-172239
403093	8954241	Plus	177083-177373,177464-177751
403177	9838213	Minus	142560-142726
403273	8018055	Plus	133809-134099
403334	8568877	Minus	137205-137350
403350	8569775	Minus	135374-135523
403356	8569930	Plus	92839-93036
403403	9438460	Plus	21240-21399
403525	7960440	Plus	152431-153243
403568	8101145	Minus	85509-85658
403647	8699843	Minus	35849-36204
403687	7387384	Plus	9009-9534
403691	7387384	Minus	88280-88463
403698	4263532	Plus	10464-10907

403741	7630932	Minus	2833-3468
403747	7658395	Minus	20493-20621
403786	8083636	Minus	73028-73217
403831	7249249	Minus	61468-61575
403891	7331467	Minus	191508-193220
403944	7711864	Minus	129213-129415
403963	8568150	Plus	149466-149665
404070	2996642	Plus	7210-7414,10043-10195
404088	9958257	Plus	184131-184295
404097	7770701	Plus	55512-55781
404166	7596822	Plus	86147-86509
404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
404340	7630856	Plus	10898-11506
404410	7342122	Plus	49052-49176,56177-56273,59384-59488
404599	8705107	Plus	110443-110733
404638	9796751	Minus	99433-99528,100035-100161
404664	9797142	Minus	104257-105215
404727	8081050	Plus	115534-115747
404767	7882827	Minus	23244-23759
404828	6580415	Minus	26291-27253
404849	7706886	Plus	144843-144964,149846-150121
404893	6850447	Plus	65083-65223
404898	7331420	Minus	177015-177328
404952	7382669	Minus	136326-136618
404972	3213020	Plus	48711-49524
404992	4662677	Minus	106104-106199,111659-111781
405071	7708797	Minus	11115-11552
405138	8576241	Plus	90303-90516
405196	7230083	Minus	135716-135851
405227	6731245	Minus	22550-22802
405277	3980473	Plus	23471-23572
405285	6139075	Minus	55744-55903,57080-57170,61478-61560
405292	3845420	Plus	33227-33442
405336	6094635	Plus	33267-33563
405362	2337862	Minus	105008-105142,105980-106091,140445-140556,142519-142641
405382	6552767	Plus	31923-32311
405454	7656675	Plus	133807-134053
405465	7767904	Plus	8935-9073,12242-12367,13364-13506,14965-15493
405472	8439781	Plus	106297-106447,108462-108596
405547	1054740	Plus	124361-124520,124914-125050
405576	4003382	Plus	84000-85009
405621	5523811	Plus	59362-59607
405636	5123990	Plus	56384-56587
405675	4557087	Plus	70304-70630
405708	4156182	Plus	55030-55604
405771	7018349	Plus	91191-91254,91510-91589
405783	5738434	Minus	27238-27885
405793	1405887	Minus	89197-89453
405800	2791346	Plus	19271-19813
405810	4938307	Minus	64543-64966
405848	7651809	Minus	28135-28244
405851	6164995	Minus	26407-27151
405867	6758731	Minus	74553-75173
405896	6758795	Plus	57311-57874
405904	7705118	Minus	16375-16584
405917	7712162	Minus	106829-107213
405982	8247790	Minus	36028-36408
406030	8312328	Minus	96123-96547
406053	6758997	Plus	30921-31532
406057	6691254	Minus	20830-21222
406149	7144791	Minus	44464-45164
406163	7158901	Plus	66690-66835
406277	5686030	Minus	4759-5490
406322	9212102	Minus	130230-130418
406349	9256007	Minus	21251-21526
406504	7711360	Minus	107068-107277
406544	7711508	Plus	46576-46757
406589	8224211	Plus	38806-38989
406592	4567182	Plus	352560-352963

TABLE 2A lists about 187 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 1A, except that the ratio was greater than or equal to 2.5, and the predicted protein contained a PFAM domain that is indicative of extracellular localization (e.g., ig, fn3, egf, 7tm domains).

TABLE 2A: ABOUT 187 UP-REGULATED OVARIAN CANCER GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: Unigene Title
PFAM domains
ratio: tumor vs. normal tissues

Pkey	Ex. Accn No.	UG ID	Title	PFAM domain	ratio
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	serpin	63.6
431938	AA938471	Hs.115242	developmentally regulated GTP-bindi	SCP	32.0
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris ant	cadherin	30.0
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molec	EGF;lectin_c;sushi	24.5
452947	AW130413		gb:xf50f04.x1 NCI_CGAP_Gas4 Hom	alpha-amylase	15.8
418092	R45154	Hs.106604	ESTs	pkinase;Activin_recp	15.1
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	Cys_knot	12.6
422330	D30783	Hs.115263	epiregulin	EGF	12.5
446745	AW118189	Hs.156400	ESTs	vwa	11.1
416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocyt	ig	10.8
432408	N39127	Hs.76391	myxovirus (influenza) resistance 1, ho	ion_trans;K_tetra	10.6
405285			predicted exon	A2M;A2M_N	10.5
405636			predicted exon	EGF;ldl_recept_a;ldl_recept_b	9.8
403093			predicted exon	fn3	9.6
446740	AI611635	Hs.192605	ESTs	RYDR_ITPR	9.2
405547			predicted exon	ABC_tran;ABC_membrane	8.5
412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT	7tm_1	8.4
404270			predicted exon	SCP	8.1
402745			predicted exon	EGF;ldl_recept_b;thyroglobulin_1	8.1
452755	AW138937	Hs.213436	ESTs	cystatin	8.0
421459	AI821539	Hs.97249	ESTs	disintegrin;Reprolysin	7.9
416151	T26661		gb:AB65C7R Infant brain, LLNL arra	laminin_G;EGF	7.8
446232	AI281848	Hs.165547	ESTs	7tm_3	7.6
431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin	connexin	7.2
424634	NM_003613	Hs.151407	cartilage intermediate layer protein, n	ig;tsp_1	7.1
400749			predicted exon	fn3;ldl_recept_a;ldl_recept_b	6.8
419054	N40340	Hs.191510	ESTs, Weakly similar to ORF2 (M.m	ig;SPRY	6.8
459170	AI905518		gb:RC-BT091-210199-098 BT091 Ho	ABC_tran;ABC_membrane	6.6
416441	BE407197		gb:601301552F1 NIH_MGC_21 Hom	SDF	6.4
410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22	6.4
402425			predicted exon	ion_trans	6.3
415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_H	Ephrin	6.0
403083			predicted exon	fn3	5.9
448995	AI613276	Hs.5662	guanine nucleotide binding protein (G	SDF	5.9
418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	serpin	5.8
424966	AU077312	Hs.153985	solute carrier family 7 (cationic amino	aa_permeases	5.8
431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (co	connexin	5.7
430563	AA481269	Hs.178381	ESTs	ABC_tran;ABC_membrane	5.6
450152	AI138635	Hs.22968	ESTs	ig;pkinase	5.6
418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	lipoxygenase;PLAT	5.6
403089			predicted exon	fn3	5.6
403687			predicted exon	tsp_1;Reprolysin	5.6
403691			predicted exon	tsp_1;Reprolysin	5.5
414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	serpin	5.4
421284	U62435	Hs.103128	cholinergic receptor, nicotinic, alpha p	neur_chan	5.3
435435	T89473	Hs.192328	ESTs	lipase;PLAT	5.3
457122	AI026157	Hs.33728	ESTs, Weakly similar to ALU1_HUM	lipoxygenase;PLAT	5.2
419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A	neur_chan	5.2
425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	ion_trans	5.2
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	EGF;DSL	5.1
457948	AI498640	Hs.159354	ESTs	G-alpha;arf	5.1
435174	AA687378	Hs.194624	ESTs	SPRY	5.0
408170	AW204516	Hs.31835	ESTs	arf;ras	5.0
434351	AW974991	Hs.191852	ESTs, Weakly similar to ALU1_HUM	arf;ras	4.9
430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	7tm_1	4.8
422597	BE245909	Hs.118634	ATP-binding cassette, sub-family B (M	ABC_tran;ABC_membrane	4.8
405545			predicted exon	ABC_tran;ABC_membrane	4.8
426471	M22440	Hs.170009	transforming growth factor, alpha	EGF	4.7
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	serpin	4.7
420206	M91463	Hs.95958	solute carrier family 2 (facilitated gluc	sugar_tr	4.6
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	Kunitz_BPTI;G-gamma	4.6
424402	M63108	Hs.1769	luteinizing hormone/choriogonadotrop	7tm_1	4.5
436480	AJ271643	Hs.87469	putative acid-sensing ion channel	ASC	4.5
430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	7tm_1	4.4
436126	AW449757	Hs.163036	ESTs	SNF	4.4
406812	AF000575	Hs.67846	leukocyte immunoglobulin-like recep	ig	4.4
409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (	TIMP	4.3
449184	AW296295	Hs.196491	ESTs	TNFR_c6	4.3
410555	U92649	Hs.64311	a disintegrin and metalloproteinase do	disintegrin;Reprolysin	4.3
422389	AF240635	Hs.115897	protocadherin 12	cadherin	4.3
405281			predicted exon	A2M;A2M_N	4.3
413548	BE147555	Hs.288541	Homo sapiens mRNA for KIAA1558	EGF;ldl_recept_a;ldl_recept_b	4.3
449535	W15267	Hs.23672	low density lipoprotein receptor-relate	ldl_recept_a;EGF;ldl_recept_b	4.3
425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	7tm_1	4.3
410611	AW954134	Hs.20924	KIAA1628 protein	Peptidase_S9	4.2
430686	NM_001942	Hs.2633	desmoglein 1	cadherin;Cadherin_C_term	4.1
418693	AI750878	Hs.87409	thrombospondin 1	vwc;TSPN	4.0
445924	AI264671	Hs.164166	ESTs	sugar_tr	3.9
457148	AF091035	Hs.184627	KIAA0118 protein	arf;ras	3.9
428568	AC004755	Hs.184922	one cut domain, family member 3	E1-E2_ATPase	3.9
412170	D16532	Hs.73729	very low density lipoprotein receptor	EGF;ldl_recept_a;ldl_recept_b	3.8
442566	R37337	Hs.12111	ESTs	ank;death;RHD;TIG	3.8
403763			predicted exon	7tm_1	3.8

403074			predicted exon	fn3	3.8
413605	BE152644		gb:CM1-HT0329-250200-128-f09 HT	alpha-amylase	3.8
442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, c	Collagen;COLFI	3.7
403661			predicted exon	7tm_3;ANF_receptor	3.7
407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Hom	pkinase;Sema;Plexin_repeat;TIG	3.7
457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocortic	7tm_1	3.7
431176	AI026984	Hs.293662	ESTs	laminin_EGF;laminin_B	3.6
436233	AI742878	Hs.124116	ESTs	ig	3.6
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived g	EGF	3.6
445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	zf-C2H2	3.6
400380	NM_018485	Hs.283079	G protein-coupled receptor C5L2	7tm_1	3.6
453893	NM_000835	Hs.36451	glutamate receptor, ionotropic, N-met	lig_chan	3.5
409402	AF208234	Hs.695	cystatin B (stefin B)	cystatin	3.5
421166	AA305407	Hs.102308	potassium inwardly-rectifying channe	IRK	3.5
445575	Z25368	Hs.172004	titin	fn3	3.5
428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway p	tsp_1;vwc;IGFBP	3.5
403909	NM_016255	Hs.95260	Homo sapiens mRNA; cDNA DKFZp	Na_H_Exchanger	3.5
403077			predicted exon	fn3	3.5
455612	BE042896	Hs.274848	ESTs	ABC_tran;ABC_membrane	3.5
424091	AF235097	Hs.139263	calcium channel, voltage-dependent, a	ion_trans	3.5
403956	W28077	Hs.79389	nel (chicken)-like 2	cadherin;Cadherin_C_term	3.4
457470	AB040973	Hs.272385	G protein-coupled receptor 72	7tm_1	3.4
401522	N47812	Hs.81360	CGI-35 protein	disintegrin;Reprolysin	3.4
404886			predicted exon	ion_trans	3.4
437692	AA176959	Hs.172004	titin	fn3	3.4
407944	R34008	Hs.239727	desmocollin 2	cadherin	3.4
407393	AB038237		gb:Homo sapiens mRNA for G protei	7tm_1	3.3
436936	AL134451	Hs.197478	ESTs	EGF;laminin_G	3.3
423309	BE006775	Hs.126782	sushi-repeat protein	sushi;HYR	3.3
402172			predicted exon	ig	3.3
447420	AI378628		gb:tc72g07.x1 Soares_NhHMPu_S1 H	ank;pkinase;death	3.3
438901	AF085834	Hs.29036	ESTs	sushi	3.3
424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp	trypsin;sushi;CUB	3.3
430453	BE387060	Hs.3903	Cdc42 effector protein 4; binder of Rh	fn3	3.3
416631	H69466		gb:yr88f07.r1 Soares fetal liver spleen	ldl_recept_a;MACPF	3.3
453174	AI633529	Hs.135238	ESTs	7tm_1	3.3
433848	AF095719	Hs.93764	carboxypeptidase A3	Zn_carbOpept;Propep_M14	3.2
408546	W49512	Hs.46348	bradykinin receptor B1	7tm_1	3.2
423573	AA328504		gb:EST31993 Embryo, 12 week I Hom	7tm_1	3.2
458662	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5	7tm_3;ANF_receptor	3.2
433430	AI863735	Hs.186755	ESTs	thyroglobulin_1;IGFBP	3.2
438850	R33727	Hs.24688	EST	ank;pkinase;death	3.2
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	Gal-bind_lectin	3.2
409968	U56102	Hs.57699	adhesion glycoprotein	ig	3.1
430630	AW269920	Hs.2621	cystatin A (stefin A)	7tm_3;ANF_receptor	3.1
420737	L08096	Hs.99899	tumor necrosis factor (ligand) superfa	TNF	3.1
422279	H69644	Hs.114231	C-type lectin-like receptor-2	lectin_c	3.1
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromely	hemopexin;Peptidase_M10	3.1
412597	AU077051	Hs.74561	alpha-2-macroglobulin	A2M;A2M_N	3.1
453420	AJ003459		gb:AJ003459 Selected chromosome 2	IRK	3.1
404243			predicted exon	zf-C3HC4;SPRY;zf-B_box	3.1
449987	AW079749	Hs.184719	ESTs, Weakly similar to AF116721 1	ABC_tran;ABC_membrane	3.1
422471	AA311027	Hs.271894	ESTs	ig	3.0
400464			predicted exon	Peptidase_S9	3.0
458713	BE044496	Hs.282707	ESTs	EGF	3.0
421340	F07783	Hs.1369	decay accelerating factor for complem	sushi	3.0
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	7tm_1	3.0
400704			predicted exon	lig_chan;ANF_receptor	3.0
416239	AL038450	Hs.48948	ESTs	E1-E2_ATPase;Hydrolase	3.0
433664	AW292176	Hs.245834	ESTs	Ricin_B_lectin	3.0
423994	X01057	Hs.1724	interleukin 2 receptor, alpha	rrm	2.9
447726	AL137638	Hs.19368	Homo sapiens mRNA; cDNA DKFZp	vwa	2.9
425483	AF231022	Hs.301273	Homo sapiens protocadherin Fat 2 (FA	EGF;cadherin;laminin_G	2.9
423513	AF035960	Hs.129719	transglutaminase 5	Transglut_core;Transglutamin_N	2.9
401537			predicted exon	ig;pkinase;LRRNT;LRRCT	2.9
405790			predicted exon	Sema;Plexin_repeat;TIG	2.9
422669	H12402	Hs.119122	ribosomal protein L13a	arf;ras;Ribosomal_S17	2.9
430793	M83181	Hs.247940	5-hydroxytryptamine (serotonin) recep	7tm_1	2.9
403411			predicted exon	ABC_tran;ABC_membrane	2.8
428188	M98447	Hs.22	transglutaminase 1 (K polypeptide ep	Transglutamin_N;Transglut_core	2.8
414482	S57498	Hs.76252	endothelin receptor type A	7tm_1	2.8
427223	BE208189	Hs.174031	cytochrome c oxidase subunit VIb	COX6B	2.8
404187			predicted exon	ig	2.8
443537	D13305	Hs.203	cholecystokinin B receptor	7tm_1	2.8
428701	NM_013276	Hs.190207	carbohydrate kinase-like	vwa;integrin_A;P2X_receptor	2.7
411213	AA676939	Hs.69285	neuropilin 1	CUB;MAM;F5_F8_type_C	2.7
453999	BE328153	Hs.240087	ESTs	kazal	2.7
401244			predicted exon	vwa;vwd;TIL	2.7
458930	NM_003612	Hs.24640	sema domain, immunoglobulin domai	Sema	2.7
434411	AA632649	Hs.201372	ESTs	sushi	2.7
400421	AF263537	Hs.287370	fibroblast growth factor 23	FGF	2.7
448999	AF179274	Hs.22791	transmembrane protein with EGF-like	kazal	2.7
417350	U50928	Hs.82001	polycystic kidney disease 2 (autosoma	ion_trans	2.6
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	pkinase;ig	2.6

401657			predicted exon	7tm_1	2.6
456711	AA033699	Hs.83938	ESTs, Moderately similar to MASP-2	sushi;trypsin;CUB	2.6
432042	AW971345	Hs.292715	ESTs	sugar_tr	2.6
433138	AB029496	Hs.59729	semaphorin sem2	Ig;Sema	2.6
452530	AI905518		gb:RC-BT091-210199-098 BT091 Ho	ABC_tran;ABC_membrane	2.6
426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syn	Collagen;C4	2.6
403796			predicted exon	cadherin	2.6
431728	NM_007351	Hs.268107	multimerin	EGF;C1q	2.6
441595	AW206035	Hs.192123	ESTs	sugar_tr	2.6
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	EGF;MAM	2.6
447197	R36075		gb:yh88b01.s1 Soares placenta Nb2H	SDF	2.5
428765	X54150	Hs.193122	Fc fragment of IgA, receptor for	ig	2.5
450245	AA007536	Hs.271767	ESTs, Moderately similar to ALU1_H	ig	2.5
416429	H54658	Hs.268942	ESTs	E1-E2_ATPase;Hydrolase	2.5
417067	AJ001417	Hs.81086	solute carrier family 22 (extraneurona	sugar_tr	2.5
433182	AB039920	Hs.127821	BWRT protein	ion_trans	2.5
403092			predicted exon	fn3	2.5
406850	AI624300	Hs.172928	collagen, type I, alpha 1	vwc;Collagen;COLFI	2.5
438698	AW297855	Hs.125815	ESTs	lipoxygenase;PLAT	2.5
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channe	IRK	2.5

TABLE 2B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409385	112523_1	AA071267 T65940 T64515 AA071334
412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
413605	1379792_1	BE152644 BE152712 BE152668 BE152659 BE152810 BE152811 BE152816 BE152643 BE152706 BE152656 BE152660 BE152715 BE152662 BE152669 BE152661 BE152672 BE152653 BE152716 BE152651 BE152767 BE152677 BE152652 BE152714 BE152708 BE152665 BE152679 BE152771 BE152775 BE152666 BE152768 BE152813 BE152664 BE152676 BE152681 BE152709 BE152667 BE152814 BE152808 BE152711 BE152707 BE152815 BE152678 BE152673 BE152782 BE152671 BE152682 BE152760 BE152809 BE152778 BE152780 BE152762 BE152776 BE152781 BE152774 BE152763 BE152769
416151	1573926_1	T26661 Z44135 H23016
416441	159480_1	BE407197 AA182474 AA180369 BE275628 BE276131
416631	1605019_1	H69466 H93884 N59684
423573	229714_1	AA328504 AA327783 AW962370
447197	711623_1	R36075 AI366546 R36167
447420	721207_1	AI378628 N32350 H85772
452530	920646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037
452947	939810_1	AW130413 AI932362
453420	966433_1	AJ003459 AJ003461
459170	920646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037

TABLE 2C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400464	9929670	Plus	22074-22214
400704	8118864	Minus	63110-63241
400749	7331445	Minus	9162-9293
401244	4827300	Minus	55359-56376
401537	7960358	Minus	186786-187029,190607-190779,198218-198348
401657	9100664	Minus	7312-8163
402172	8575911	Minus	143378-143671
402425	9796347	Minus	50224-50395
402745	9212200	Minus	76516-76690
403074	8954241	Plus	143375-143561
403077	8954241	Plus	146923-147222,147326-147628
403083	8954241	Plus	163070-163351
403089	8954241	Plus	171964-172239
403092	8954241	Plus	174720-175016,175104-175406,175508-175813
403093	8954241	Plus	177083-177373,177464-177751
403411	9438635	Minus	104247-104420
403661	8705027	Minus	30268-30482
403687	7387384	Plus	9009-9534
403691	7387384	Minus	88280-88463
403763	7229888	Minus	43575-43887
403796	8099896	Minus	75073-77664
404187	4481839	Plus	7644-7991
404243	5672609	Plus	74695-75123
404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
404886	4884062	Plus	30058-30596
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405285	6139075	Minus	55744-55903,57080-57170,61478-61560
405545	1054740	Plus	118677-118807,119091-119296,121626-121823
405547	1054740	Plus	124361-124520,124914-125050
405636	5123990	Plus	56384-56587

405790 1203968 Plus 136364-136509,136579-136699,136805-136941

TABLE 3A lists about 1643 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 1A, except that the ratio was greater than or equal to 15, and the denominator was the arithmetic mean value for various non-malignant ovary specimens obtained.

TABLE 3A: ABOUT 1643 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: Unigene Title
PFAM domains
ratio: tumor vs. normal tissues

Pkey	Ex. Accn No.	UG ID	Title	ratio
420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	219.9
422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin B)	180.2
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	165.0
424799	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-associated)	161.5
442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	150.2
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human, odontogenic k	149.5
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (antileukoprotein	144.9
430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	136.6
428471	X57348	Hs.184510	stratifin	129.5
421978	AJ243662	Hs.110196	NICE-1 protein	108.7
437191	NM_006846	Hs.5476	serine protease inhibitor, Kazal type, 5	106.2
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	105.5
441565	AW953575	Hs.169902	solute carrier family 2 (facilitated glucose transporter),	103.6
431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (connexin 26)	102.1
419329	AY007220	Hs.288998	S100-type calcium binding protein A14	95.3
430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fundus d	87.0
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	86.1
412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	85.0
417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated protein	84.8
426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	84.5
452669	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced product u	84.4
406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	83.8
406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	81.0
432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	81.0
416889	AW250318	Hs.80395	mal, T-cell differentiation protein	77.8
409453	AI885516	Hs.95612	ESTs	75.3
424670	W61215	Hs.116651	epithelial V-like antigen 1	67.5
417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium protein, calv	67.0
423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	65.7
442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, protein-glutamine-g	64.7
456898	NM_001928	Hs.155597	D component of complement (adipsin)	64.6
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, clade B (ovalbu	63.6
447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cys-Cys), memb	60.7
424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from	60.3
414438	AI879277	Hs.76136	thioredoxin	59.9
420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	58.9
433336	AF017986	Hs.31386	ESTs, Highly similar to JE0174 frizzled protein-2 [H.sa	58.8
403741			predicted exon	57.0
430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizzarin)	56.1
424098	AF077374	Hs.139322	small proline-rich protein 3	55.8
441591	AF055992	Hs.183	Duffy blood group	55.6
426521	AF161445	Hs.170219	hypothetical protein	55.5
406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	55.3
406725	D51245	Hs.288061	actin, beta	54.1
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	54.1
406755	N80129	Hs.94360	metallothionein 1L	54.0
425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	53.3
442257	AW503831		gb:UI-HF-BN0-alb-b-05-0-UI.r1 NIH_MGC_50 Homo	53.1
421957	AW068637	Hs.109857	hypothetical protein DKFZp434H0820	52.3
447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte chemotactic pro	51.2
406722	H27498	Hs.283305	Homo sapiens SNC73 protein (SNC73) mRNA, comple	51.0
427223	BE208189	Hs.174031	cytochrome c oxidase subunit VIb	51.0
414420	AA043424	Hs.76095	immediate early response 3	50.9
417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	50.3
414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	49.5
436906	H95990	Hs.181244	major histocompatibility complex, class I, A	49.0
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	49.0
414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, clade B (ovalbu	48.8
432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma cluster 4 antig	48.8
421948	L42583	Hs.111758	keratin 6A	48.7
414662	AL036058	Hs.76807	major histocompatibility complex, class II, DR alpha	48.5
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	48.5
404767			predicted exon	48.4
418327	U70370	Hs.84136	paired-like homeodomain transcription factor 1	48.2
436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	47.7
414183	AW957446	Hs.301711	ESTs	47.2
400163			predicted exon	47.0
433423	BE407127	Hs.8997	heat shock 70kD protein 1A	46.9
423457	F08208	Hs.155606	paired mesoderm homeo box 1	46.6

414085	AA114016	Hs.75746	aldehyde dehydrogenase 6	46.0
423189	M59371	Hs.171596	EphA2	45.6
438240	N92638	Hs.124004	ESTs	45.5
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	45.3
412774	AA120865	Hs.23136	ESTs	45.1
407242	M18728		gb:Human nonspecific crossreacting antigen mRNA, co	44.8
431292	AA370141	Hs.251453	Human DNA sequence from clone 967N21 on chromos	44.8
403695			predicted exon	43.5
417365	D50683	Hs.82028	transforming growth factor, beta receptor II (70-80kD)	43.4
432331	W37862	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586I1524 (from c	43.4
424479	AF064238	Hs.149098	smoothelin	43.3
444726	NM_006147	Hs.11801	interferon regulatory factor 6	43.2
432314	AA533447	Hs.285173	ESTs	43.2
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	43.1
441406	Z45957	Hs.7837	Homo sapiens cDNA FLJ10457 fis, clone NT2RP1001	42.7
412969	AI373162	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	42.6
423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL02160	42.5
400111			predicted exon	42.4
407207	T03651	Hs.179661	tubulin, beta polypeptide	42.4
417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein A/B	42.2
424971	AA479005	Hs.154036	tumor suppressing subtransferable candidate 3	41.9
439394	AA149250	Hs.56105	ESTs, Weakly similar to WDNM RAT WDNM1 PROT	41.9
406657	AI678644	Hs.277477	major histocompatibility complex, class I, C	41.8
451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein, partial cds	41.6
412596	AA161219	Hs.799	diphtheria toxin receptor (heparin-binding epidermal gro	41.6
422103	AA984330	Hs.111676	protein kinase H11; small stress protein-like protein HS	41.5
428785	AI015953	Hs.125265	ESTs	41.3
450988	BE618571	Hs.429	ATP synthase, H+ transporting, mitochondrial F0 comp	41.0
414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	40.8
405022			predicted exon	40.8
408221	AA912183	Hs.47447	ESTs	40.8
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome	40.7
421416	BE302950	Hs.104125	adenylyl cyclase-associated protein	40.6
412247	AF022375	Hs.73793	vascular endothelial growth factor	40.5
410541	AA065003	Hs.64179	hypothetical protein	40.5
406658	AI920965	Hs.77961	major histocompatibility complex, class I, B	40.0
420225	AW243046	Hs.94789	ESTs	40.0
406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	39.4
443623	AA345519	Hs.9641	complement component 1, q subcomponent, alpha poly	39.4
404201	AF059566	Hs.103983	solute carrier family 5 (sodium iodide symporter), mem	39.3
405138			predicted exon	39.1
408733	AW264812	Hs.254290	ESTs	39.0
414044	BE614194	Hs.75721	profilin 1	38.9
430152	AB001325	Hs.234642	aquaporin 3	38.8
428121	AB006622	Hs.182536	Homo sapiens cDNA: FLJ21370 fis, clone COL03092	38.8
434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MAMMA10	38.7
406140			predicted exon	38.5
432918	AF077200	Hs.279813	hypothetical protein	38.4
420107	AL043980	Hs.7886	pellino (Drosophila) homolog 1	38.4
427693	BE546832	Hs.180370	cofilin 1 (non-muscle)	38.1
448835	BE277929	Hs.11081	ESTs, Weakly similar to S57447 HPBRII-7 protein [H.	38.1
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PLACE1010	37.9
428383	BE616599	Hs.184029	hypothetical protein DKFZp761A052	37.7
436258	AW867491	Hs.107125	ESTs, Weakly similar to S57447 HPBRII-7 protein [H.	37.7
420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis; keratosis palm	37.7
400327	M18679	Hs.247942	Human variant 5S rRNA-like gene and ORF, complete	37.6
401781			predicted exon	37.6
448257	AW772070	Hs.253146	ESTs	37.3
428415	AA337211	Hs.184222	Down syndrome critical region gene 1	37.2
424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vascular adhesion p	37.2
406812	AF000575	Hs.67846	leukocyte immunoglobulin-like receptor, subfamily B (	37.2
425882	U83115	Hs.161002	absent in melanoma 1	37.2
432501	BE546532	Hs.287329	Fas binding protein 1	37.1
421786	AI188653	Hs.21351	ESTs	37.1
427981	BE275986	Hs.181311	asparaginyl-tRNA synthetase	37.0
410143	AA188169	Hs.288819	Homo sapiens cDNA: FLJ21022 fis, clone CAE06383	36.8
451328	AW853606	Hs.109012	ESTs	36.7
414135	NM_004419	Hs.2128	dual specificity phosphatase 5	36.7
414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from	36.7
401785			predicted exon	36.5
411469	T09997	Hs.70327	cysteine-rich protein 2	36.2
419693	AA133749	Hs.92323	FXYD domain-containing ion transport regulator 3	36.1
417039	AA302180	Hs.80986	ATP synthase, H+ transporting, mitochondrial F0 comp	36.1
406718	AA505525	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	36.0
402543			predicted exon	36.0
408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antig	35.9
414987	AA524394	Hs.165544	ESTs	35.9
445810	AW265700	Hs.155660	ESTs	35.9
406653	AA574074	Hs.77961	major histocompatibility complex, class I, B	35.7
407498	U28131		gb:Human HMGI-C chimeric transcript mRNA, partial	35.6
412524	AA417813	Hs.11177	ESTs	35.5
401521			predicted exon	35.4
408948	AW296713	Hs.221441	ESTs	35.1
406728	AI936345	Hs.183704	ubiquitin C	34.9

440669	AI206964		gb:qr30g06.x1 NCI_CGAP_GC6 Homo sapiens cDNA	34.8
422658	AF231981	Hs.250175	homolog of yeast long chain polyunsaturated fatty acid	34.8
452924	AW580939	Hs.97199	complement component C1q receptor	34.7
428600	AW863261	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC095 [H.sapi	34.7
409828	AW501137		gb:UI-HF-BP0p-ail-e-12-0-UI.r1 NIH_MGC_51 Homo	34.5
459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens cDNA	34.5
445055	BE512856	Hs.109051	glycoprotein, synaptic 2	34.3
411789	AF245505	Hs.72157	Homo sapiens adlican mRNA, complete cds	34.3
410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens cDNA	34.2
410706	AI732404	Hs.68846	ESTs	34.2
419273	BE271180	Hs.293490	ESTs	34.2
407839	AA045144	Hs.161566	ESTs	34.0
444286	AI625304	Hs.190312	ESTs	34.0
449226	AB002365	Hs.23311	KIAA0367 protein	34.0
414290	AI568801	Hs.71721	ESTs	33.9
401245			predicted exon	33.9
425222	M85430	Hs.155191	villin 2 (ezrin)	33.8
409950	R42678	Hs.301669	KIAA0564 protein	33.8
437201	F29279	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-II,	33.7
406566	AF088886	Hs.11590	cathepsin F	33.7
405071			predicted exon	33.7
455426	AW937792		gb:QV3-DT0045-140200-082-b07 DT0045 Homo sapi	33.6
415160	T82802		gb:yd38a04.r1 Soares fetal liver spleen 1NFLS Homo s	33.5
424995	Z45023		gb:HSC2FA041 normalized infant brain cDNA Homo s	33.5
453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone LNG10019	33.5
433470	AW960564	Hs.3337	transmembrane 4 superfamily member 1	33.4
428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epidermal type I, pro	33.3
417409	BE272506	Hs.82109	syndecan 1	33.3
425389	AW974499	Hs.192183	ESTs	33.3
434658	AI624436	Hs.194488	ESTs	33.2
456562	AA306049	Hs.102669	DKFZP434O125 protein	33.1
447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	33.0
432360	BE045243	Hs.274416	NADH dehydrogenase (ubiquinone) 1 alpha subcomple	32.9
424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	32.7
419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	32.7
429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	32.6
451541	BE279383	Hs.26557	plakophilin 3	32.6
424499	N90344	Hs.149436	kinesin family member 5B	32.4
402144			predicted exon	32.4
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	32.4
400231			predicted exon	32.3
437712	X04588	Hs.85844	neurotrophic tyrosine kinase, receptor, type 1	32.3
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	32.2
419659	AB023206	Hs.92186	Leman coiled-coil protein	32.0
428582	BE336699	Hs.185055	BENE protein	32.0
421401	AW410478	Hs.104019	transforming, acidic coiled-coil containing protein 3	32.0
414064	BE245289	Hs.16165	expressed in activated T/LAK lymphocytes	32.0
431938	AA938471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
411930	F06485		gb:HSC19G051 normalized infant brain cDNA Homo s	31.9
428150	AW950547	Hs.182684	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	31.8
401887			predicted exon	31.8
412570	AA033517	Hs.74047	electron-transfer-flavoprotein, beta polypeptide	31.7
422738	X80915	Hs.1573	growth differentiation factor 5 (cartilage-derived morph	31.6
453092	X64838	Hs.31638	restin (Reed-Steinberg cell-expressed intermediate filam	31.5
413924	AL119964	Hs.75616	KIAA0018 gene product	31.4
420231	R06866	Hs.19813	ESTs	31.3
434715	BE005346	Hs.116410	ESTs	31.3
422831	R02504		gb:ye86f06.r1 Soares fetal liver spleen 1NFLS Homo sa	31.2
416854	H40164	Hs.80296	Purkinje cell protein 4	31.2
422976	AU076657	Hs.1600	sec61 homolog	31.1
426356	BE536836		gb:601064837F1 NIH_MGC_10 Homo sapiens cDNA	31.0
433935	AF112208	Hs.44163	13kDa differentiation-associated protein	30.8
430040	AW503115	Hs.227823	pM5 protein	30.8
406340	AA299679	Hs.180370	cofilin 1 (non-muscle)	30.8
426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcription factor, epith	30.7
425105	BE280066	Hs.24956	hypothetical protein FLJ22056	30.7
402066			predicted exon	30.7
429538	BE182592	Hs.139322	small proline-rich protein 3	30.6
418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	30.4
421251	Z28913	Hs.102948	enigma (LIM domain protein)	30.3
456084	AA155859	Hs.79708	ESTs	30.3
402023			predicted exon	30.3
404356			predicted exon	30.2
415973	R24707	Hs.260201	ESTs	30.2
445983	AI269107	Hs.132219	ESTs	30.1
450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	30.1
458789	AL157468	Hs.20157	Homo sapiens cDNA FLJ20848 fis, clone ADKA01732	30.1
400842			predicted exon	30.1
406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	30.0
423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (from c	30.0
451383	AW239364	Hs.20242	hypothetical protein FLJ12788	30.0
437042	AK000702	Hs.5420	hypothetical protein FLJ20695	30.0
459399	BE407712		gb:601299745F1 NIH_MGC_21 Homo sapiens cDNA	30.0
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	30.0

416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membrane protein	29.9
431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 30)	29.7
436651	BE045962	Hs.275998	ESTs	29.6
419766	BE243101	Hs.22391	chromosome 20open reading frame 3	29.5
420747	BE294407	Hs.99910	phosphofructokinase, platelet	29.5
436895	AF037335	Hs.5338	carbonic anhydrase XII	29.5
412765	AK000620	Hs.74571	ADP-ribosylation factor 1	29.4
419223	X60111	Hs.1244	CD9 antigen (p24)	29.4
413796	AW408094	Hs.75545	interleukin 4 receptor	29.4
447795	AW295151	Hs.163612	ESTs	29.4
431103	M57399	Hs.44	pleiotrophin (heparin binding growth factor 8, neurite g	29.4
415314	N88802	Hs.5422	glycoprotein M6B	29.3
428411	AW291464	Hs.10338	ESTs	29.3
430580	AA806105	Hs.140	immunoglobulin heavy constant gamma 3 (Gm marker)	29.3
430451	AA836472	Hs.249982	cathepsin B	29.2
453949	AU077146	Hs.36927	heat shock 105kD	29.2
413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme 4	29.2
407845	AL036518	Hs.118598	ESTs	29.1
453500	AI478427	Hs.43125	ESTs	29.1
456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens cDNA	29.0
453467	AI535997	Hs.30089	ESTs	29.0
411794	AL118577	Hs.75658	phosphorylase, glycogen; brain	28.9
421773	W69233	Hs.112457	ESTs	28.9
423621	BE002904		gb:QV4-BN0090-070400-163-c07 BN0090 Homo sapi	28.8
408935	BE539706	Hs.285363	ESTs	28.8
450847	NM_003155	Hs.25590	stanniocalcin 1	28.8
431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	28.7
423225	AA852604	Hs.125359	Thy-1 cell surface antigen	28.7
433469	F12741		gb:HSC3DG061 normalized infant brain cDNA Homo	28.7
405783			predicted exon	28.7
417308	H60720	Hs.81892	KIAA0101 gene product	28.7
400749			predicted exon	28.7
413442	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sapiens c	28.6
404828			predicted exon	28.6
407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein heavy ch	28.6
418529	AW005695	Hs.250897	TRK-fused gene (NOTE: non-standard symbol and nam	28.6
413787	AI352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	28.5
450690	AA296696	Hs.25334	FXYD domain-containing ion transport regulator 5	28.5
402430			predicted exon	28.4
413929	BE501689	Hs.75617	collagen, type IV, alpha 2	28.2
423803	NM_005709	Hs.132945	PDZ-73 protein	28.2
406086			predicted exon	28.2
416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	28.2
417055	N39489	Hs.7258	Homo sapiens cDNA: FLJ22021 fis, clone HEP08253	28.1
449184	AW296295	Hs.196491	ESTs	28.1
446542	NM_004281	Hs.15259	BCL2-associated athanogene 3	28.1
412793	AW997986		gb:RC1-BN0056-230200-021-e11 BN0056 Homo sapie	28.0
452818	W21909	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subunit	28.0
402869			predicted exon	27.9
436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) homolog	27.9
402075			predicted exon	27.9
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	27.8
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell adhesion molecul	27.8
439766	AB033492	Hs.301241	Homo sapiens mRNA; cDNA DKFZp586A0424 (from	27.7
424482	BE268621	Hs.149155	voltage-dependent anion channel 1	27.6
420737	L08096	Hs.99899	tumor necrosis factor (ligand) superfamily, member 7	27.6
414663	BE396326		gb:601289258F1 NIH_MGC_8 Homo sapiens cDNA c	27.6
409703	NM_006187	Hs.56009	2'-5'oligoadenylate synthetase 3	27.6
446108	AL036596	Hs.102773	ESTs	27.5
428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	27.5
445688	AI248205	Hs.153244	ESTs	27.5
405411			predicted exon	27.5
410275	U85658	Hs.61796	transcription factor AP-2 gamma (activating enhancer-b	27.5
424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	27.3
450455	AL117424	Hs.25035	chloride intracellular channel 4	27.3
414855	AA156986	Hs.104640	HIV-1 inducer of short transcripts binding protein	27.2
433578	BE336886	Hs.3416	adipose differentiation-related protein	27.2
401994			predicted exon	27.2
445033	AV652402	Hs.155145	ESTs	27.2
402277			predicted exon	27.1
428106	BE620016	Hs.182470	PTD010 protein	27.1
448625	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fis, clone HSI08080	27.1
422587	AI879352	Hs.118625	hexokinase 1	27.0
457204	BE264152	Hs.221994	ESTs	27.0
444094	AI695764	Hs.202394	ESTs	27.0
414053	BE391635	Hs.75725	transgelin 2	26.9
430511	BE018156	Hs.2575	calpain 1, (mu/I) large subunit	26.9
434039	L32977	Hs.3712	ubiquinol-cytochrome c reductase, Rieske iron-sulfur po	26.9
424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, partial cds	26.9
414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens cDNA	26.9
404675			predicted exon	26.8
401597	AA172106	Hs.110950	Rag C protein	26.8
401405			predicted exon	26.8
411541	W03940		gb:za62b02.r1 Soares fetal liver spleen 1NFLS Homo sa	26.8

412025	AI827451	Hs.24143	ESTs	26.7
414276	BE297862		gb:601174780F1 NIH_MGC_17 Homo sapiens cDNA	26.7
444065	AW449415	Hs.10260	Homo sapiens cDNA FLJ11341 fis, clone PLACE1010	26.7
447981	R53772	Hs.8929	hypothetical protein FLJ11362	26.7
410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	26.5
400982			predicted exon	26.5
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone HRC08686	26.5
407233	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecul	26.4
430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit, alpha type, 7	26.3
448218	AI188489		gb:qd09b12.x1 Soares_placenta_8to9weeks_2NbHP8to	26.3
413511	AI627178	Hs.75412	Arginine-rich protein	26.2
459511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sapiens cDNA	26.2
410668	BE379794	Hs.65403	hypothetical protein	26.2
458662	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5)	26.2
451219	AA054209	Hs.167904	ESTs	26.2
448939	BE267795	Hs.22595	hypothetical protein FLJ10637	26.2
400800	Y10262	Hs.46925	eyes absent (Drosophila) homolog 3	26.2
446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from c	26.2
421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (from	26.1
433848	AF095719	Hs.93764	carboxypeptidase A3	26.1
448497	BE613269	Hs.21893	ESTs, Weakly similar to glycerol 3-phosphate permease	26.1
415279	F04237	Hs.1447	glial fibrillary acidic protein	26.0
419323	AI092379	Hs.135275	ESTs	26.0
430265	L36033	Hs.237356	stromal cell-derived factor 1	25.9
437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	25.9
425535	AB007937	Hs.158287	KIAA0468 gene product	25.8
412923	AA179922	Hs.75056	adaptor-related protein complex 3, delta 1 subunit	25.8
447980	AI703397	Hs.202355	ESTs	25.8
419118	AA234223	Hs.139204	ESTs	25.8
421224	AW402154	Hs.125812	ESTs	25.8
414890	BE281095	Hs.77573	uridine phosphorylase	25.8
447330	BE279949	Hs.18141	ladinin 1	25.7
405610			predicted exon	25.7
447604	AW089933	Hs.293674	ESTs	25.7
445677	H96577	Hs.6838	ras homolog gene family, member E	25.7
456088	BE177320	Hs.156148	Homo sapiens cDNA: FLJ23082 fis, clone LNG06451	25.7
417120	N79687	Hs.46616	ESTs	25.6
405194			predicted exon	25.6
410687	U24389	Hs.65436	lysyl oxidase-like 1	25.6
421888	AA299780	Hs.121036	ESTs	25.6
420459	AF016045	Hs.97905	ovo (Drosophila) homolog-like 1	25.5
416323	N72630	Hs.33981	Homo sapiens genomic DNA, chromosome 21q, section	25.5
446292	AF081497	Hs.279682	Rh type C glycoprotein	25.5
416274	AW160404	Hs.79126	guanine nucleotide binding protein 10	25.5
430028	BE564110	Hs.227750	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	25.5
438450	AI050866	Hs.65853	nodal, mouse, homolog	25.5
400215			predicted exon	25.4
430014	H59354	Hs.182485	actinin, alpha 4	25.4
453582	AW854339	Hs.33476	hypothetical protein FLJ11937	25.4
405867			predicted exon	25.4
459170	AI905518		gb:RC-BT091-210199-098 BT091 Homo sapiens cDNA	25.4
407944	R34008	Hs.239727	desmocollin 2	25.4
415748	D90086	Hs.979	pyruvate dehydrogenase (lipoamide) beta	25.3
423287	H38340		gb:yp70h07.r1 Soares adult brain N2b4HB55Y Homo s	25.3
450944	AA554989	Hs.209061	sudD (suppressor of bimD6, Aspergillus nidulans) homo	25.3
432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	25.3
400104			predicted exon	25.3
449019	AI949095	Hs.67776	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	25.3
406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, partial cds.	25.3
402639			predicted exon	25.3
447147	AA910353	Hs.292815	ESTs	25.3
453379	AA035261	Hs.61753	ESTs	25.3
414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone LNG09846	25.3
430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	25.3
406685	M18728		gb:Human nonspecific crossreacting antigen mRNA, co	25.3
444747	AW450407	Hs.257291	ESTs, Weakly similar to PSS8_HUMAN PROSTASIN	25.2
417883	R22519	Hs.23398	ESTs	25.2
430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	25.2
459001	AI761313	Hs.204605	ESTs	25.2
434368	AW519020	Hs.212640	Homo sapiens cDNA FLJ13265 fis, clone OVARC1000	25.2
415917	Z43912		gb:HSC1OA111 normalized infant brain cDNA Homo	25.2
444409	AI792140	Hs.49265	ESTs	25.2
428578	BE391797	Hs.82148	hypothetical protein	25.1
433417	AA587773	Hs.136494	ESTs	25.1
426372	BE304680	Hs.169531	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21	25.1
402131			predicted exon	25.1
450545	AW135582	Hs.201767	ESTs	25.0
434162	AI221214	Hs.116136	ESTs	25.0
406571			predicted exon	24.9
427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (P	24.9
409402	AF208234	Hs.695	cystatin B (stefin B)	24.9
400135			predicted exon	24.9
428403	AI393048	Hs.239894	leucine rich repeat (in FLII) interacting protein 1	24.9
403223			predicted exon	24.8

435236	T03890	Hs.157208	ESTs, Highly similar to Arx homeoprotein [M.musculu	24.8
457439	AW410408	Hs.271167	L-pipecolic acid oxidase	24.8
448667	Z78394	Hs.4896	Homo sapiens cDNA: FLJ22046 fis, clone HEP09276	24.8
440605	Z40094	Hs.185698	ESTs	24.8
426724	AA383623	Hs.293616	ESTs	24.8
403359			predicted exon	24.7
442826	AI018777	Hs.131241	ESTs	24.7
411503	AW190338	Hs.28029	purinergic receptor P2X, ligand-gated ion channel, 4	24.6
414540	BE379050		gb:601236655F1 NIH_MGC_44 Homo sapiens cDNA	24.6
421595	AB014520	Hs.105958	Homo sapiens cDNA: FLJ22735 fis, clone HUV00180	24.5
438802	AA825976	Hs.136954	ESTs	24.5
400491	H25530	Hs.50868	solute carrier family 22 (organic cation transporter), me	24.5
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	24.5
426383	BE537380		gb:601064570F1 NIH_MGC_10 Homo sapiens cDNA	24.4
418408	AA219321	Hs.173294	ESTs	24.4
416186	W87575	Hs.269177	ESTs	24.4
416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	24.4
453857	AL080235	Hs.35861	DKFZP586E1621 protein	24.4
439706	AW872527	Hs.59761	ESTs	24.4
441619	NM_014056	Hs.7917	DKFZP564K247 protein	24.4
417198	F11533	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 comp	24.3
433662	W07162	Hs.150826	CATX-8 protein	24.3
453986	M13232	Hs.36989	coagulation factor VII (serum prothrombin conversion a	24.3
457123	AA770021	Hs.16332	ESTs	24.3
433864	AA931550	Hs.192785	ESTs	24.3
409865	AW502208		gb:UI-HF-BR0p-aju-e-09-0-UI.r1 NIH_MGC_52 Hom	24.3
448175	BE296174	Hs.225160	Homo sapiens cDNA FLJ13102 fis, clone NT2RP3002	24.3
406277			predicted exon	24.3
451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PLACE1006	24.3
408802	AL048269	Hs.288544	Homo sapiens cDNA: FLJ20882 fis, clone ADKA0320	24.2
401757			predicted exon	24.2
444751	AI207406	Hs.11866	hypothetical protein PRO1197	24.2
408647	AW245831		gb:2822937.5prime NIH_MGC_7 Homo sapiens cDNA	24.2
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fusin)	24.2
436913	AA789074	Hs.187478	ESTs	24.2
434745	AW974445	Hs.185155	ESTs, Weakly similar to HuEMAP [H.sapiens]	24.2
451743	AW074266	Hs.23071	ESTs	24.2
421853	AL117472	Hs.108924	DKFZP586P1422 protein	24.2
407926	AW956382	Hs.59771	ESTs	24.1
413973	BE279858	Hs.128417	Homo sapiens cDNA FLJ14009 fis, clone Y79AA1002	24.1
439078	AF085936		gb:Homo sapiens full length insert cDNA clone YR58F	24.1
401913			predicted exon	24.1
435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo sapiens cDNA	24.1
405311			predicted exon	24.0
413127	BE066529	Hs.83484	SRY (sex determining region Y)-box 4	24.0
430793	M83181	Hs.247940	5-hydroxytryptamine (serotonin) receptor 1A	24.0
434445	AI349306	Hs.11782	ESTs	24.0
418166	AI754416	Hs.260024	Cdc42 effector protein 3	24.0
431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	23.9
401167			predicted exon	23.9
454163	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo sapi	23.9
403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic reticulum/	23.9
410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac muscle, beta	23.9
450796	NM_001988	Hs.25482	envoplakin	23.8
442199	BE277633	Hs.286027	etoposide-induced mRNA	23.8
402699			predicted exon	23.8
426143	BE379836	Hs.167106	proteasome (prosome, macropain) subunit, alpha type, 3	23.8
437592	NM_003851	Hs.5710	cellular repressor of E1A-stimulated genes	23.8
433598	AI762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN ALU SU	23.8
401088			predicted exon	23.8
445924	AI264671	Hs.164166	ESTs	23.8
420902	AA742277		gb:ny28e09.s1 NCI_CGAP_GCB1 Homo sapiens cDN	23.8
426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog	23.8
458698	AW452189	Hs.257528	ESTs	23.7
422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	23.7
413460	R61610	Hs.21527	ESTs, Weakly similar to KIAA0918 protein [H.sapiens	23.6
401575			predicted exon	23.6
431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	23.6
427276	AA400269	Hs.49598	ESTs	23.6
417069	AA442192	Hs.81097	cytochrome c oxidase subunit VIII	23.5
400161			predicted exon	23.5
417190	NM_001359	Hs.81548	2,4-dienoyl CoA reductase 1, mitochondrial	23.5
443667	AI129066	Hs.135457	ESTs	23.5
413544	BE147225		gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapie	23.5
400685			predicted exon	23.5
422090	W05345	Hs.293884	ESTs	23.4
432517	AF275816	Hs.283096	PR domain containing 9	23.4
405307			predicted exon	23.4
416328	H48389	Hs.268886	ESTs	23.4
427174	AA398848	Hs.97541	ESTs	23.4
426148	AI751071	Hs.167135	Homo sapiens cDNA FLJ10728 fis, clone NT2RP3001	23.3
452544	AW851888		gb:QV0-CT0225-131099-034-d05 CT0225 Homo sapie	23.3
404890			predicted exon	23.3
408725	AA131539	Hs.15669	ESTs	23.3

428362	AA426555	Hs.169333	ESTs	23.3
425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5-phosphate ep	23.3
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11 (aldose redu	23.3
410962	BE273749	Hs.752	FK506-binding protein 1A (12kD)	23.2
411796	AA807197	Hs.6918	ESTs	23.2
458954	AW379075	Hs.141742	Homo sapiens cDNA FLJ12211 fis, clone MAMMA10	23.2
408896	AI610447	Hs.48778	niban protein	23.2
457024	AA397546	Hs.119151	ESTs	23.2
414591	AI888490	Hs.55902	ESTs	23.2
437846	AA773866	Hs.244569	ESTs	23.2
401220			predicted exon	23.1
421747	AI816224	Hs.107747	DKFZP566C243 protein	23.1
452950	AA428123	Hs.7745	17kD fetal brain protein	23.1
414327	BE408145	Hs.185254	ESTs, Moderately similar to NAC-1 protein [R.norvegic	23.1
405256			predicted exon	23.1
452416	AA026115	Hs.114777	ESTs	23.1
440684	AI253123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NESTI [H.sap	23.1
445603	H08345	Hs.106234	ESTs	23.1
436306	AA805939	Hs.117927	ESTs	23.1
434867	AF159442	Hs.103382	phospholipid scramblase 3	23.0
404727			predicted exon	23.0
407317	AI204033	Hs.271461	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	23.0
405580			predicted exon	23.0
437898	W81260	Hs.43410	ESTs	22.9
448781	AW243419	Hs.254048	ESTs	22.9
457297	AW968188	Hs.290999	ESTs	22.9
405545			predicted exon	22.9
431562	AI884334	Hs.11637	ESTs	22.9
440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (from c	22.9
439848	AW979249		gb:EST391359 MAGE resequences, MAGP Homo sap	22.9
418149	AA811473	Hs.291877	ESTs	22.9
439332	AW842747	Hs.293314	ESTs, Highly similar to unnamed protein product [H.sa	22.8
401566			predicted exon	22.8
425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	22.8
406684	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecul	22.8
421651	AW860612	Hs.283586	ESTs	22.8
421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced protein 2	22.8
441249	AA971585	Hs.166250	ESTs	22.8
457624	AA809159	Hs.287581	Homo sapiens cDNA FLJ13544 fis, clone PLACE1006	22.8
407395	AF005082		gb:Homo sapiens skin-specific protein (xp33) mRNA, p	22.8
459006	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
436827	H72187	Hs.5322	guanine nucleotide binding protein (G protein), gamma	22.7
418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	22.7
418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin transporter), mem	22.7
456035	N54956	Hs.271726	ESTs	22.7
457867	AA045767	Hs.5300	bladder cancer associated protein	22.7
440401	AI126341	Hs.143887	ESTs	22.7
400126			predicted exon	22.7
414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (from	22.7
406719	AI832962	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	22.6
439675	W95357	Hs.138860	Rho GTPase activating protein 1	22.6
456058	N94587	Hs.55063	ESTs	22.6
441926	AI015051	Hs.130953	ESTs	22.6
428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen exchanger), is	22.6
438518	BE561958	Hs.285823	immunoglobulin heavy constant mu	22.6
420674	NM_000055	Hs.1327	butyrylcholinesterase	22.6
422160	AW582898		gb:la07e04.y1 Human Pancreatic Islets Homo sapiens c	22.5
412408	D51103	Hs.73851	ATP synthase, H+ transporting, mitochondrial F0 comp	22.5
400964			predicted exon	22.5
434360	AW015415	Hs.127780	ESTs	22.5
427977	AW630727	Hs.181307	H3 histone, family 3A	22.4
450339	AI693281	Hs.54547	ESTs	22.4
424059	AW451266	Hs.107418	ESTs	22.4
414626	BE410589		gb:601303308F1 NIH_MGC_21 Homo sapiens cDNA	22.4
401991			predicted exon	22.4
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	22.3
457952	U25750	Hs.210783	Human chromosome 17q21 mRNA clone 1046:1-1	22.3
422597	BE245909	Hs.118634	ATP-binding cassette, sub-family B (MDR/TAP), mem	22.3
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	22.3
447306	AI373163	Hs.170333	ESTs	22.3
424966	AU077312	Hs.153985	solute carrier family 7 (cationic amino acid transporter,	22.3
422739	H20106	Hs.119591	adaptor-related protein complex 2, sigma 1 subunit	22.2
432504	AL121015	Hs.277704	oxygen regulated protein (150kD)	22.2
423804	AW403448	Hs.1706	interferon-stimulated transcription factor 3, gamma (48k	22.2
404683	AI924294	Hs.173259	uncharacterized bone marrow protein BM033	22.2
441624	AF220191	Hs.179666	uncharacterized hypothalamus protein HSMNP1	22.2
425751	T19239	Hs.1940	crystallin, alpha B	22.2
452976	R44214	Hs.101189	ESTs	22.2
414642	AA150350		gb:zl03h01.r1 Soares_pregnant_uterus_NbHPU Homo	22.2
437452	AL390127	Hs.7104	Homo sapiens mRNA; cDNA DKFZp761P06121 (from	22.2
417426	NM_002291	Hs.82124	laminin, beta 1	22.2
414774	X02419	Hs.77274	plasminogen activator, urokinase	22.1
424631	AA688021	Hs.179808	ESTs	22.1
413967	AW204431	Hs.117853	ESTs	22.1

400174			predicted exon	22.1
431837	T79326	Hs.298262	ESTs, Weakly similar to dJ68J8.1 [H.sapiens]	22.1
401628			predicted exon	22.1
418374	AJ011916	Hs.84359	hypothetical protein	22.0
429297	X82494	Hs.198862	fibulin 2	22.0
403508			predicted exon	22.0
432638	AI017717	Hs.126525	chromosome 21 open reading frame 15	22.0
407382	AA503620		gb:ne49b08.s1 NCI_CGAP_Co3 Homo sapiens cDNA	22.0
411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	22.0
420185	AL044056	Hs.158047	ESTs	22.0
409545	BE296182		gb:601177324F1 NIH_MGC_17 Homo sapiens cDNA	22.0
426662	AA879474	Hs.122710	ESTs	22.0
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	22.0
443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDNA clone EU	21.9
422447	AA310711	Hs.124340	ESTs	21.9
421574	AJ000152	Hs.105924	defensin, beta 2	21.9
435302	AI076259	Hs.190337	ESTs	21.9
414527	BE241739	Hs.76359	catalase	21.9
441436	AW137772	Hs.185980	ESTs	21.9
454178	AW177274		gb:CM2-CT0128-230899-005-a02 CT0128 Homo sapie	21.8
448838	BE614761		gb:601281335F1 NIH_MGC_39 Homo sapiens cDNA	21.8
427889	AI400968	Hs.181046	dual specificity phosphatase 3 (vaccinia virus phosphat	21.8
441114	AA917466	Hs.126600	ESTs	21.8
451831	NM_001674	Hs.460	activating transcription factor 3	21.8
405600			predicted exon	21.8
446981	AI652743	Hs.197497	ESTs	21.8
432839	AA579465	Hs.287332	ESTs	21.8
405208			predicted exon	21.8
435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeast) homolog	21.7
413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro	21.7
423515	AA327017	Hs.162204	ESTs	21.7
452329	N36626	Hs.29106	mitogen-activated protein kinase phosphatase x	21.7
423050	AA320946		gb:EST23529 Adipose tissue, brown Homo sapiens cD	21.7
413679	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo sapie	21.7
442166	AW845280	Hs.204723	ESTs	21.6
445585	AI243836	Hs.147066	ESTs	21.6
406160			predicted exon	21.6
433025	AA374743	Hs.279920	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	21.6
446598	AW250546		gb:2821774.5prime NIH_MGC_7 Homo sapiens cDNA	21.6
434493	AA635305	Hs.121574	ESTs	21.6
429582	AI569068	Hs.22247	ESTs	21.6
403796			predicted exon	21.6
405028			predicted exon	21.6
426597	AA382250	Hs.145601	ESTs	21.6
437308	AA749417	Hs.292353	ESTs	21.6
447384	AI377221	Hs.40528	ESTs	21.6
429060	AW139155	Hs.194995	hypothetical protein DKFZp434O0320	21.6
437068	AA743643	Hs.291427	ESTs	21.6
418509	AB028624	Hs.85539	ATP synthase, H+ transporting, mitochondrial F0 comp	21.5
432999	BE294029	Hs.279903	Ras homolog enriched in brain 2	21.5
407663	NM_016429	Hs.37482	COPZ2 for nonclathrin coat protein zeta-COP	21.5
446627	AI973016	Hs.15725	hypothetical protein SBBI48	21.5
413605	BE152644		gb:CM1-HT0329-250200-128-f09 HT0329 Homo sapie	21.5
427286	AW732802	Hs.2132	epidermal growth factor receptor pathway substrate 8	21.5
405226			predicted exon	21.4
402570			predicted exon	21.4
457960	AA771881	Hs.298149	ESTs	21.4
400684			predicted exon	21.4
425943	H46986	Hs.31861	ESTs	21.4
434240	AF119912	Hs.258119	hypothetical protein PRO3073	21.4
448376	AI494332	Hs.196963	ESTs	21.4
408089	H59799	Hs.42644	thioredoxin-like	21.4
400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33) mRNA, part	21.4
412652	AI801777	Hs.6774	ESTs	21.4
428373	AI751656	Hs.183986	poliovirus receptor-related 2 (herpesvirus entry mediato	21.3
416138	C18946	Hs.79026	myeloid leukemia factor 2	21.3
425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen included)	21.3
411028	AW813703		gb:RC3-ST0197-130100-014-h09 ST0197 Homo sapien	21.3
417438	Z43989	Hs.82141	Human clone 23612 mRNA sequence	21.3
417534	NM_004998	Hs.82251	myosin IC	21.3
427767	AI879283	Hs.180714	cytochrome c oxidase subunit VIa polypeptide 1	21.2
433300	AA582307		gb:nn49d09.s1 NCI_CGAP_Kid6 Homo sapiens cDNA	21.2
452061	AI074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	21.2
411939	AI365585	Hs.146246	ESTs	21.2
435060	AI422719	Hs.233349	ESTs, Weakly similar to fork head like protein [H.sapie	21.2
432412	AI470549	Hs.162201	ESTs	21.2
407491	S82769		gb:GABAA receptor gamma 3 subunit [human, fetal bra	21.2
418960	NM_004494	Hs.89525	hepatoma-derived growth factor (high-mobility group p	21.1
426254	BE018103	Hs.168541	Homo sapiens mRNA full length insert cDNA clone EU	21.1
458188	AW297226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOMEOB	21.1
406215			predicted exon	21.1
425461	AK000602	Hs.157938	hypothetical protein FLJ20595	21.1
448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT2RM4002	21.1
409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone CAE07155	21.1

408546	W49512	Hs.46348	bradykinin receptor B1	21.1
450008	H52970	Hs.36688	WAP four-disulfide core domain 1	21.1
430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	21.1
438901	AF085834	Hs.29036	ESTs	21.1
440500	AA972165	Hs.150308	ESTs	21.1
413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo sapie	21.1
447452	BE618258	Hs.102480	ESTs	21.1
412446	AI768015	Hs.92127	ESTs	21.1
418975	T75496	Hs.296980	ESTs	21.0
454961	AW847807		gb:IL3-CT0213-190200-040-E12 CT0213 Homo sapien	21.0
401072			predicted exon	21.0
401204			predicted exon	21.0
433626	AF078859	Hs.86347	hypothetical protein	21.0
418047	R37633	Hs.4847	ESTs	21.0
443380	AI792478	Hs.135377	ESTs	21.0
427424	AA402453	Hs.113011	ESTs	21.0
433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (yeast)	21.0
422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A) expressed in	20.9
435656	R93409	Hs.120759	ESTs	20.9
413745	AW247252	Hs.75514	nucleoside phosphorylase	20.9
418874	T60872		gb:yb72h11.s1 Stratagene ovary (937217) Homo sapien	20.9
452574	AF127481	Hs.35093	lymphoid blast crisis oncogene	20.9
400332	S66407	Hs.248032	FLT4	20.9
402421			predicted exon	20.9
427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.9
432038	AA524746	Hs.162110	ESTs	20.8
423711	AF059194	Hs.131953	v-maf musculoaponeurotic fibrosarcoma (avian) oncoge	20.8
402297			predicted exon	20.8
405133			predicted exon	20.8
436661	AI125270	Hs.128069	ESTs, Weakly similar to similar to collagen [C.elegans]	20.8
437836	BE269291	Hs.292458	ESTs	20.8
437329	AA811977	Hs.291761	ESTs	20.8
445830	H10451	Hs.42656	Homo sapiens cDNA FLJ12667 fis, clone NT2RM4002	20.8
406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	20.7
421271	AW170057	Hs.133179	ESTs	20.7
400256			predicted exon	20.7
414028	AA782576	Hs.4944	Homo sapiens cDNA FLJ12783 fis, clone NT2RP2001	20.7
456728	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	20.7
417707	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	20.7
438713	H16902	Hs.6749	ESTs	20.7
450306	AL080080	Hs.24766	DKFZP564E1962 protein	20.7
438898	AI819863	Hs.106243	ESTs	20.7
403273			predicted exon	20.7
414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens cDNA	20.7
401283			predicted exon	20.7
403703			predicted exon	20.6
416969	AI815443	Hs.283404	organic cation transporter	20.6
442400	AW381148	Hs.3593	ESTs	20.6
447563	BE536115	Hs.160983	ESTs	20.5
419754	H52299	Hs.75243	bromodomain-containing 2	20.5
408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, member 3	20.5
450507	AW295603	Hs.250891	ESTs	20.5
429612	AF062649	Hs.252587	pituitary tumor-transforming 1	20.5
413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo sapie	20.5
432140	AK000404	Hs.272688	hypothetical protein FLJ20397	20.5
400642			predicted exon	20.4
431582	F07136	Hs.261828	G protein-coupled receptor kinase 7	20.4
442724	AA355525	Hs.159604	cysteinyl-tRNA synthetase	20.4
417861	AA334551	Hs.82767	sperm specific antigen 2	20.4
402948			predicted exon	20.4
411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapie	20.4
435478	AA682622		gb:zj20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Ho	20.4
447955	BE544271	Hs.288390	Homo sapiens cDNA: FLJ22795 fis, clone KAIA2543	20.3
433592	NM_004642	Hs.3436	deleted in oral cancer (mouse, homolog) 1	20.3
420865	N73241	Hs.100001	solute carrier family 17 (sodium phosphate), member 1	20.3
449482	AI784266	Hs.28774	ESTs	20.3
400807			predicted exon	20.3
419942	U25138	Hs.93841	potassium large conductance calcium-activated channel	20.3
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7 (galectin 7)	20.3
402986	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (beta)	20.3
451375	AI792066	Hs.283902	Homo sapiens BAC clone RP11-481J13 from 2	20.3
453586	AA248089	Hs.50841	ESTs, Weakly similar to tuftelin [M.musculus]	20.3
433090	AI720050	Hs.145362	Immortalization-upregulated protein	20.3
425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homologous to yeast	20.3
412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral protein, 28kD)	20.3
409738	BE222975	Hs.56205	insulin induced gene 1	20.3
428245	AF151048	Hs.183180	hypothetical protein	20.2
412582	BE270631	Hs.74077	proteasome (prosome, macropain) subunit, alpha type, 6	20.2
406207			predicted exon	20.2
400931			predicted exon	20.2
410709	AL122109	Hs.65735	Homo sapiens mRNA; cDNA DKFZp434M1827 (from	20.2
428438	NM_001955	Hs.2271	endothelin 1	20.2
446918	AL135125	Hs.13913	KIAA1577 protein	20.2
417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.2

429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (prostaglandin G	20.2
414511	AA148725	Hs.12969	hypothetical protein	20.2
451546	AF051782	Hs.26584	Homo sapiens clone CDABP0038 mRNA sequence	20.1
441899	AI372588	Hs.8022	TU3A protein	20.1
425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	20.1
411014	AW816072		gb:MR3-ST0220-070100-021-h07 ST0220 Homo sapie	20.1
451400	BE160479		gb:QV1-HT0413-210200-081-g05 HT0413 Homo sapi	20.1
459247	N46243	Hs.110373	ESTs	20.1
441633	AW958544	Hs.112242	ESTs	20.1
427466	AA523543	Hs.7678	cellular retinoic acid-binding protein 1	20.0
406893	M22406		gb:Human intestinal mucin mRNA, partial cds, clone SM	20.0
406268			predicted exon	20.0
403348			predicted exon	20.0
400970			predicted exon	20.0
414045	NM_002951	Hs.75722	ribophorin II	20.0
427169	AA398823	Hs.97549	EST	20.0
405586			predicted exon	20.0
445834	AI913290	Hs.145532	ESTs, Weakly similar to Gag polyprotein [M.musculus	20.0
422525	AA758797	Hs.192807	ESTs	20.0
425383	D83407	Hs.156007	Down syndrome critical region gene 1-like 1	20.0
454590	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HEMBA100	20.0
411529	AA430348	Hs.288837	Homo sapiens cDNA FLJ12927 fis, clone NT2RP2004	20.0
425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	20.0
403234			predicted exon	19.9
427267	AI201185	Hs.119164	ESTs	19.9
400203			predicted exon	19.9
449296	AL137257	Hs.23458	Homo sapiens mRNA; cDNA DKFZp434C1613 (from	19.9
406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac muscle, beta	19.9
423083	AA321774	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTEIN PH	19.9
422112	BE540240	Hs.111783	Lsm1 protein	19.9
413282	BE078159		gb:CM0-BT0615-140200-175-e06 BT0615 Homo sapie	19.9
453702	AA037637	Hs.42128	ESTs	19.9
403065			predicted exon	19.9
440633	AI140686	Hs.263320	ESTs	19.9
456994	AA383623	Hs.293616	ESTs	19.9
458260	R41782	Hs.22279	ESTs	19.9
452388	BE019696	Hs.29287	retinoblastoma-binding protein 8	19.9
422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	19.9
441989	AA306207	Hs.286241	Homo sapiens cDNA: FLJ22698 fis, clone HSI12044	19.9
418758	AW959311	Hs.87019	ESTs	19.9
406646	M33600	Hs.180255	major histocompatibility complex, class II, DR beta 1	19.8
433053	BE301909	Hs.279952	glutathione S-transferase subunit 13 homolog	19.8
414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid ceramidase)	19.8
452321	AW844498	Hs.289052	Homo sapiens LENG8 mRNA, variant C, partial sequen	19.8
449713	AW027025	Hs.239262	ESTs	19.8
458827	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fis, clone HSI08080	19.8
414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	19.8
441730	AI243276	Hs.149017	ESTs	19.8
420701	N42919	Hs.88630	ESTs, Weakly similar to AC007228 1 R31665 2 [H.sap	19.8
403642			predicted exon	19.8
408987	H85615		gb:yt03f11.r1 Soares retina N2b5HR Homo sapiens cD	19.8
446712	AW204789	Hs.209828	ESTs	19.8
403286			predicted exon	19.8
434439	AI022360	Hs.190583	ESTs	19.8
404067			predicted exon	19.7
455694	BE067300		gb:PM2-BT0349-161299-001-h10 BT0349 Homo sapie	19.7
403287			predicted exon	19.7
434633	AI189587	Hs.120915	ESTs	19.7
408199	AA132637	Hs.15396	ESTs	19.7
420080	M94065	Hs.94925	dihydroorotate dehydrogenase	19.7
408852	AW291435	Hs.254961	ESTs	19.7
403786			predicted exon	19.7
416839	H94900	Hs.17882	ESTs	19.7
434385	AA631946	Hs.259580	ESTs	19.7
446845	AI343645	Hs.156108	ESTs	19.7
425612	BE004257		gb:CM0-BN0103-180300-296-c04 BN0103 Homo sapi	19.7
402520			predicted exon	19.6
436098	R20597	Hs.9739	ESTs	19.6
438974	AF089816	Hs.6454	chromosome 19 open reading frame 3	19.6
447751	AA339541	Hs.24956	hypothetical protein FLJ22056	19.6
451310	AW250651	Hs.26213	ESTs, Moderately similar to dJ447F3.3 [H.sapiens]	19.6
435961	BE293127	Hs.283722	GTT1 protein	19.6
452937	BE410390	Hs.288940	five-span transmembrane protein M83	19.6
404850			predicted exon	19.6
438360	H74149	Hs.288193	hypothetical protein FLJ10375	19.6
436508	AW604381	Hs.121121	ESTs	19.6
430486	BE062109	Hs.241551	chloride channel, calcium activated, family member 2	19.6
407824	AA147884	Hs.9812	ESTs	19.6
406388			predicted exon	19.6
430204	AA618335	Hs.146137	ESTs, Weakly similar to putative [C.elegans]	19.5
457560	AI801934	Hs.163909	ESTs	19.5
429521	BE048708	Hs.50949	ESTs	19.5
429758	AW137722	Hs.246804	ESTs	19.5
441473	AA934995	Hs.184846	ESTs, Weakly similar to R28830 1 [H.sapiens]	19.5

411724	AA770559	Hs.71618	polymerase (RNA) II (DNA directed) polypeptide L (7.	19.5
450453	AA009883	Hs.50186	ESTs	19.5
419687	AI638859	Hs.227699	ESTs, Weakly similar to Yhr217cp [S.cerevisiae]	19.5
442162	AW294966	Hs.150849	ESTs	19.5
435056	AW023337	Hs.5422	glycoprotein M6B	19.5
417412	X16896	Hs.82112	interleukin 1 receptor, type I	19.5
413825	BE299181	Hs.75564	CD151 antigen	19.4
422687	AW068823	Hs.119206	insulin-like growth factor binding protein 7	19.4
435551	AF212365	Hs.5470	IL-17B receptor	19.4
440069	BE617892	Hs.6895	actin related protein 2/3 complex, subunit 3 (21 kD)	19.4
432277	AI669790	Hs.161825	ESTs	19.4
428044	AA093322	Hs.182225	RNA binding motif protein 3	19.4
456064	AA256213	Hs.72010	ESTs	19.4
424897	D63216	Hs.153684	frizzled-related protein	19.4
424673	AA345051	Hs.294092	ESTs	19.4
403852			predicted exon	19.3
405699			predicted exon	19.3
433096	AU076803	Hs.282975	carboxylesterase 2 (intestine, liver)	19.3
400344	NM_012368	Hs.258574	olfactory receptor, family 2, subfamily C, member 1	19.3
417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig), short basic	19.3
400449			predicted exon	19.3
453801	AL134751	Hs.23450	mRNA for FLJ00023 protein	19.3
435849	BE305242	Hs.112442	ESTs, Weakly similar to CLDE_HUMAN CLAUDIN-	19.3
454181	AW177377		gb:CM4-CT0129-190899-007-e09 CT0129 Homo sapie	19.3
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	19.3
406326			predicted exon	19.3
421921	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	19.3
416700	AW498958	Hs.79572	cathepsin D (lysosomal aspartyl protease)	19.2
458857	AI627342	Hs.224601	ESTs	19.2
405501			predicted exon	19.2
416601	R08652	Hs.20205	hemoglobin, beta pseudogene 1	19.2
426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	19.2
425590	AI954686	Hs.158321	beaded filament structural protein 2, phakinin	19.2
428151	AA422028		gb:zv26g06.r1 Soares_NhHMPu_S1 Homo sapiens cDN	19.2
426420	BE383808	Hs.169829	KIAA1180 protein	19.2
414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	19.2
404601			predicted exon	19.2
403861			predicted exon	19.2
448363	BE174595	Hs.366	6-pyruvoyltetrahydropterin synthase	19.2
406655	M21533	Hs.181244	major histocompatibility complex, class I, A	19.1
435372	AA809591	Hs.106486	ESTs, Highly similar to CIKG_HUMAN VOLTAGE-G	19.1
413154	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo sapie	19.1
443021	AA368546	Hs.8904	Ig superfamily protein	19.1
412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,40, sulfated	19.1
412633	AF001691	Hs.74304	periplakin	19.1
402071			predicted exon	19.1
410387	AI277367	Hs.47094	ESTs	19.1
423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-like)	19.1
407032	U73799		gb:Human dynactin mRNA, partial cds.	19.0
404034			predicted exon	19.0
456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudogene	19.0
446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse homolog) 6	19.0
426410	BE298446	Hs.180372	BCL2-like 1	19.0
419618	AA528295		gb:nh26e06.s1 NCI_CGAP_Pr3 Homo sapiens cDNA c	19.0
457632	AW292151	Hs.112689	ESTs	19.0
417138	AA193646	Hs.65771	Homo sapiens chromosome 19, BAC CIT-HSPC_204F	19.0
417933	X02308	Hs.82962	thymidylate synthetase	19.0
458808	AW134832	Hs.246295	ESTs	19.0
415860	D56051	Hs.78888	diazepam binding inhibitor (GABA receptor modulator	18.9
440919	AW291274	Hs.262826	ESTs	18.9
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	18.9
401747			predicted exon	18.9
454209	AW179083		gb:MR4-ST0065-270899-006-A07 ST0065 Homo sapi	18.8
417661	T84155	Hs.15464	Homo sapiens cDNA: FLJ21351 fis, clone COL02762	18.8
426499	C14937	Hs.11169	Gene 33/Mig-6	18.8
404240			predicted exon	18.8
439718	AA307634	Hs.6650	vacuolar protein sorting 45B (yeast homolog)	18.8
401789			predicted exon	18.8
456952	AW445081	Hs.301469	ESTs	18.8
439739	AI199391	Hs.124464	ESTs	18.8
437974	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	18.8
427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	18.8
443482	AW188093	Hs.250385	ESTs	18.8
411420	BE390652		gb:601286820F1 NIH_MGC_44 Homo sapiens cDNA	18.8
435196	F35675	Hs.188128	ESTs, Moderately similar to ALU8_HUMAN !!!! ALU	18.8
417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain family 2	18.8
413531	AL036958	Hs.75416	DAZ associated protein 2	18.7
428981	BE313077	Hs.93135	ESTs	18.7
421598	AW630942	Hs.106061	RD RNA-binding protein	18.7
443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding protein	18.7
406754	AA477223	Hs.75922	brain protein I3	18.7
400661			predicted exon	18.7
442638	AI088742	Hs.134713	ESTs	18.7
434169	AA683752	Hs.179724	ESTs	18.7

424126	AA335635	Hs.96917	ESTs	18.7
408473	BE259039	Hs.129953	Ewing sarcoma breakpoint region 1	18.7
401962			predicted exon	18.7
447326	AW002252	Hs.201395	ESTs	18.7
459053	AI807052	Hs.210361	ESTs	18.7
403362			predicted exon	18.7
427697	T18997	Hs.180372	BCL2-like 1	18.7
402061	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	18.7
433785	BE044593	Hs.112704	ESTs	18.7
405423			predicted exon	18.6
429259	AA420450	Hs.292911	ESTs	18.6
444071	AI627808	Hs.110524	ESTs	18.6
410512	AA085603	Hs.250570	ESTs	18.6
440376	AI024452	Hs.236816	ESTs	18.6
457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotropic hormone)	18.6
432749	NM_014438	Hs.278909	Interleukin-1 Superfamily e	18.6
415602	F12920	Hs.165575	ESTs	18.6
407891	AA486620	Hs.41135	endomucin-2	18.6
455910	Z43712		gb:HSC1JA121 normalized infant brain cDNA Homo s	18.6
426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig), short basic	18.6
444246	H93281	Hs.10710	hypothetical protein FLJ20417	18.6
428125	AA393071	Hs.182579	leucine aminopeptidase	18.6
406457			predicted exon	18.5
446625	AI333070	Hs.156141	ESTs	18.5
423334	AK000906	Hs.127273	hypothetical protein FLJ10044	18.5
423103	AA322029		gb:EST24685 Cerebellum II Homo sapiens cDNA 5' en	18.5
443549	T89608	Hs.16601	ESTs	18.5
419299	AI311085	Hs.62406	Homo sapiens cDNA: FLJ22573 fis, clone HSI02387	18.5
411942	AW877015		gb:QV2-PT0010-250300-096-f12 PT0010 Homo sapien	18.5
442440	BE464435	Hs.146180	ESTs, Weakly similar to non-receptor protein tyrosine k	18.5
454574	AW809109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo sapie	18.5
454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library	18.5
422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic subunit of DNA p	18.5
421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondroplasia, tha	18.5
420603	AB042636	Hs.4775	junctophilin 3	18.4
401373			predicted exon	18.4
402292			predicted exon	18.4
444118	AA458542	Hs.10326	coatomer protein complex, subunit epsilon	18.4
408310	AW179023		gb:PM3-ST0036-170899-001-e08 ST0036 Homo sapie	18.4
411236	AW833752		gb:QV4-TT0008-130100-077-b07 TT0008 Homo sapie	18.4
431405	AI470895	Hs.252574	ribosomal protein L10a	18.4
441408	AI733249	Hs.126897	ESTs	18.4
453994	BE180964	Hs.165590	ribosomal protein S13	18.4
444518	AI160278	Hs.146884	ESTs	18.4
402407			predicted exon	18.4
404270			predicted exon	18.4
409103	AF251237	Hs.112208	XAGE-1 protein	18.4
415198	AW009480	Hs.943	natural killer cell transcript 4	18.3
430771	BE387244	Hs.2664	flavin containing monooxygenase 4	18.3
432636	AA340864	Hs.278562	claudin 7	18.3
433504	NM_014874	Hs.3363	KIAA0214 gene product	18.3
415606	W70022		gb:zd51e10.r1 Soares_fetal_heart_NbHH19W Homo sa	18.3
401401	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R28379	18.3
420758	AW297536	Hs.33053	ESTs	18.3
457520	AA553495	Hs.162264	ESTs	18.3
432323	AK001409	Hs.274356	hypothetical protein FLJ10547	18.3
404750			predicted exon	18.3
450645	AL117441	Hs.25264	DKFZP434N126 protein	18.3
445160	AI299144	Hs.150797	ESTs	18.3
418461	BE242781	Hs.288037	Homo sapiens cDNA FLJ12999 fis, clone NT2RP3000	18.3
401809			predicted exon	18.3
458121	S42416	Hs.74647	Human T-cell receptor active alpha-chain mRNA from	18.3
435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box protein Fbx	18.3
448398	AW444655	Hs.170838	ESTs	18.3
428145	BE243327	Hs.182626	chromosome 22 open reading frame 5	18.2
445302	AK001537	Hs.12488	hypothetical protein FLJ10675	18.2
407352	H47860		gb:yp76h12.r1 Soares fetal liver spleen 1NFLS Homo s	18.2
413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma 2 subunit	18.2
436371	AI821912	Hs.113912	ESTs	18.2
400965			predicted exon	18.2
433427	AI816449	Hs.171889	cholinephosphotransferase 1	18.2
427504	AA776743	Hs.191589	ESTs	18.2
426759	AI590401	Hs.21213	ESTs	18.2
423792	AW135866	Hs.245854	ESTs	18.2
406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	18.1
406659	AA663985	Hs.277477	major histocompatibility complex, class I, C	18.1
437453	AI761350	Hs.181391	hypothetical protein DKFZp761G2113	18.1
409276	AW372097	Hs.278429	hepatocellular carcinoma-associated antigen 59	18.1
449628	AI697676	Hs.197713	ESTs	18.1
421043	BE379455	Hs.89072	ESTs	18.1
442344	AI022925	Hs.301212	ESTs	18.1
448744	AL135424	Hs.9469	phosphoinositol 3-phosphate binding protein-1	18.1
416062	AA724811	Hs.74427	p53-induced protein	18.1
414500	W24087	Hs.76285	DKFZP564B167 protein	18.1

427272	NM_001096	Hs.174140	ATP citrate lyase	18.1
403964			predicted exon	18.1
433217	AB040914	Hs.278628	KIAA1481 protein	18.1
427902	AI809202	Hs.208343	ESTs, Weakly similar to cerebroside sulfotransferase (H	18.1
449586	AI863918	Hs.195078	ESTs	18.1
430826	U10061	Hs.248019	POU domain, class 4, transcription factor 3	18.1
414195	BE263293		gb:601144881F2 NIH_MGC_19 Homo sapiens cDNA	18.1
416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	18.1
411088	BE247593	Hs.145053	ESTs	18.1
419407	AW410377	Hs.41502	Homo sapiens cDNA: FLJ21276 fis, clone COL01829	18.1
407938	AA905097	Hs.85050	phospholamban	18.1
449360	AI640623	Hs.252720	ESTs	18.1
417286	AA122237	Hs.81874	microsomal glutathione S-transferase 2	18.0
405515			predicted exon	18.0
439319	AW016401	Hs.233476	ESTs	18.0
419387	BE378356	Hs.90107	cell membrane glycoprotein, 110000M(r) (surface antig	18.0
414015	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C)	18.0
447778	BE620592	Hs.71190	ESTs	18.0
435523	T62849	Hs.11090	high affinity immunoglobulin epsilon receptor beta sub	18.0
429230	AF088991	Hs.198274	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	18.0
457822	AA970001	Hs.150319	ESTs	18.0
442424	AI342715	Hs.129569	ESTs, Moderately similar to B34087 hypothetical prote	18.0
418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	18.0
413477	AI815825	Hs.48756	ESTs, Moderately similar to neuronal-STOP protein (M	18.0
405277			predicted exon	18.0
450192	AA263143	Hs.24596	RAD51-interacting protein	18.0
442191	W95186	Hs.8136	endothelial PAS domain protein 1	18.0
429490	AI971131	Hs.293684	ESTs, Weakly similar to alternatively spliced product u	18.0
406744	AA554082	Hs.279860	hypothetical protein FLJ20030	17.9
425205	NM_005854	Hs.155106	receptor (calcitonin) activity modifying protein 2	17.9
414387	AL043148	Hs.186257	ESTs	17.9
411811	AW864370		gb:PM4-SN0016-100500-004-h09 SN0016 Homo sapie	17.9
433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro	17.9
414333	BE274897		gb:601122959F1 NIH_MGC_20 Homo sapiens cDNA	17.9
403747			predicted exon	17.9
435542	AA687376	Hs.269533	ESTs	17.9
403093			predicted exon	17.9
412088	AI689496	Hs.108932	ESTs	17.9
450506	NM_004460	Hs.418	fibroblast activation protein, alpha	17.9
404763			predicted exon	17.9
454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo sapien	17.9
440788	AI806594	Hs.128577	ESTs	17.9
411800	N39342	Hs.5184	TH1 drosophila homolog	17.9
441361	BE263308	Hs.7797	TERF1 (TRF1)-interacting nuclear factor 2	17.8
422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted in velocardiof	17.8
405333			predicted exon	17.8
408297	R17710	Hs.113314	ESTs	17.8
403036			predicted exon	17.8
417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	17.8
417091	AA193283	Hs.291990	ESTs	17.8
440789	AB007857	Hs.7416	KIAA0397 gene product	17.8
438397	AA806478	Hs.123206	ESTs	17.8
435948	AA702675	Hs.114135	ESTs	17.8
450273	AW296454	Hs.24743	hypothetical protein FLJ20171	17.8
435969	W85773	Hs.191386	ESTs	17.8
427031	AA397601	Hs.125147	ESTs	17.8
454505	AW801365		gb:IL5-UM0067-240300-050-a01 UM0067 Homo sapi	17.8
403447			predicted exon	17.8
433297	AV658581	Hs.282633	ESTs	17.8
443326	BE156494	Hs.188478	ESTs	17.8
448283	AI340462	Hs.182979	ribosomal protein L12	17.8
458067	AA393603	Hs.36752	Homo sapiens cDNA: FLJ22834 fis, clone KAIA4314	17.8
452359	BE167229	Hs.29206	Homo sapiens clone 24659 mRNA sequence	17.8
434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapiens cDN	17.8
450911	AA011586	Hs.272097	ESTs	17.7
410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, receptor for; gamma	17.7
407082	Z47055		gb:Human partial cDNA sequence, farnesyl pyrophosph	17.7
415271	X94232	Hs.78335	microtubule-associated protein, RP/EB family, member	17.7
417413	AA197072	Hs.86092	Human DNA sequence from clone RP11-243J16 on chr	17.7
408937	AA210734	Hs.291386	ESTs	17.7
433459	AA593498		gb:nn27b05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA	17.7
459536	AI254723	Hs.145496	ESTs	17.7
428500	AI815395	Hs.184641	delta-6 fatty acid desaturase	17.7
433463	R41963	Hs.4197	ESTs	17.7
406537			predicted exon	17.7
410003	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937221) Homo	17.7
440857	AA907808	Hs.135556	ESTs	17.7
451072	AA013451	Hs.117929	ESTs	17.7
418693	AI750878	Hs.87409	thrombospondin 1	17.7
443624	BE616129	Hs.9651	related RAS viral (r-ras) oncogene homolog	17.6
422626	AA344932	Hs.118786	metallothionein 2A	17.6
410756	AB037820	Hs.66159	KIAA1399 protein	17.6
436621	AI266254	Hs.132929	ESTs	17.6
453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	17.6

456828	AF156889	Hs.148427	LIM homeobox protein 3	17.6
421486	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	17.6
428834	AW899713	Hs.10338	ESTs	17.6
451419	R36309	Hs.174369	EST	17.6
448413	AI745379	Hs.42911	ESTs	17.6
424323	AA338791	Hs.146763	nascent-polypeptide-associated complex alpha polypept	17.6
423943	AF163570	Hs.135756	polymerase (DNA-directed) kappa	17.6
439423	BE536678	Hs.147099	ESTs	17.6
434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	17.6
408246	N55669	Hs.43946	L13 protein	17.6
441579	AW468847	Hs.127194	ESTs	17.5
420867	NM_014183	Hs.100002	HSPC162 protein	17.5
453680	AL079647	Hs.14485	ESTs	17.5
400202			predicted exon	17.5
410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	17.5
409932	AI376750	Hs.57600	adaptor-related protein complex 1, sigma 1 subunit	17.5
425563	AF084199	Hs.299837	ESTs	17.5
440475	AI807671	Hs.128343	ESTs	17.5
452767	AW014195	Hs.61472	ESTs, Weakly similar to unknown [S.cerevisiae]	17.5
410570	AI133096	Hs.64593	ATP synthase, H+ transporting, mitochondrial F1F0, su	17.4
419600	AA448958	Hs.91481	NEU1 protein	17.4
419588	AI347205	Hs.91375	Human clone 23614 mRNA sequence	17.4
428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase kinase 6	17.4
448928	AI350260	Hs.5384	Homo sapiens cDNA FLJ11743 fis, clone HEMBA100	17.4
403924			predicted exon	17.4
419889	AA251600		gb:zs10d12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA	17.4
405023	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	17.4
426065	N32049		gb:yw96g08.s1 Soares_placenta_8to9weeks_2NbHP8to	17.4
453199	AI336266	Hs.301854	Homo sapiens PRO0412 mRNA, complete cds	17.4
455132	AW857955		gb:PM0-CT0325-151299-002-A12 CT0325 Homo sapi	17.4
442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger domain, 1A	17.4
432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), catalytic subunit	17.3
444652	BE513613	Hs.11538	actin related protein 2/3 complex, subunit 1A (41 kD)	17.3
417935	R53697	Hs.170044	ESTs	17.3
430050	AA430993	Hs.227913	API5-like 1	17.3
446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrate 1	17.3
425996	W67330	Hs.81256	S100 calcium-binding protein A4 (calcium protein, calv	17.3
416964	D87467	Hs.80620	guanine nucleotide exchange factor for Rap1; M-Ras-re	17.3
437418	AI478954	Hs.59459	ESTs	17.3
447255	AI884908	Hs.158607	ESTs	17.3
402203			predicted exon	17.3
417611	AW993983		gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapie	17.3
426560	AA381661	Hs.119878	ESTs	17.3
446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PLACE1010	17.3
445017	AI205493	Hs.176860	ESTs	17.3
438658	AI222068	Hs.123571	ESTs	17.3
442238	AW135374	Hs.270949	ESTs	17.3
443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002	17.3
442609	AL020996	Hs.8518	selenoprotein N	17.2
416591	AA091976	Hs.79387	proteasome (prosome, macropain) 26S subunit, ATPase	17.2
403674			predicted exon	17.2
430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1 protein	17.2
411696	AW857404		gb:CM3-CT0313-291199-046-c11 CT0313 Homo sapie	17.2
434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	17.2
422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68kD	17.2
414364	D38521	Hs.75935	KIAA0077 protein	17.2
409119	AA531133	Hs.4253	G protein-coupled receptor 44	17.2
425640	U34051	Hs.299204	ESTs, Highly similar to CD5S_HUMAN CYCLIN-DE	17.2
436044	BE247571	Hs.15627	Nit protein 2	17.2
401657			predicted exon	17.2
449763	AI822112	Hs.118241	ESTs	17.2
409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	17.2
449636	AI656608	Hs.281328	ESTs	17.2
444958	AW292643	Hs.167047	ESTs	17.2
429978	AA249027	Hs.241507	ribosomal protein S6	17.2
453043	AW136440	Hs.224277	ESTs	17.2
458640	AI284935		gb:qk55g09.x1 NCI_CGAP_Co8 Homo sapiens cDNA	17.1
456329	T41418		gb:ph1h3_19/1TV Outward Alu-primed hncDNA librar	17.1
414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	17.1
403662			predicted exon	17.1
411651	AW855392		gb:CM3-CT0275-191099-024-e12 CT0275 Homo sapie	17.1
404097			predicted exon	17.1
447252	R90916		gb:yn01e10.r1 Soares adult brain N2b4HB55Y Homo s	17.1
430024	AI808780	Hs.227730	integrin, alpha 6	17.1
412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerst	17.1
444558	AW181975	Hs.165892	ESTs	17.1
420869	X58964	Hs.123638	regulatory factor X, 1 (influences HLA class II expressi	17.1
448812	H30775	Hs.22140	BM88 antigen	17.0
431777	AA570296	Hs.105470	found in inflammatory zone 1	17.0
422007	AI739435	Hs.39168	ESTs	17.0
403051			predicted exon	17.0
402427			predicted exon	17.0
417408	F17211	Hs.86092	Human DNA sequence from clone RP11-243J16 on chr	17.0
450598	AF151076	Hs.25199	hypothetical protein	17.0

421121	AA459028	Hs.86228	TRIAD3 protein	17.0
458488	AL040565	Hs.209544	ESTs	17.0
417158	AW965223	Hs.110062	ESTs, Weakly similar to ACR3_HUMAN 30 KD ADIP	17.0
439318	AW837046	Hs.6527	G protein-coupled receptor 56	17.0
428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE2000	17.0
447572	AI631546	Hs.159732	ESTs	17.0
434434	AA633516	Hs.157201	ESTs	17.0
409994	D86864	Hs.57735	acetyl LDL receptor; SREC	17.0
408927	AW295650	Hs.255453	ESTs	17.0
439093	AA534163	Hs.5476	serine protease inhibitor, Kazal type, 5	17.0
454466	AA984138	Hs.279895	Homo sapiens mRNA for KIAA1578 protein, partial cd	17.0
426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone HEP03447,	17.0
436659	AI217900	Hs.144464	ESTs	17.0
422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3) Homo s	17.0
429294	AA095971	Hs.198793	KIAA0750 gene product	17.0
432847	BE266941	Hs.279554	proteasome (prosome, macropain) 26S subunit, non-AT	16.9
416977	AW130242	Hs.293476	ESTs	16.9
406827	AA971409	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	16.9
453758	U83527		gb:HSU83527 Human fetal brain (M.Lovett) Homo sap	16.9
431314	AI732204	Hs.105423	ESTs	16.9
423185	BE299590	Hs.125078	ornithine decarboxylase antizyme 1	16.9
435086	AW975243	Hs.122596	ESTs	16.9
447383	N24231		gb:yx22a11.r1 Soares melanocyte 2NbHM Homo sapie	16.9
456251	R13326	Hs.21303	ESTs	16.9
456327	H68741	Hs.38774	ESTs	16.9
450594	N31036		gb:yx51g04.r1 Soares melanocyte 2NbHM Homo sapie	16.9
428177	AA423967	Hs.178113	ESTs, Moderately similar to kinesin like protein 9 [M.m	16.9
453250	AI346520	Hs.121619	chromosome 11 open reading frame 15	16.9
418294	AF061739	Hs.83954	protein associated with PRK1	16.9
446546	BE167687	Hs.156628	ESTs	16.9
421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone COLF6967	16.9
455993	BE179085		gb:RC0-HT0613-140300-021-d06 HT0613 Homo sapie	16.9
459375	BE251770		gb:601112470F1 NIH_MGC_16 Homo sapiens cDNA	16.9
454803	AW860148		gb:RC0-CT0379-290100-032-b10 CT0379 Homo sapie	16.9
445474	AI240014	Hs.259558	ESTs	16.9
443198	AI039813		gb:ox49d06.x1 Soares_total_fetus_Nb2HF8_9w Homo	16.9
441557	AW452647	Hs.270462	ESTs	16.9
420206	M91463	Hs.95958	solute carrier family 2 (facilitated glucose transporter),	16.9
442202	BE272862	Hs.106534	Homo sapiens cDNA: FLJ22625 fis, clone HSI06009	16.9
416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapie	16.9
419355	AA428520	Hs.90061	progesterone binding protein	16.9
452975	M85521	Hs.69469	dendritic cell protein	16.9
432525	AI796096	Hs.109414	ESTs	16.8
453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	16.8
437270	R18087	Hs.11282	ESTs, Weakly similar to cleft lip and palate transmemb	16.8
408007	AW135965	Hs.246783	ESTs	16.8
450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying protein 3	16.8
402958			predicted exon	16.8
445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H	16.8
410684	AA088500	Hs.170298	ESTs	16.8
437669	AI358105	Hs.123164	ESTs, Weakly similar to match to ESTs AA667999 [H.	16.8
447869	AW139113	Hs.164307	ESTs	16.8
458025	AI275406		gb:ql63c10.x1 Soares_NhHMPu_S1 Homo sapiens cDN	16.8
445614	AV660763	Hs.110675	apolipoprotein C-IV	16.8
454610	AW810224		gb:MR4-ST0125-021199-017-e07 ST0125 Homo sapie	16.8
449303	AK001495	Hs.23467	hypothetical protein FLJ10633	16.8
422105	AI929700	Hs.111680	endosulfine alpha	16.8
444788	AI871122	Hs.202821	ESTs	16.8
414057	AI815559	Hs.75730	signal recognition particle receptor ('docking protein')	16.8
408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OVARC1000	16.8
433379	AA586368	Hs.190232	ESTs	16.8
441552	AA937975		gb:oc08e12.s1 NCI_CGAP_GCB1 Homo sapiens cDN	16.8
403582			predicted exon	16.8
433871	W02410	Hs.205555	ESTs	16.8
439509	AF086332	Hs.58314	ESTs	16.8
431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.8
430129	BE301708	Hs.233955	hypothetical protein FLJ20401	16.8
401465			predicted exon	16.8
448913	AA194422	Hs.22564	myosin VI	16.8
410261	AF145713	Hs.61490	schwannomin interacting protein 1	16.8
421199	BE244219	Hs.102497	paxillin	16.7
450489	AI697990	Hs.224375	ESTs	16.7
410186	AW602528		gb:RC5-BT0562-260100-011-A02 BT0562 Homo sapi	16.7
447224	BE617125		gb:601441664F1 NIH_MGC_65 Homo sapiens cDNA	16.7
403010			predicted exon	16.7
404881			predicted exon	16.7
445572	AI243445	Hs.189654	ESTs	16.7
419440	AB020689	Hs.90419	KIAA0882 protein	16.7
443406	AI056238	Hs.143316	ESTs	16.7
457901	AW207023	Hs.250497	ESTs, Highly similar to dJ745C22.1 [H.sapiens]	16.7
448364	T08958	Hs.16561	HSPC141 protein	16.6
407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor, subfamily B (	16.6
401847			predicted exon	16.6
429523	AK000788	Hs.205280	Homo sapiens cDNA FLJ20781 fis, clone COL04235	16.6

432845	AI989751	Hs.150378	ESTs	16.6
400246			predicted exon	16.6
404971			predicted exon	16.6
422954	AW998605	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP like prot	16.6
415042	NM_006759	Hs.77837	UDP-glucose pyrophosphorylase 2	16.6
432201	AI538613	Hs.135657	ESTs	16.6
456993	AL134577	Hs.200302	ESTs	16.6
456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	16.6
444060	AA340277	Hs.10248	Homo sapiens cDNA FLJ20167 fis, clone COL09512	16.6
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial)	16.6
448199	AI953278	Hs.170557	ESTs	16.6
443422	R10288	Hs.301529	ESTs	16.6
401117			predicted exon	16.6
400613			predicted exon	16.6
431214	AA294921	Hs.250811	v-ral simian leukemia viral oncogene homolog B (ras re	16.6
431649	AL133077	Hs.266746	Homo sapiens cDNA: FLJ22615 fis, clone HSI05118	16.5
421335	X99977	Hs.103505	ARS component B	16.5
427154	AL137262	Hs.288991	Homo sapiens cDNA: FLJ22523 fis, clone HRC12507	16.5
401010			predicted exon	16.5
436678	BE512828	Hs.5273	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30k	16.5
401589			predicted exon	16.5
402538			predicted exon	16.5
430478	NM_014349	Hs.241535	TNF-inducible protein CG12-1	16.5
437623	D63880	Hs.5719	chromosome condensation-related SMC-associated pro	16.5
401244			predicted exon	16.5
415167	AA160784	Hs.26410	ESTs	16.5
438291	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fis, clone HRC07453,	16.5
405183			predicted exon	16.5
436480	AJ271643	Hs.87469	putative acid-sensing ion channel	16.5
456691	AI023428	Hs.205696	ESTs	16.5
418332	R34976	Hs.78293	ESTs	16.5
446052	AA358760		gb:EST67699 Fetal lung II Homo sapiens cDNA 5' end	16.5
444859	AW449137	Hs.157487	ESTs	16.5
437192	AW975786	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yea	16.5
400891			predicted exon	16.5
448372	AW445166	Hs.170802	ESTs	16.5
425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens cDNA 5' en	16.5
459253	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (from c	16.5
420746	AW195932	Hs.197488	ESTs	16.4
414717	BE271039	Hs.77060	proteasome (prosome, macropain) subunit, beta type, 6	16.4
400727			predicted exon	16.4
422691	NM_003365	Hs.119251	ubiquinol-cytochrome c reductase core protein I	16.4
405639			predicted exon	16.4
414444	BE298594		gb:601119754F1 NIH_MGC_17 Homo sapiens cDNA	16.4
456146	AL034349	Hs.79005	protein tyrosine phosphatase, receptor type, K	16.4
414610	BE388044		gb:601283747F1 NIH_MGC_44 Homo sapiens cDNA	16.4
414267	AL078459	Hs.289109	dimethylarginine dimethylaminohydrolase 1	16.4
401268			predicted exon	16.4
403613			predicted exon	16.4
414203	BE262170		gb:601150419F1 NIH_MGC_19 Homo sapiens cDNA	16.4
454315	AW373564	Hs.251928	nuclear pore complex interacting protein	16.4
452114	N22687	Hs.8236	ESTs	16.4
404638			predicted exon	16.4
404600			predicted exon	16.3
448855	AF070574	Hs.22316	Homo sapiens clone 24819 mRNA sequence	16.3
406629	AW277078	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	16.3
450957	BE515202	Hs.21497	Homo sapiens mRNA for FLJ00042 protein, partial cds	16.3
449966	H60542	Hs.37848	ESTs	16.3
402585			predicted exon	16.3
436008	AI078428	Hs.58785	ESTs	16.3
401492			predicted exon	16.3
412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140kD, antigen C	16.3
405088			predicted exon	16.3
437345	BE259522	Hs.5556	NADH dehydrogenase (ubiquinone) 1, alpha/beta subco	16.3
432280	BE440142	Hs.2943	signal recognition particle 19kD	16.3
419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase	16.3
428801	AW277121	Hs.254881	ESTs	16.3
431394	AK000692	Hs.252351	HERV-H LTR-associating 2	16.3
452998	BE019681	Hs.6019	Homo sapiens cDNA: FLJ21288 fis, clone COL01927	16.3
439938	AI147392	Hs.124607	ESTs	16.3
418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	16.3
446081	AA972412	Hs.13755	f-box and WD-40 domain protein 2	16.3
443534	AI076123		gb:oy92e04.x1 Soares_fetal_liver_spleen_1NFLS_S1 H	16.3
459510	AA076706		gb:7B01B02 Chromosome 7 Fetal Brain cDNA Library	16.3
450517	AI523755	Hs.59236	ESTs, Weakly similar to B35049 ankyrin 1, erythrocyte	16.3
451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-binding (negativ	16.3
454478	AW805749		gb:QV1-UM0105-180400-162-f10 UM0105 Homo sap	16.2
407214	AA412048	Hs.279574	CGI-39 protein; cell death-regulatory protein GRIM19	16.2
406580			predicted exon	16.2
409452	BE336714	Hs.289271	cytochrome c-1	16.2
416841	N33878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	16.2
458710	AV660856		gb:AV660856 GLC Homo sapiens cDNA clone GLCG	16.2
450657	AK001579	Hs.25277	hypothetical protein FLJ21065	16.2
404230			predicted exon	16.2

439471	W69839	Hs.58033	ESTs	16.2
400848			predicted exon	16.2
428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (from c	16.2
416272	AA178882		gb:zp38b09.r1 Stratagene muscle 937209 Homo sapiens	16.2
444465	AI206592	Hs.143843	ESTs	16.2
431257	AF039597		gb:Homo sapiens Ku86 autoantigen related protein 1 (K	16.2
447775	BE179318		gb:RC1-HT0615-290300-021-g05 HT0615 Homo sapie	16.2
403833			predicted exon	16.2
444140	AV648089	Hs.282383	ESTs	16.2
446102	AW168067	Hs.252956	ESTs	16.2
416475	T70298		gb:yd26g02.s1 Soares fetal liver spleen 1NFLS Homo s	16.2
430783	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	16.2
414070	AW963783		gb:EST375856 MAGE resequences, MAGH Homo sap	16.2
444283	AI138971	Hs.154636	ESTs	16.2
405599	X92715	Hs.3057	zinc finger protein 74 (Cos52)	16.2
409427	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo sapien	16.2
409417	AA156247	Hs.295908	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	16.2
435380	AA679001	Hs.192221	ESTs	16.2
406752	AI285598	Hs.217493	annexin A2	16.2
406096	F12200	Hs.5811	chromosome 21 open reading frame 59	16.2
417551	AI816291	Hs.82273	hypothetical protein	16.2
441252	AW360901	Hs.183047	ESTs, Weakly similar to unnamed protein product [H.s	16.2
419608	AL037237	Hs.91586	transmembrane 9 superfamily member 1	16.1
438894	AI630819	Hs.300431	ESTs	16.1
451287	AK002158	Hs.26194	hypothetical protein FLJ11296	16.1
412499	AW956916	Hs.11238	KIAA0622 protein; Drosophila "multiple asters" (Mast	16.1
433355	AI808235		gb:wf44e01.x1 Soares_NFL_T_GBC_S1 Homo sapien	16.1
416818	AI986408	Hs.204766	ESTs, Weakly similar to B48013 proline-rich proteogly	16.1
438765	AI031888	Hs.132594	ESTs	16.1
424470	BE244261	Hs.5615	nuclear RNA export factor 1	16.1
416194	H27114	Hs.301212	ESTs	16.1
446702	R44518	Hs.143496	ESTs	16.1
414222	AL135173	Hs.878	sorbitol dehydrogenase	16.1
443122	AI806656	Hs.209022	ESTs, Weakly similar to Pro-Pol-dUTPase polyprotein	16.1
448648	BE614345	Hs.159089	ESTs	16.1
456394	W28506		gb:48f1 Human retina cDNA randomly primed sublibra	16.1
445887	AI263105	Hs.145597	ESTs	16.1
412332	AW937661	Hs.288324	Homo sapiens cDNA FLJ13283 fis, clone OVARC1001	16.1
403912			predicted exon	16.1
441446	R66269	Hs.28714	ESTs	16.1
403153			predicted exon	16.0
444907	AW772596	Hs.148586	ESTs	16.0
421946	R99629	Hs.109773	hypothetical protein FLJ20625	16.0
437513	AW410681	Hs.5648	proteasome (prosome, macropain) 26S subunit, non-AT	16.0
407752	AA573581	Hs.13328	ESTs	16.0
447953	AI804218	Hs.209614	Homo sapiens cDNA: FLJ22343 fis, clone HRC06043	16.0
425708	AK001342	Hs.14570	Homo sapiens cDNA: FLJ22530 fis, clone HRC12866	16.0
421449	AA713491	Hs.291501	ESTs	16.0
418323	NM_002118	Hs.1162	major histocompatibility complex, class II, DM beta	16.0
447787	BE620108		gb:601483015F1 NIH_MGC_69 Homo sapiens cDNA	16.0
422716	AI702835	Hs.124475	ESTs	16.0
443958	BE241880	Hs.10029	cathepsin C	16.0
417908	AA207221		gb:zq55h04.s1 Stratagene neuroepithelium (937231) Ho	16.0
438542	AA810131	Hs.123317	ESTs	16.0
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor, alpha polypeptid	16.0
456825	H67220	Hs.146406	nitrilase 1	16.0
431360	NM_000427	Hs.251680	loricrin	16.0
414266	BE267834		gb:601124428F1 NIH_MGC_8 Homo sapiens cDNA c	16.0
440571	AA904461	Hs.130798	ESTs	16.0
426075	AW513691	Hs.270149	ESTs	16.0
413488	BE144017	Hs.184693	transcription elongation factor B (SIII), polypeptide 1 (1	16.0
446767	AI380107	Hs.158954	ESTs	16.0
418008	W56044	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone HEP16248	16.0
404239			predicted exon	16.0
458401	AW236939	Hs.172154	ESTs	16.0
412955	BE241849	Hs.75082	ras homolog gene family, member G (rho G)	15.9
423072	AI792946	Hs.123116	solute carrier family 12 (sodium/potassium/chloride tran	15.9
444954	AW247076	Hs.12163	eukaryotic translation initiation factor 2, subunit 2 (beta	15.9
449023	AI623261	Hs.248875	ESTs	15.9
435729	BE048886	Hs.275017	EST	15.9
438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	15.9
413047	H02209		gb:yj38c09.r1 Soares placenta Nb2HP Homo sapiens cD	15.9
425997	AK000086	Hs.165948	hypothetical protein FLJ20079	15.9
446863	AW614370	Hs.254620	ESTs	15.9
448564	AL044962	Hs.21453	Homo sapiens mRNA for inositol 1,4,5-trisphosphate 3	15.9
455640	BE064059		gb:QV3-BT0296-010300-111-e04 BT0296 Homo sapie	15.9
404345	AA730407	Hs.159156	protocadherin 11	15.9
418512	AW498974	Hs.89981	diacylglycerol kinase, zeta (104kD)	15.9
411551	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo sapien	15.9
446726	AW300144	Hs.209209	Homo sapiens cDNA FLJ11629 fis, clone HEMBA100	15.9
410748	BE383816	Hs.136005	ESTs, Highly similar to bG115G20.2 [H.sapiens]	15.9
449618	AI076459	Hs.14366	Homo sapiens cDNA FLJ12819 fis, clone NT2RP2002	15.9
429697	AW296451	Hs.24605	ESTs	15.9
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homology to p53	15.9

403151			predicted exon	15.8
452363	AI582743	Hs.94953	ESTs, Highly similar to C1QC_HUMAN COMPLEME	15.8
425971	AF135024	Hs.165296	kallikrein 13	15.8
432826	X75363	Hs.250770	kallikrein 15	15.8
431972	AI805145	Hs.191711	ESTs	15.8
400269			predicted exon	15.8
404703	AI904493	Hs.99890	polymerase (DNA directed), delta 1, catalytic subunit (1	15.8
449335	AW150717	Hs.296176	STAT induced STAT inhibitor 3	15.8
418443	NM_005239	Hs.85146	v-ets avian erythroblastosis virus E26 oncogene homolo	15.8
445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (from	15.8
433782	AF090945		gb:Homo sapiens clone HQ0670	15.8
406473			predicted exon	15.8
420831	AA280824	Hs.190035	ESTs	15.8
402939			predicted exon	15.8
405196			predicted exon	15.8
452947	AW130413		gb:xf50f04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA	15.8
414170	AA335996	Hs.3743	matrix metalloproteinase 24 (membrane-inserted)	15.8
437133	AB018319	Hs.5460	KIAA0776 protein	15.8
458356	AI024855	Hs.131575	ESTs	15.8
407857	AI928445	Hs.92254	hypothetical protein FLJ20163	15.8
405687			predicted exon	15.8
415189	L34657	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antig	15.8
408662	AW247699	Hs.105897	ESTs	15.7
448338	AI492857		gb:th72h08.x1 Soares_NhHMPu_S1 Homo sapiens cDN	15.7
402694			predicted exon	15.7
430224	AW675175	Hs.235975	hypothetical protein DKFZp434D0412	15.7
458792	N56666		gb:yw75e02.r1 Soares_placenta_8to9weeks_2NbHP8to	15.7
402944			predicted exon	15.7
422675	BE018517	Hs.119140	eukaryotic translation initiation factor 5A	15.7
408661	AW247625		gb:2820094.5prime NIH_MGC_7 Homo sapiens cDNA	15.7
423238	AA323569	Hs.280482	ESTs	15.7
421517	AB018352	Hs.105399	KIAA0809 protein	15.7
429865	AB023217	Hs.225968	KIAA1000 protein	15.7
440815	AW071945	Hs.7436	putative acyltransferase	15.7
400634			predicted exon	15.7
451034	AL050341	Hs.25846	zinc metalloproteinase, STE24 (yeast, homolog)	15.7
457571	AI375726	Hs.279918	hypothetical protein	15.7
450105	BE281124	Hs.288013	similar to yeast BET3 (S. cerevisiae)	15.7
407464	AJ276396		gb:Homo sapiens mRNA for matrix extracellular phosp	15.7
439465	AF086285		gb:Homo sapiens full length insert cDNA clone ZD47B	15.7
451837	T92157	Hs.16970	ESTs	15.7
435313	AI769400	Hs.189729	ESTs	15.7
402738			predicted exon	15.7
432966	AA650114		gb:ns92h09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA c	15.7
457666	AW470302	Hs.129663	ESTs	15.7
401269			predicted exon	15.7
427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a ligand)	15.7
418846	AI821602	Hs.115127	ESTs	15.6
448891	AI587332	Hs.209115	ESTs	15.6
445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	15.6
421254	AK001724	Hs.102950	coat protein gamma-cop	15.6
447073	AW204821	Hs.157726	ESTs	15.6
445438	AB014578	Hs.12707	KIAA0678 protein	15.6
432126	AA865239	Hs.55144	ESTs	15.6
424091	AF235097	Hs.139263	calcium channel, voltage-dependent, alpha 1F subunit	15.6
440832	AI057548	Hs.128224	ESTs	15.6
449228	AJ403107	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-004 [H.sapie	15.6
434253	AI393345	Hs.116215	ESTs	15.6
459270	AL039604		gb:DKFZp434E2211_r1 434 (synonym: htes3) Homo s	15.6
454425	AW300927	Hs.27192	hypothetical protein dJ1057B20.2	15.6
412055	AA099907	Hs.271806	ESTs	15.6
400837			predicted exon	15.6
458866	BE616694	Hs.288042	Homo sapiens cDNA FLJ14299 fis, clone PLACE1010	15.6
417124	BE122762	Hs.25338	ESTs	15.6
414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [H.sapiens]	15.6
418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo sapie	15.6
454128	AL031259	Hs.41639	programmed cell death 2	15.6
441074	AW500001	Hs.4783	Homo sapiens cDNA: FLJ22035 fis, clone HEP08838	15.6
451742	T77609	Hs.117970	ankyrin 2, neuronal	15.6
403687			predicted exon	15.6
431838	AI097229	Hs.217484	ESTs	15.6
402855			predicted exon	15.6
449635	AI989942	Hs.232150	ESTs	15.6
434392	AW983709	Hs.268051	ESTs	15.6
444301	AK000136	Hs.10760	hypothetical protein FLJ20129	15.6
414973	C19089		gb:C19089 Human placenta cDNA (TFujiwara) Homo	15.5
428374	AW405156	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isoform	15.5
415745	AI301107	Hs.150790	ESTs	15.5
432532	AW058459	Hs.162246	ESTs	15.5
417112	AA193439		gb:zr41b09.s1 Soares_NhHMPu_S1 Homo sapiens cDN	15.5
418101	AL047476	Hs.98485	gap junction protein, beta 4 (connexin 30.3)	15.5
453110	AW384928	Hs.225160	Homo sapiens cDNA FLJ13102 fis, clone NT2RP3002	15.5
458506	AJ239397		gb:AJ239397 Uni-ZAP XR retinal pigment epithelium H	15.5
436989	AA741028	Hs.256155	ESTs	15.5

407396	AF011757		gb:Homo sapiens RAGE binding protein (P12) mRNA,	15.5
449684	AI659166	Hs.207144	ESTs	15.5
454666	AW812994		gb:RC3-ST0186-230300-019-g02 ST0186 Homo sapien	15.5
430492	U15197	Hs.300803	Human histo-blood group ABO protein mRNA, partial	15.5
439460	AA836220	Hs.13774	ESTs	15.5
449231	BE410360		gb:601302340F1 NIH_MGC_21 Homo sapiens cDNA	15.5
453060	AW294092	Hs.21594	ESTs	15.5
416961	BE391476	Hs.80617	ribosomal protein S16	15.5
439988	AA860119	Hs.255976	ESTs	15.5
400917			predicted exon	15.5
424585	AA464840		gb:zx43h11.r1 Soares_total_fetus_Nb2HF8_9w Homo	15.5
431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q3	15.5
441680	AW444598	Hs.7940	RAP1, GTP-GDP dissociation stimulator 1	15.5
437830	AB020658	Hs.5867	KIAA0851 protein	15.5
409479	BE163800	Hs.136912	ESTs	15.5
409885	AW503068		gb:UI-HF-BP0p-aje-g-10-0-UI.r1 NIH_MGC_51 Homo	15.4
459090	AA443323	Hs.107812	ESTs, Weakly similar to SPOP [H.sapiens]	15.4
429324	AA488101	Hs.199245	inactivation escape 1	15.4
403766			predicted exon	15.4
413970	U59309	Hs.75653	fumarate hydratase	15.4
456674	BE266120	Hs.269358	ESTs	15.4
417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	15.4
430125	U46418	Hs.233950	serine protease inhibitor, Kunitz type 1	15.4
452154	AW953265	Hs.271277	hypothetical protein from EUROIMAGE 363668	15.4
422984	W28614	Hs.75984	chorionic somatomammotropin hormone 2	15.4
408649	BE242232	Hs.26045	protein tyrosine phosphatase, receptor type, A	15.4
417497	AW402482	Hs.82212	CD53 antigen	15.4
404666			predicted exon	15.4
456847	AI360456	Hs.37776	ESTs	15.4
426995	AA400646	Hs.221988	ESTs	15.4
445350	AF052112	Hs.12540	lysophospholipase I	15.4
450214	BE439763	Hs.227571	regulator of G-protein signalling 4	15.4
449733	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 fis, clone HEMBB100	15.4
411660	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapie	15.4
442653	BE269247	Hs.170226	Homo sapiens clone 23579 mRNA sequence	15.4
447552	AI394125	Hs.160413	ESTs	15.4
448712	W01046	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone LNG15735	15.4
420180	AI004035	Hs.25191	ESTs	15.4
440099	AL080058	Hs.6909	DKFZP564G202 protein	15.4
427550	BE242818	Hs.179606	nuclear RNA helicase, DECD variant of DEAD box fam	15.4
432894	AW167668	Hs.279772	brain specific protein	15.3
412113	AW161274	Hs.74427	p53-induced protein	15.3
431614	AI189827		gb:qd19d07.x1 Soares_placenta_8to9weeks_2NbHP8to	15.3
445870	AW410053	Hs.13406	syntaxin 18	15.3
424347	AA723883	Hs.145513	Homo sapiens mRNA; cDNA DKFZp434L0435 (from	15.3
425132	AW250114		gb:2821134.5prime NIH_MGC_7 Homo sapiens cDNA	15.3
439756	AL359651	Hs.283852	Homo sapiens mRNA full length insert cDNA clone EU	15.3
432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	15.3
406130			predicted exon	15.3
453359	AA448787	Hs.24872	ESTs, Weakly similar to aortic carboxypeptidase-like p	15.3
405491			predicted exon	15.3
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	15.3
446826	AK000626	Hs.16230	hypothetical protein FLJ20619	15.3
441211	AW946155	Hs.7750	hypothetical protein AL133206	15.3
418711	AW247977	Hs.87595	translocase of inner mitochondrial membrane 22 (yeast)	15.3
457301	AA469146		gb:nc67e03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA c	15.3
449999	AI679421	Hs.231098	ESTs, Highly similar to ALU4_HUMAN ALU SUBFA	15.3
439090	H65724	Hs.271663	ESTs	15.3
416586	D44643	Hs.14144	secreted modular calcium-binding protein 1	15.3
411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo sapie	15.3
407639	AW205369	Hs.252936	ESTs	15.3
458012	AI424899	Hs.188211	ESTs	15.3
426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	15.3
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	15.3
437371	AK000868	Hs.5570	hypothetical protein FLJ10006	15.3
437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) homolog	15.3
441890	AI809547	Hs.128075	ESTs	15.3
409442	AA310162	Hs.169248	cytochrome c	15.3
407078	Z26256		gb:H.sapiens isoform 1 gene for L-type calcium channe	15.2
436553	AW407157	Hs.181125	immunoglobulin lambda locus	15.2
443177	BE268461	Hs.202	benzodiazapine receptor (peripheral)	15.2
448771	BE315511	Hs.296244	SNARE protein	15.2
436837	AI968248	Hs.187869	ESTs	15.2
423623	AB011117	Hs.129943	KIAA0545 protein	15.2
422651	NM_015670	Hs.118926	DKFZP586K0919 protein	15.2
403221	AL134878	Hs.119500	karyopherin alpha 4 (importin alpha 3)	15.2
431620	AA126109	Hs.264981	2'-5'oligoadenylate synthetase 2	15.2
404794	NM_000078	Hs.89538	cholesteryl ester transfer protein, plasma	15.2
412944	AA384110	Hs.197143	ESTs	15.2
450817	N71597	Hs.29698	ESTs	15.2
418666	AF001434	Hs.155119	EH domain containing 1	15.2
451636	AW173270	Hs.140444	ESTs	15.2
426302	AA459085	Hs.275163	non-metastatic cells 2, protein (NM23B) expressed in	15.2
454485	AW795322		gb:PM0-UM0018-120400-002-h01 UM0018 Homo sap	15.2

440617	AA894880	Hs.181181	ESTs	15.2
449718	AA459480	Hs.23956	hypothetical protein FLJ20502	15.2
405227			predicted exon	15.2
431006	BE152871		gb:CM1-HT0333-101299-064-d12 HT0333 Homo sapi	15.2
443476	AW068594	Hs.133878	ESTs, Weakly similar to AF151889 1 CGI-131 protein	15.2
438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	15.2
407634	AW016569	Hs.301280	ESTs, Highly similar to AF241831 1 intracellular hyalu	15.2
436857	AA732647		gb:nz89d01.s1 NCI_CGAP_GC81 Homo sapiens cDN	15.2
431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	15.1
447386	NM_006289	Hs.18420	KIAA1027 protein	15.1
436573	AA723297	Hs.127138	ESTs	15.1
432858	BE618609	Hs.279591	Homo sapiens clone 25056 mRNA sequence	15.1
437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	15.1
413209	AW083791	Hs.21263	Homo sapiens cDNA FLJ13152 fis, clone NT2RP3003	15.1
407376	AA993138	Hs.142287	ESTs, Weakly similar to ALUF_HUMAN !!!! ALU CL	15.1
430475	BE387420	Hs.241531	pellin	15.1
446764	AW291276	Hs.285532	ESTs	15.1
425868	AB017548	Hs.160100	Homo sapiens gene for Sepiapterin Reductase, partial c	15.1
453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying protein 1	15.1
447246	AW449032	Hs.170257	ESTs	15.1
401780			predicted exon	15.1
434063	AA018893	Hs.3727	unr-interacting protein	15.1
416114	AI695549	Hs.183868	glucuronidase, beta	15.1
441018	AI809587	Hs.148782	ESTs	15.1
425972	BE391563	Hs.165433	ESTs, Highly similar to T17342 hypothetical protein D	15.1
426062	N57014	Hs.44013	ESTs	15.1
451234	AI914901	Hs.24052	ESTs	15.1
429565	AB020719	Hs.207802	KIAA0912 protein	15.1
418092	R45154	Hs.106604	ESTs	15.1
424550	AI650541	Hs.115298	ESTs	15.1
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipid G-protein-coup	15.1
445213	AW204314	Hs.170784	ESTs	15.1
418102	R58958	Hs.26608	ESTs	15.0
450082	AI908894	Hs.245893	ESTs	15.0
446749	NM_016069	Hs.16089	CGI-136 protein	15.0
406124			predicted exon	15.0
457408	AL137507	Hs.255348	Homo sapiens mRNA; cDNA DKFZp761P211 (from c	15.0
410051	U25773	Hs.218182	ESTs, Weakly similar to dJ1042K10.2 [H.sapiens]	15.0
440965	AI523646	Hs.169859	ESTs	15.0
440190	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214 Homo sapien	15.0
417437	U52682	Hs.82132	interferon regulatory factor 4	15.0
454249	AW249008		gb:2821048.5prime NIH_MGC_7 Homo sapiens cDNA	15.0
432276	AF163302	Hs.274255	somatostatin receptor-interacting protein	15.0
401116			predicted exon	15.0
423960	AA164516	Hs.136309	CGI-61 protein	15.0
451661	AB020650	Hs.26777	KIAA0843 protein	15.0
450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	15.0
446187	AK001241	Hs.14229	hypothetical protein FLJ10379	15.0
404122			predicted exon	15.0
411299	BE409857	Hs.69499	hypothetical protein	15.0
403077			predicted exon	15.0
438000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	15.0
447118	AB014599	Hs.17411	KIAA0699 protein	15.0
417878	U90916	Hs.82845	Human clone 23815 mRNA sequence	15.0
444079	H09048	Hs.23606	ESTs	15.0
458234	BE551408	Hs.127196	ESTs	15.0
434208	T92641	Hs.127648	hypothetical protein PRO2176	15.0
423136	AW375506	Hs.124147	ESTs	15.0
403177			predicted exon	15.0
448699	AI857269	Hs.227351	ESTs	15.0
425248	AW957442	Hs.252766	ESTs	15.0
429430	AI381837	Hs.155335	ESTs	15.0

TABLE 38:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408310	1051011_1	AW179023 AW179010
408647	1071855_1	AW245831 AW273207
408661	1073036_1	AW247625 AW249214
408987	109306_1	H85615 H86300 H86263 H86282 AA059278 H86304
409427	1129667_1	AW389668 AW389657 AW609198 AW389649
409545	1138823_1	BE296182 AW629821
409828	1155571_1	AW501137 AW501295 AW501212
409865	1156518_1	AW502208 AW502366 AW502148
409885	1157385_1	AW503068 AW503789
410003	116761_1	AA079487 AA128547 AA128291 AA079587 AA079600
410186	1182096_1	AW602528 BE073859 Z38412
410626	1212621_-1	BE407727
411004	1228975_1	AW813242 BE146089 AW813195 AW813173 AW813206 BE145953 BE146212 AW813196 AW854582 AW813241 BE061582
411014	1229091_1	AW816072 AW813375 AW813385 AW813372 AW813436 AW816148 AW813475 AW816107 AW813398 AW813479 AW814475 AW813317
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411236	1236374_1	AW833752 AW833633 AW833776 AW833719 AW833362 AW833749
411420	1245222_-1	BE390652
411541	1249044_1	W03940 T98335 AW850705
411551	1249196_1	AW851309 AW850888 AW851419 AW851412 AW851299
411651	1252835_1	AW855392 AW855559 AW855423
411660	1253078_1	AW855718 AW855740 AW855748
411696	1254304_1	AW857404 AW857401 BE144856
411811	1259427_1	AW864370 AW864319 AW864504
411930	1266070_1	F06485 AW876454
411940	1266262_1	AW876686 AW876717 AW877215 AW876691 AW876722 AW877218 AW876694 AW876725
411942	1266449_1	AW877015 AW877133 AW876978 AW877071 AW876988 AW877069 AW877063 AW877013
412793	1327636_-1	AW997986
413047	1346806_1	H02209 BE062154 BE062032
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413154	1351077_1	BE067870 BE067866 BE165133 BE165334 BE165329 BE165332
413282	1358147_1	BE078159 BE078276 BE078163 BE078277 BE078279 BE078158
413442	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
413544	1375671_1	BE147225 BE147205 BE147234
413605	1379792_1	BE152644 BE152712 BE152668 BE152659 BE152810 BE152811 BE152816 BE152643 BE152706 BE152656 BE152660 BE152715 BE152662 BE152669 BE152661 BE152672 BE152653 BE152716 BE152651 BE152767 BE152677 BE152652 BE152714 BE152708 BE152665 BE152679 BE152771 BE152775 BE152666 BE152768 BE152813 BE152664 BE152676 BE152681 BE152709 BE152667 BE152814 BE152808 BE152711 BE152707 BE152815 BE152678 BE152673 BE152782 BE152671 BE152682 BE152760 BE152809 BE152778 BE152780 BE152762 BE152776 BE152781 BE152774 BE152763 BE152769
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414266	1430984_1	BE267834 BE514180 BE514096
414276	1432115_-1	BE297862
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414539	1460320_1	BE379046 BE395459
414540	1460324_-1	BE379050
414605	1465790_-1	BE390440
414610	1466027_1	BE388044 BE391117 BE391530
414626	1467232_1	BE410589 BE390949 BE408297 BE389529
414642	146960_1	AA150350 AA361174 AW959038
414663	1472628_-1	BE396326
414973	1510755_1	C19089 C18814 C16621
415160	1525766_1	T82802 D78670 R08505
415606	1540470_1	W70022 R35201 F12763 T74725 H63485 Z45782 H61126
415917	1561575_1	Z43912 H09194
416272	158407_1	AA178882 AA179898 AA178897
416475	1596398_1	T70298 H58072 R02750
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
417112	165068_1	AA193439 AA193537 AW814128
417611	168900_1	AW993983 AW994798 AW993990 AW993999 AW993989 AA204755
417908	170764_1	AA207221 BE538271
418636	177402_1	AW749855 AA225995 AW750208 AW750206
418874	1799516_1	T60872 T60906
419618	186533_1	AA528295 AW971284 AA247945
419889	188798_1	AA251600 AA279607
420902	197525_1	AA742277 AW976493 AA281585
422160	212412_1	AW582898 AA305114
422731	220507_1	AL138411 AL138412 AA315860
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423050	224288_1	AA320946 H92114 BE144449 BE144438
423103	225019_1	AA322029 BE315237
423287	226793_1	H38340 H39081 AA324112
423621	230314_1	BE002904 H64880 AA328679
424585	241151_1	AA464840 AA343628
424995	245794_1	Z45023 AA349514
425132	247059_1	AW250114 Z43124 AA431421 AI879054 AA351616 AA351035 AL048999
425612	253969_1	BE004257 AW811190 AA360576 BE172402 BE181703
425798	256586_1	AA364002 AI522307
426065	260276_1	N32049 R34821 R78237
426356	265381_1	BE536836 AA376153
426383	266126_1	BE537380 BE255215
428151	287658_1	AA422028 W79191
431006	326833_1	BE152871 BE152870 AA490552
431257	33049_1	AF039597 BE243938
431614	335668_1	AI189827 AW860554 AW860552 AA508543
431822	338082_1	AA516049 AW004922
432966	356839_1	AA650114 AW974148 AA572946
433300	362452_1	AA582307 BE273018
433355	364004_1	AI808235 AI024295 AA584528
433459	366899_1	AA593498 AW749647 AW749630
433469	367263_1	F12741 T75155 AA594014
433782	37414_1	AF090945 AW996754 AI064870
434098	380006_1	AA625499 AA625269 AA625184
435138	401159_1	BE314734 AA666393
435478	406683_1	AA682622 BE141696

436857	428068_1	AA732647 BE008970 BE009028
439078	46841_1	AF085936 H64070 H64017
439465	47272_1	AF086285 W69587 W69421
439848	477806_1	AW979249 D63277 AA846968
440190	488021_1	AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700
440669	499861_1	AI206964 AI350890 AA902772 AI768881
441552	520138_1	AA937975 F11215 BE005635
442257	53699_1	AW503831 AW503317 BE565665
443198	562655_1	AI039813 AI684642 Z40121 AI951414 BE501049
443534	572957_1	AI076123 AI244834 AI695239
446052	65988_1	AA358760 AA158850 AW062737 AW062738 AV656291
446598	68463_1	AW250546 BE257108 BE251006 BE255957 BE250926 BE513012 AV659318
447224	71279_-1	BE617125
447252	714160_1	R90916 AL120023 R18429 Z42095 AI369730 R90824
447383	71990_1	N24231 BE617964 N36313
447775	73665_1	BE179318 BE620044
447787	73719_1	BE620108 BE312062 AW896316 BE262546
448218	75525_1	AI188489 BE622201
448338	758968_1	AI492857 AW070478 AI885157
448838	78409_4	BE614761 AA263136 W00335 W00327
449231	80303_1	BE410360 AA442408 AA315540
450594	83962_1	N31036 N42915 F07753 AA010329
451400	868459_1	BE160479 BE160478 BE069211 AW861059 AI793147
452544	921467_1	AW851888 AW851889 AW852147
452947	939810_1	AW130413 AI932362
453758	980026_1	U83527 AL120938 U83522
454163	1048369_1	AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
454178	1049458_1	AW177274 AW177249 AW177223 AW177216 AW177233
454181	1049567_1	AW177377 AW177357 AW177359 AW177385 AW177358 AW177395 AW177394 AW177396 AW177383 AW177333 AW177384 AW177382 AW177360 AW177356
454209	1051071_1	AW179083 AW179085 AW179087 AW179081 AW179084 AW179086 AW179082 AW801493 AW801658 AW801714
454249	1073933_1	AW249008 BE295653 BE296765
454377	114761_1	AA076811 AW814764
454478	1214744_1	AW805749 AW805872 AW794466 AW798102 AW796921 AW794538 AW794380
454485	1215381_1	AW795322 AW795308 AW795311 AW795310 AW795314 AW795321
454505	1219564_1	AW801365 AW801435 AW801372
454574	1225636_1	AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
454610	1226543_1	AW810224 AW810337 AW810295 AW810333 AW810335 AW810296 AW816053
454633	1227504_1	AW811380 AW811385
454666	1228600_1	AW812994 AW812723 AW812930
454803	1235520_1	AW860148 AW862380 AW821887 AW821863 AW821870 AW821894 AW862351 AW862378
454961	1246745_1	AW847807 AW847935 AW847636
455132	1254686_1	AW857955 AW861636 AW857967 AW857958 AW857943 AW857945 AW857963 AW857968 AW857959 AW857961 AW857956 BE072135 AW857972 BE072137 AW857952 AW857935 AW857940 AW857944 AW857947 AW857934
455426	1289303_1	AW937792 BE072250 BE072251 BE072264
455640	1348141_1	BE064059 BE063903 BE063838 BE063863 BE064056 BE063974 BE063904 BE063898 BE063896 BE063906 BE063980
455694	1350650_1	BE067300 BE067293 BE067279
455910	1382504_1	Z43712 BE156729 BE156538 BE156731 BE156673 BE156539 BE156674 BE156430 BE156672 BE156675 BE156432 BE156541
455993	1398665_1	BE179085 BE179084 BE179086 BE179264
456054	1452761_1	BE313241 BE383148
456329	1789807_1	T41418 T41320 T41379
456394	1843275_-2	W28506
457301	314434_1	AA469146 AA469396 AA469218 AA469395
458025	46409_1	AI275406 L23206
458606	65568_1	AJ239397 AV655764
458640	670076_1	AI284935 AW409822 BE408182
458710	69727_1	AV660856 BE167375
458792	748294_1	N56666 AI460076
459170	920646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037
459270	969232_1	AL039604 AL039497

TABLE 3C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400449	9887692	Minus	50889-51188
400613	9864507	Plus	92278-92472
400634	8567750	Minus	101102-101223,101886-102018
400642	8117693	Plus	10475-10845
400661	8118474	Plus	84912-85187
400684	8118768	Plus	58189-58323
400685	8118768	Minus	72969-73050,73713-73800
400727	6705887	Plus	106175-107016
400749	7331445	Minus	9162-9293
400807	8567878	Plus	69375-70295
400837	9188531	Plus	144778-144838,145582-145670,146656-146751,147255-147419,147682-147807
400842	1927148	Plus	90462-90673
400848	1927148	Plus	107149-107339,110873-111171
400891	9958279	Minus	140073-140427
400917	7283186	Minus	173258-173631

400931	7651921	Minus	142145-142353,144311-144721
400964	7139719	Minus	155282-155403
400965	7770576	Minus	173043-173564
400970	7960452	Minus	92744-92895
400982	8078794	Minus	119245-119471
401010	8117391	Minus	83967-84180
401072	3687273	Plus	64370-64524
401088	8492704	Plus	194659-195179
401116	9966559	Plus	123579-124447
401117	8570083	Minus	28948-29204
401167	9438381	Plus	18944-19176
401204	9743388	Minus	33694-33872
401220	9929324	Minus	48079-48279
401244	4827300	Minus	55359-56376
401245	4827300	Minus	59373-59531
401268	9797154	Plus	152272-152483,157312-157418,158025-158205,158838-158974,160716-160952
401269	8954206	Plus	2259-2591
401283	9800093	Minus	47256-47456
401373	7248205	Minus	84211-84336
401405	7768126	Minus	69276-69452,69548-69958
401465	6682292	Plus	25676-25800
401492	7341778	Plus	171020-171282,171858-172241
401521	7705251	Plus	9127-9234
401566	8469090	Minus	96277-96420,96979-97160
401575	7229804	Minus	76253-76364
401589	9966292	Plus	135969-136263
401628	8575954	Minus	210617-210796
401657	9100664	Minus	7312-8163
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401757	7239630	Plus	88641-88751
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401789	7249213	Minus	70399-70629,70941-71055
401809	7342191	Minus	107548-108298
401847	7139731	Plus	85447-85593
401887	7229981	Plus	93973-94120
401913	9369520	Minus	33753-33904
401962	3176728	Minus	71433-71648,76711-76833,78677-78845,79585-79763,82349-82485
401991	4156128	Plus	2398-2513
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402023	7528158	Minus	132872-133040
402066	6649269	Plus	135543-136031
402071	8117361	Plus	85924-86039
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402131	7704961	Minus	33114-33209,33496-33678
402144	7242326	Plus	115425-115977
402203	8576119	Minus	8124-8285
402277	2894631	Plus	16980-17152,17933-18018,18170-18306
402292	2447220	Plus	33880-34029,34176-34336,34953-35103
402297	6598824	Plus	35279-35405,35573-35659
402407	3962498	Minus	115812-116187
402421	9796341	Minus	46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924
402427	9796372	Plus	16266-16431
402430	9796372	Minus	62382-62552
402520	7596899	Minus	171761-171996
402538	9801137	Minus	96314-96539
402543	9838066	Minus	89684-90893
402570	9884747	Minus	12649-12866
402585	9908890	Minus	174893-175050,183210-183435
402639	9958129	Minus	20167-22383
402694	8569867	Plus	2218-2440
402699	8570304	Minus	182773-182883,184551-184732
402738	7331557	Minus	8725-8859
402855	9662953	Minus	59763-59909
402869	6434643	Minus	138639-139335
402939	9187334	Minus	18329-18535
402944	9368423	Plus	110411-110716,111173-111640
402948	9368458	Minus	143456-143626,143808-143935
402958	9368493	Plus	13324-13507
403010	3132346	Plus	78385-79052
403036	3132360	Plus	66545-66712
403051	4827080	Minus	5269-5411
403065	8954197	Minus	71615-71773,73930-74144
403077	8954241	Plus	146923-147222,147326-147628
403093	8954241	Plus	177083-177373,177464-177751
403151	7407965	Minus	14055-14264
403153	9799871	Minus	42232-43389
403177	9838213	Minus	142560-142726
403223	7630969	Plus	81529-81692
403234	7637801	Plus	180641-180822
403273	8018055	Plus	133809-134099
403286	8080320	Plus	118369-118872

403287	8080320	Minus	126097-126411
403348	7239527	Plus	13809-13968
403359	8570207	Minus	108939-109229
403362	8571772	Plus	64099-64260
403447	9837821	Minus	159072-159387
403508	7630896	Plus	5570-5719
403582	8101186	Plus	18308-18458
403613	8493504	Plus	81290-81465
403642	8699671	Plus	7062-7311
403662	5823349	Plus	58627-59062,59222-59548
403674	7321642	Plus	104988-105623,107394-107590
403687	7387384	Plus	9009-9534
403695	3046276	Plus	168272-168514
403703	4966380	Plus	83681-84042
403741	7630932	Minus	2833-3468
403747	7658395	Minus	20493-20621
403766	7229888	Plus	136283-136830
403786	8083636	Minus	73028-73217
403796	8099896	Minus	75073-77664
403833	887461	Plus	13522-13664
403852	7708872	Minus	124007-124202
403861	7708966	Plus	58363-58649
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
403924	7711688	Minus	89369-89592
403964	7596976	Plus	178174-178300
404034	8567760	Minus	44635-47010
404067	3282162	Plus	1415-2071
404097	7770701	Plus	55512-55781
404122	9796270	Plus	90540-92977
404230	7981448	Minus	92934-93093
404239	5002624	Plus	94841-95095
404240	5002624	Minus	116132-116407,116653-116922
404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
404356	7630858	Minus	126433-126623
404600	8705107	Plus	118354-118444,118649-118792
404601	8705107	Plus	128449-128693,129085-129249,130525-130733
404638	9796751	Minus	99433-99528,100035-100161
404666	7272179	Minus	18677-18993
404675	9797204	Minus	48532-48645,49808-49975,51088-51369,54944-55063
404727	8081050	Plus	115534-115747
404750	7596836	Plus	181879-182198
404763	7882612	Plus	50981-51392
404767	7882827	Minus	23244-23759
404828	6580415	Minus	26291-27253
404850	5420148	Minus	35145-35413,40635-41062
404881	5931510	Minus	36360-36608
404890	7329390	Plus	101280-101408
404971	3212939	Minus	74585-75532
405022	7330304	Plus	217163-217439
405028	7533974	Minus	110588-110847,110933-111115
405071	7708797	Minus	11115-11552
405088	8072518	Minus	115690-117621
405133	8516055	Minus	28127-28288
405138	8576241	Plus	90303-90516
405183	7209940	Plus	12335-12653
405194	7230072	Plus	190465-190645,193346-193610
405196	7230083	Minus	135716-135851
405208	7230142	Plus	8068-8214
405226	7248966	Plus	53547-54128
405227	6731245	Minus	22550-22802
405256	7329310	Plus	26070-26309
405277	3980473	Plus	23471-23572
405307	3638954	Plus	39195-39429
405311	3638954	Plus	46313-46496
405333	3165399	Plus	149905-150215
405411	3451356	Minus	17503-17778,18021-18290
405423	4753276	Plus	6162-6983
405491	5801645	Plus	81857-82045
405501	9211311	Minus	49085-49400,49565-49679,50117-50262
405515	9454624	Plus	37329-37469
405545	1054740	Plus	118677-118807,119091-119296,121626-121823
405580	4512267	Plus	169232-169647
405586	5002511	Plus	38810-39017
405600	5923640	Plus	26662-27225
405610	5757553	Minus	71907-72080
405639	5091650	Plus	211184-211350
405687	6249668	Minus	54787-54891,55844-55917
405699	4165331	Plus	100727-100859
405783	5738434	Minus	27238-27885
405867	6758731	Minus	74553-75173
406086	7107817	Plus	9418-9573
406124	9149714	Minus	1331-1774
406130	9161404	Minus	32394-32498
406140	9168231	Minus	49887-50219

406160	7144945	Plus	55498-56268
406207	5923650	Minus	162607-162800
406215	7342161	Plus	310-432
406268	6682695	Minus	6605-7072
406277	5686030	Minus	4759-5490
406326	9212385	Plus	84508-84655
406388	9256205	Plus	85153-85277
406457	9755793	Plus	44966-45406
406473	9795566	Minus	109669-109931
406537	7711478	Plus	32904-33017
406571	7711622	Minus	65634-65912,66116-66596
406580	7711838	Minus	96654-97640

TABLE 4A lists about 131 genes up-regulated in ovarian cancer compared to normal ovaries that are likely to be extracellular or cell-surface proteins. These were selected as for Table 3A, except that the ratio was greater than or equal to 10, and the predicted protein contained a PFAM domain that is indicitive of extracellular localization.

TABLE 4A: ABOUT131 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL OVARY
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: Unigene Title
PFAM domains
ratio: tumor vs. normal ovary

Pkey	Ex. Accn	UG ID	Title	PFAM	ratio
403077			predicted exon	fn3	15.0
426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TP	Kunitz_BPTI	14.9
403089			predicted exon	fn3	14.9
457148	AF091035	Hs.184627	KIAA0118 protein	arf;ras	14.8
431176	AI026984	Hs.293662	ESTs	laminin_EGF;laminin_B;	14.8
434293	NM_004445	Hs.3796	EphB6	fn3;pkinase;EPH_lbd	14.8
408482	NM_000676	Hs.45743	adenosine A2b receptor	7tm_1	14.6
428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	7tm_1	14.5
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) ho	EGF	14.4
423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxy	sugar_tr;MCT	14.3
422125	NM_003459	Hs.111967	solute carrier family 30 (zinc transporte	Cation_efflux	14.2
407483	NM_012368		(NONE)	7tm_1	14.2
446689	AW594695	Hs.167046	ESTs	7tm_1	14.1
410184	AW503667	Hs.59545	ring finger protein 15	zf-C3HC4;SPRY;zf-B_box	14.0
423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermoly	fn3;vwa	14.0
405448	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp5	trypsin;sushi;CUB	14.0
450684	AA872605	Hs.25333	interleukin 1 receptor, type II	ig	14.0
406692	L36607		gb:Homo sapiens (clone 22) pregnancy	ig	13.9
425549	U64863	Hs.158297	programmed cell death 1	ig	13.8
452755	AW136937	Hs.213436	ESTs	cystatin	13.8
427637	AK000816	Hs.179986	flotillin 1	Band_7	13.7
424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	7tm_1	13.7
405024			predicted exon	TGF-beta;TGFb_propeptide	13.7
405285			predicted exon	A2M;A2M_N	13.7
412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lym	7tm_1	13.7
420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascu	cadherin;Cadherin_C_term	13.6
420511	AF052692	Hs.98485	gap junction protein, beta 4 (connexin 3	connexin	13.5
448638	R17122	Hs.21639	nuclear protein, marker for differentiat	ig	13.4
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	EGF;DSL	13.4
439285	AL133916	Hs.298998	ESTs	ig;pkinase;LRRNT;LRRCT	13.4
424283	AA338246	Hs.301678	ESTs	E1-E2_ATPase;Hydrolase	13.3
436233	AI742878	Hs.124116	ESTs	ig	13.3
443859	NM_013409	Hs.9914	follistatin	kazal	13.2
410016	AA297977	Hs.57907	small inducible cytokine subfamily A (	IL8	13.2
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologo	IL8	13.2
400242			predicted exon	Ephrin	13.0
429057	AF156557	Hs.194816	stomatin-like protein 1	Band_7;SCP2	12.9
438294	AI693753	Hs.143004	ESTs	E1-E2_ATPase;Hydrolase	12.9
458493	AV649408	Hs.282418	ESTs	RYDR_ITPR	12.8
444181	AB033063	Hs.10491	KIAA1237 protein	fn3;ig;PH;RhoGEF	12.8
422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin	cadherin	12.7
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	serpin	12.7
407000	U12139		gb:Human alpha1(XI) collagen (COL1	TSPN;Collagen;COLFI	12.6
417064	W02903	Hs.15440	ESTs	lectin_c	12.6
439389	AA318940	Hs.56004	ESTs	hemopexin;Peptidase_M10	12.6
407786	AA687538	Hs.38972	tetraspan 1	transmembrane4	12.5
410498	AA355749		gb:EST64459 Jurkat T-cells VI Homo	aa_permeases	12.5
422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	vwd	12.5
422330	D30783	Hs.115263	epiregulin	EGF	12.5
402425			predicted exon	ion_trans	12.4
414875	H42679	Hs.77522	major histocompatibility complex, clas	ig	12.2
424239	M67439	Hs.143526	dopamine receptor D5	7tm_1	12.2
442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	EGF;ank;notch	12.2
405368			predicted exon	7tm_1	12.2
402406			predicted exon	Gal-bind_lectin	12.1
426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteoge	TGF-beta;TGFb_propeptide	12.1
406811	U82979	Hs.67846	leukocyte immunoglobulin-like recepto	ig	12.0
416441	BE407197		gb:601301552F1 NIH_MGC_21 Homo	SDF	12.0

433221	AB040917	Hs.97860	KIAA1484 protein	fn3;ig;LRRCT	11.9
442915	AA852875	Hs.8850	a disintegrin and metalloproteinase dom	disintegrin;Reprolysin;	11.9
423613	AF036035	Hs.129910	hyaluronoglucosaminidase 3	ig;Sema;Acetyltransf	11.9
411213	AA676939	Hs.69285	neuropilin 1	CUB;MAM;F5_F8_type_C	11.9
425483	AF231022	Hs.301273	Homo sapiens protocadherin Fat 2 (FA	EGF;cadherin;laminin_G	11.8
421258	AA286731		gb:zs53d08.r1 NCI_CGAP_GCB1 Hom	7tm_3	11.8
423795	AW849759		gb:IL3-CT0216-240200-077-C04 CT0	arf;ras	11.7
422424	AI186431	Hs.116577	prostate differentiation factor	TGF-beta	11.7
443296	AI765286		gb:wi73b05.x1 NCI_CGAP_Kid12 Ho	ig	11.7
448999	AF179274	Hs.22791	transmembrane protein with EGF-like	kazal	11.7
414878	AA341040	Hs.77541	ADP-ribosylation factor 5	arf;ras	11.5
429344	R94038	Hs.199538	inhibin, beta C	TGF-beta	11.5
402114			predicted exon	laminin_EGF;laminin_G	11.5
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (	IL8	11.5
430263	D12614	Hs.36	lyphotoxin alpha (TNF superfamily, m	TNF	11.4
400464			predicted exon	Peptidase_S9	11.4
456841	AA875863	Hs.152345	poliovirus receptor-related 1 (herpesvir	ig	11.4
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kal	laminin_EGF;laminin_B	11.4
418043	AW377752	Hs.83341	H.sapiens mRNA for tyrosine kinase re	fn3;ig;pkinase	11.3
426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrog	Na_H_Exchanger	11.3
446051	BE048061	Hs.153315	ESTs	Reprolysin;disintegrin	11.3
439710	AF086543		gb:Homo sapiens full length insert cDN	Xlink	11.3
416602	NM_006159	Hs.79389	nel (chicken)-like 2	vwc;TSPN	11.3
418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	integrin_B	11.3
425721	AC002115	Hs.159309	uroplakin 1A,	transmembrane4;COX6B;Ets	11.2
409757	NM_001898	Hs.123114	cystatin SN	cystatin	11.2
430630	AW269920	Hs.2621	cystatin A (stefin A)	7tm_3;ANF_receptor	11.2
429630	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perleca	laminin_EGF;ig;ldl_recept_a	11.1
427289	AI097346	Hs.174203	solute carrier family 1 (glutamate/neutr	SDF	11.1
401248	AB028989	Hs.88500	mitogen-activated protein kinase 8 inte	vwa;vwd;TIL	11.1
412627	BE391959	Hs.74276	chloride intracellular channel 1	G-patch;ig;MutS_C	11.1
420104	U09825	Hs.1287	zinc finger protein 173	zf-C3HC4;SPRY;zf-B_box	11.1
405275	AB028989	Hs.88500	mitogen-activated protein kinase 8 inte	vwa;vwd;TIL	11.1
425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	7tm_1	11.1
446745	AW118189	Hs.156400	ESTs	vwa	11.1
441834	AL138034	Hs.7979	KIAA0736 gene product	sugar_tr	11.0
450986	BE241845	Hs.25744	Novel human gene mapping to chomos	PH;RhoGAP;Gal-bind_lectin	11.0
416118	N52773	Hs.167721	ESTs	hemopexin;Peptidase_M10	11.0
443071	AL080021	Hs.8986	complement component 1, q subcompo	C1q;Collagen	10.9
431247	AL021578	Hs.278489	matrilin 4	EGF;vwa	10.9
431449	M55994	Hs.256278	tumor necrosis factor receptor superfam	TNFR_c6	10.9
457044	S73899	Hs.2131	arginine vasopressin receptor 1A	7tm_1	10.9
416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocyte	ig	10.8
402172			predicted exon	ig	10.7
424218	AF031824	Hs.143212	cystatin F (leukocystatin)	cystatin	10.6
409208	Y00093	Hs.51077	integrin, alpha X (antigen CD11C (p15	vwa	10.6
426330	M77235	Hs.169331	sodium channel, voltage-gated, type V,	ion_trans;IQ	10.6
439758	AA845235	Hs.124470	ESTs	transmembrane4	10.6
412429	AV650262	Hs.75765	GRO2 oncogene	IL8	10.6
449987	AW079749	Hs.184719	ESTs, Weakly similar to AF116721 11	ABC_tran;ABC_membrane	10.6
432408	N39127	Hs.76391	myxovirus (influenza) resistance 1, hom	ion_trans;K_tetra	10.6
406672	M26041	Hs.198253	major histocompatibility complex, clas	ig;MHC_II_alpha	10.5
419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like	kazal;thyroglobulin_1	10.5
419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	fn3;wap	10.5
425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	fn3;ig;Y_phosphatase;MAM	10.5
423869	BE409301	Hs.134012	C1q-related factor	GTP_EFTU;EFG_C	10.4
430209	AF177941	Hs.235368	Pro-(alpha)3(V) collagen	Collagen;COLFI;TSPN	10.4
400834			predicted exon	IRK	10.4
442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	Cys_knot;tsp_1;vwc;IGFBP	10.4
403691			predicted exon	tsp_1;Reprolysin;	10.4
430776	AJ011021	Hs.247905	potassium voltage-gated channel, subfa	ion_trans	10.3
432342	AL036128	Hs.274404	plasminogen activator, tissue	EGF;fn1;kringle;trypsin	10.3
413731	BE243845	Hs.75511	connective tissue growth factor	Cys_knot;tsp_1;vwc	10.3
423309	BE006775	Hs.126782	sushi-repeat protein	sushi;HYR	10.3
431728	NM_007351	Hs.268107	multimerin	EGF;C1q	10.3
450245	AA007536	Hs.271767	ESTs, Moderately similar to ALU1_HU	ig	10.2
446983	AA157484	Hs.97199	complement component C1q receptor	EGF;Xlink	10.2
414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	death;ank;ZU5	10.1
400253			predicted exon	7tm_1	10.0
406694	M94891	Hs.225932	pregnancy specific beta-1-glycoprotein	ig	10.0
418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1	EGF	10.0
410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22	10.0
427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	pkinase;ig	10.0

TABLE 4B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410498	120611_1	AA355749 AA085520 AW966333 AA340319 BE170936
416441	159480_1	BE407197 AA182474 AA180369 BE275628 BE276131
421258	200725_1	AA286731 AA287621 AW188228 AW137774
423795	232093_1	AW849759 AW849758 T89549 AA331069

439710	47550_1	AF086543 W96291 W96225
443296	56539_2	AI765286 AW297086 BE568658

TABLE 4C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400464	9929670	Plus	22074-22214
400834	8705192	Plus	121963-122288
402114	8318586	Plus	71578-71715
402172	8575911	Minus	143378-143671
402406	3970929	Plus	10872-11123,12932-13048
402425	9796347	Minus	50224-50395
403077	8954241	Plus	146923-147222,147326-147628
403089	8954241	Plus	171964-172239
403691	7387384	Minus	88280-88463
405024	7107727	Plus	88500-88697
405285	6139075	Minus	55744-55903,57080-57170,61478-61560
405368	2104517	Plus	46055-47188

TABLE 5A lists about 685 genes down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 3A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal ovary).

TABLE 5A: 685 DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene Title
ratio: ration normal ovary vs tumor

Pkey	Ex. Accn	UG ID	Title	ratio
421013	M62397	Hs.1345	mutated in colorectal cancers	14.8
439360	AA448488	Hs.55346	ESTs, Weakly similar to Z141_HUMAN ZINC FINGE	12.8
407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, member 2	12.6
424851	AA676441	Hs.119059	ESTs	11.6
455056	AW853057		gb:RC1-CT0249-170200-025-h04 CT0249 Homo sapie	11.5
420727	H75701	Hs.99886	complement component 4-binding protein, beta	11.3
451617	C01056	Hs.168000	ESTs	10.0
401308			predicted exon	9.9
440987	AA911705	Hs.130229	ESTs	9.7
409725	T40760	Hs.90459	EST	9.7
415752	BE314524	Hs.78776	putative transmembrane protein	9.7
437690	AA804362	Hs.180544	ESTs	9.6
437787	AI908263	Hs.291625	ESTs	9.5
459054	AW798466	Hs.82396	2',5'-oligoadenylate synthetase 1	9.2
435330	R16769	Hs.185689	ESTs	9.2
436642	AA724430	Hs.127960	ESTs	9.1
453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2) Homo sa	9.1
451683	AI808964	Hs.207673	ESTs	9.1
401464	AF039241	Hs.9028	histone deacetylase 5	9.0
436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Hom	8.7
410758	BE535988		gb:601062418F1 NIH_MGC_10 Homo sapiens cDNA	8.7
412637	AA115097	Hs.261313	ESTs	8.4
419166	AA234638	Hs.293584	ESTs	8.3
423739	AA398155	Hs.97600	ESTs	8.1
413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	8.1
416211	R14625		gb:yg45c03.r1 Soares infant brain 1NIB Homo sapiens	8.0
443131	AI033833	Hs.132689	ESTs	7.9
415866	T10115	Hs.92423	KIAA1566 protein	7.9
410130	AI912097	Hs.163208	ESTs	7.9
439426	AI131502	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE	7.8
408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	7.7
419015	T79262	Hs.14463	ESTs	7.6
441573	BE563966	Hs.6529	ESTs	7.5
419386	AA236867	Hs.143868	ESTs	7.5
430562	D78260	Hs.285097	ESTs	7.5
434738	AA836265		gb:od17e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	7.4
403283			predicted exon	7.4
415861	Z43123	Hs.144513	ESTs	7.4
412732	AW993300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo sapie	7.4
441247	AW118681	Hs.128051	ESTs	7.4
442865	N57659	Hs.114541	ESTs, Weakly similar to neuronal thread protein AD7c-	7.3
409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo sapie	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens cDNA	7.3
421418	AA806639		gb:ob88g05.s1 NCI_CGAP_GCB1 Homo sapiens cDN	7.2
413597	AW302885	Hs.117183	ESTs	7.2
454102	AW752363		gb:RC0-CT0201-270999-011-f03 CT0201 Homo sapien	7.1
445487	AI806287	Hs.201217	ESTs	7.1
457604	AI004397	Hs.130558	ESTs, Weakly similar to similar to O-sialoglycoprotein	7.1

400942			predicted exon	6.9
407596	R86913		gb:yq30f05.r1 Soares fetal liver spleen 1NFLS Homo sa	6.9
422046	AI638562		gb:ts50a10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA c	6.9
441284	AA927676	Hs.196542	ESTs	6.9
446224	AW450551	Hs.13308	ESTs	6.9
424943	AU077260	Hs.153924	death-associated protein kinase 1	6.9
453967	AW009077	Hs.232947	ESTs	6.9
448683	AA167642	Hs.14632	ESTs	6.8
431877	AA521204	Hs.105507	ESTs	6.8
411337	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapie	6.8
410596	AA374186		gb:EST86290 HSC172 cells I Homo sapiens cDNA 5' e	6.8
417762	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937233) Homo	6.7
406364			predicted exon	6.7
452238	F01811	Hs.187931	ESTs, Moderately similar to S22703 voltage-gated pota	6.7
415288	R15794	Hs.141027	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	6.7
407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cds.	6.7
439126	AF085984		gb:Homo sapiens full length insert cDNA clone YT99F	6.6
452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapiens cDNA	6.6
431800	AW452768	Hs.162045	ESTs	6.5
426380	AI291267	Hs.149990	ESTs, Weakly similar to unnamed protein product [H.sa	6.5
449529	AI990559	Hs.232033	ESTs	6.4
437755	AW204256	Hs.291887	ESTs	6.4
448307	AI480289	Hs.211026	ESTs	6.4
439586	AA922936	Hs.110039	ESTs	6.4
420051	N35696	Hs.44745	ESTs	6.4
425806	AI522299	Hs.173369	ESTs	6.4
433923	AI823453	Hs.146625	ESTs	6.4
408159	H63977	Hs.118526	ESTs	6.3
434844	AF157116	Hs.301355	hypothetical protein LOC56757	6.3
430197	AA468888	Hs.187697	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	6.3
440332	AI218517	Hs.188051	ESTs	6.3
450061	AI797034	Hs.201115	ESTs	6.3
454994	AW850176		gb:IL3-CT0219-271099-022-H04 CT0219 Homo sapien	6.3
402105			predicted exon	6.3
409090	W56067	Hs.103105	ESTs	6.2
405752			predicted exon	6.2
408074	R20723	Hs.124764	ESTs	6.2
459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	6.1
416310	T81421	Hs.221396	ESTs	6.1
421976	AL138443	Hs.23450	mRNA for FLJ00023 protein	6.1
429755	NM_001364	Hs.215839	discs, large (Drosophila) homolog 2 (chapsyn-110)	6.0
448732	BE614063		gb:601503993F1 NIH_MGC_71 Homo sapiens cDNA	6.0
453909	AW004045	Hs.203365	ESTs	6.0
431178	AA493884	Hs.218008	Homo sapiens cDNA: FLJ21440 fis, clone COL04389	6.0
449671	AW959755	Hs.288896	Homo sapiens cDNA FLJ12977 fis, clone NT2RP20062	6.0
421349	W01715	Hs.102958	ESTs, Weakly similar to Lpg6p [S.cerevisiae]	6.0
453282	AK000043	Hs.32922	hypothetical protein FLJ20036	5.9
420618	AA278781	Hs.280698	ESTs	5.9
412480	BE142364		gb:CM0-HT0143-270999-062-d12 HT0143 Homo sapi	5.9
449858	AW205979	Hs.196065	ESTs	5.9
429884	AL049925	Hs.225984	DKFZP547G0910 protein	5.9
416453	H56968	Hs.114593	ESTs	5.9
459497	AA825742	Hs.87517	ESTs	5.9
433773	AA759293	Hs.112692	ESTs	5.9
458942	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (meltrin a	5.9
436054	AI076262	Hs.119813	ESTs	5.9
410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF H	5.8
403277			predicted exon	5.8
444302	AI140115	Hs.225130	ESTs	5.8
439834	AI754576	Hs.124523	ESTs	5.8
404020			predicted exon	5.8
454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and coiled/coil domains 1(cy	5.7
430922	AW373747	Hs.183337	ESTs	5.7
420289	N55394	Hs.96398	8-oxoguanine DNA glycosylase	5.7
428498	AA429575	Hs.243032	ESTs	5.7
445597	H65649		gb:yr72d10.r1 Soares fetal liver spleen 1NFLS Homo sa	5.7
411543	AW851248		gb:IL3-CT0220-160200-066-F01 CT0220 Homo sapien	5.7
408354	AI382803	Hs.159235	ESTs	5.7
444431	AW513324	Hs.42280	ESTs	5.7
406605			predicted exon	5.7
405541	AF039241	Hs.9028	histone deacetylase 5	5.6
458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKHEAD	5.6
454529	Z45439	Hs.270425	ESTs	5.6
445832	AI261545		gb:qz30a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA	5.6
441223	AI475067	Hs.132499	ESTs	5.6
432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	5.6
443650	AI698330	Hs.151444	ESTs	5.6
403714			predicted exon	5.6
444165	AL137443	Hs.10441	hypothetical protein FLJ11236	5.6
458914	BE327696	Hs.280922	ESTs	5.6
420620	AA278807	Hs.173343	ESTs	5.5
458228	AA934995	Hs.184846	ESTs, Weakly similar to R28830 1 [H.sapiens]	5.5
448067	R68568	Hs.183373	src homology 3 domain-containing protein HIP-55	5.5
427000	AI187420	Hs.145221	ESTs	5.5

452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W Homo sa	5.5
459359	N99545		gb:za40a05.r1 Soares fetal liver spleen 1NFLS Homo sa	5.5
408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.5
450938	AW753734	Hs.277215	ESTs	5.5
431888	H99557	Hs.2864	early endosome antigen 1, 162kD	5.4
459418	W96550	Hs.26418	ESTs	5.4
416718	R83017	Hs.204828	ESTs	5.4
413236	H16442	Hs.127376	KIAA0266 gene product	5.4
439063	AF085922	Hs.113968	ESTs	5.4
446361	AI291234	Hs.282241	ESTs	5.4
458253	AW296952	Hs.196802	ESTs	5.4
433682	AA642418	Hs.17381	ESTs	5.4
455790	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo sapie	5.4
445755	AW294870	Hs.223672	ESTs	5.3
436513	AJ278110	Hs.125507	DEAD-box protein	5.3
416671	N94087	Hs.26073	ESTs, Moderately similar to HG14_HUMAN NONHIS	5.3
440231	AW015420	Hs.163323	ESTs	5.3
429866	AA460104	Hs.99540	ESTs	5.3
437779	AA345232	Hs.21227	ESTs	5.3
424029	AB014594	Hs.137579	KIAA0694 gene product	5.3
425614	AI334963	Hs.156256	ESTs	5.3
430653	AW902062	Hs.30280	ESTs	5.2
408855	T83061	Hs.279604	desmin	5.2
410454	AW749041		gb:RC3-BT0319-100100-012-c05 BT0319 Homo saple	5.2
438116	AI904105	Hs.122016	ESTs	5.2
409138	W73159	Hs.58290	ESTs	5.2
423047	NM_005323	Hs.123064	H1 histone family, member T (testis-specific)	5.2
440212	AW300959	Hs.126216	ESTs, Weakly similar to good similarity to E. coli hypo	5.2
404108			predicted exon	5.2
456253	T12198		gb:A588F Heart Homo sapiens cDNA clone A588, mRN	5.2
409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	5.1
444013	T08531	Hs.44404	hypothetical protein PRO1488	5.1
454071	AI041793	Hs.42502	ESTs	5.1
419761	M17373	Hs.93177	interferon, beta 1, fibroblast	5.1
451250	AA491275	Hs.236940	Homo sapiens cDNA FLJ12542 fis, clone NT2RM4000	5.1
405290			predicted exon	5.1
454487	AW796342		gb:PM2-UM0027-230200-002-h02 UM0027 Homo sap	5.1
444131	AI806600	Hs.207119	EST, Weakly similar to intrinsic factor-B12 receptor pr	5.1
441679	BE502267	Hs.65996	ESTs	5.1
450077	AA523752	Hs.120855	ESTs	5.1
421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	5.1
445140	AI650599	Hs.197913	ESTs	5.1
421126	M74587	Hs.102122	insulin-like growth factor binding protein 1	5.1
447037	AI357568	Hs.157612	ESTs	5.1
407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB Homo sapiens	5.0
436196	AK001084		gb:Homo sapiens cDNA FLJ10222 fis, clone HEMBB1	5.0
442772	AW503680	Hs.300513	ESTs, Weakly similar to T15B7.2 [C.elegans]	5.0
444138	AI701572	Hs.151153	ESTs	5.0
458589	AV654623	Hs.288141	Homo sapiens cDNA FLJ13016 fis, clone NT2RP30006	5.0
451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on chromos	5.0
441318	AI078234	Hs.176130	ESTs	5.0
407490	S79281		gb:pancreatic ribonuclease [human, mRNA Recombinan	4.9
438224	AA933999		gb:on91f04.s1 Soares_NFL_T_GBC_S1 Homo sapiens	4.9
451638	AW798466	Hs.82396	2',5'-oligoadenylate synthetase 1	4.9
457356	AA489621	Hs.191670	ESTs	4.9
430679	R44428	Hs.22801	ESTs	4.9
445747	AI820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	4.9
409036	T88693	Hs.226410	ESTs	4.9
433382	T64293	Hs.291453	ESTs	4.9
401287			predicted exon	4.9
424188	AW954552	Hs.142634	zinc finger protein	4.9
404868			predicted exon	4.9
410152	AW593104	Hs.23681	ESTs	4.9
444997	AI204451	Hs.146196	ESTs	4.9
431075	BE267477		gb:601189542F2 NIH_MGC_7 Homo sapiens cDNA cl	4.8
429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolog 6	4.8
414337	BE386606		gb:601273980F1 NIH_MGC_20 Homo sapiens cDNA	4.8
410336	BE391510	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	4.8
445283	AW515763	Hs.246872	ESTs	4.8
434792	AA649253	Hs.132458	ESTs	4.8
433403	AF040247		gb:Homo sapiens erythroid differentiation-related factor	4.8
454940	AW846202		gb:QV0-CT0179-011299-061-f10 CT0179 Homo saple	4.8
455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo sapl	4.8
416437	N48990	Hs.37204	ESTs	4.8
433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo sapiens cDNA	4.8
434977	AI734233	Hs.226142	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	4.8
416192	NM_005036	Hs.998	peroxisome proliferative activated receptor, alpha	4.8
459218	AA812633	Hs.10845	ESTs	4.8
402109			predicted exon	4.8
444490	AI151080	Hs.146830	ESTs	4.8
432632	AW973801	Hs.134656	ESTs	4.8
438683	AA813982	Hs.291842	ESTs	4.8
404044			predicted exon	4.8
449862	AI672277	Hs.199475	ESTs	4.8

419002	T78625	Hs.268594	ESTs	4.7
425582	AL157686	Hs.293737	ESTs	4.7
416086	H18252	Hs.227263	ESTs	4.7
441133	AA918191	Hs.194457	ESTs	4.7
446323	AI288274	Hs.149868	ESTs	4.7
440347	AI125590	Hs.142864	ESTs	4.7
439481	AF086294	Hs.125844	ESTs	4.6
456388	W28557		gb:48d8 Human retina cDNA randomly primed sublibra	4.6
441864	R34177	Hs.181315	ESTs, Moderately similar to ALU4_HUMAN ALU SU	4.6
445910	R93483	Hs.260273	ESTs	4.6
403531			predicted exon	4.6
429773	AI332482	Hs.218791	proteoglycan 4, (megakaryocyte stimulating factor, artic	4.6
422563	BE299342	Hs.19348	Homo sapiens cDNA FLJ13119 fis, clone NT2RP30026	4.6
422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial carrier; phospha	4.6
453663	AL048807	Hs.180714	cytochrome c oxidase subunit VIa polypeptide 1	4.6
447839	N72050	Hs.164144	ESTs	4.5
415612	F12893	Hs.13301	ESTs	4.5
433371	T25451		gb:PTHI188 HTCDL1 Homo sapiens cDNA 5'/3' simila	4.5
410667	AW936099		gb:QV0-DT0020-210100-095-d04 DT0020 Homo sapie	4.5
410890	AW809575		gb:MR4-ST0121-060200-002-a12 ST0121 Homo sapie	4.5
404451			predicted exon	4.5
441705	AI087052	Hs.55993	ESTs	4.5
439597	W79579	Hs.58552	ESTs	4.5
407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.5
423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) ho	4.5
456278	BE300369	Hs.42643	ESTs, Weakly similar to KIAA1016 protein [H.sapiens	4.5
424719	H90452		gb:yv01c03.r1 Soares fetal liver spleen 1NFLS Homo sa	4.5
439542	AW297571	Hs.17646	ESTs	4.5
444433	AV649844	Hs.282436	ESTs	4.5
438831	BE263273	Hs.301128	ESTs	4.5
410065	AW812744		gb:RC3-ST0186-181099-012-c09 ST0186 Homo sapien	4.5
453895	AA039843	Hs.61948	ESTs	4.5
458250	AI807339	Hs.152174	ESTs, Weakly similar to Z140_HUMAN ZINC FINGE	4.5
423403	AA325483		gb:EST28475 Cerebellum II Homo sapiens cDNA 5' en	4.5
454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo sapien	4.5
445368	AI221631	Hs.166788	ESTs	4.5
401004			predicted exon	4.5
425837	AF007567	Hs.159609	insulin receptor substrate 4	4.5
420497	AW206285	Hs.253548	ESTs	4.5
449438	AA927317	Hs.176719	ESTs	4.5
429409	AI694817	Hs.155980	ESTs	4.5
447959	AI452784	Hs.270270	ESTs	4.4
407340	AA810168	Hs.232119	ESTs	4.4
424326	NM_014479	Hs.145296	disintegrin protease	4.4
443479	AF027219	Hs.9443	zinc finger protein 202	4.4
443246	T75157	Hs.285516	ESTs, Weakly similar to hypothetical protein [H.sapien	4.4
414475	BE302955	Hs.119598	ribosomal protein L3	4.4
432075	AW972934		gb:EST385030 MAGE resequences, MAGM Homo sap	4.4
417906	R24769	Hs.23725	ESTs	4.4
406518	W28077	Hs.79389	nel (chicken)-like 2	4.4
441460	AI962478	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU	4.4
450549	T49427	Hs.181244	major histocompatibility complex, class I, A	4.4
426528	AA380828		gb:EST93827 Activated T-cells VII Homo sapiens cDN	4.4
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo sapi	4.4
408479	BE047329	Hs.144483	ESTs	4.3
448636	AI557139	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PLACE10090	4.3
411280	N50617		gb:yy89h02.r1 Soares_multiple_sclerosis_2NbHMSP H	4.3
440790	AW593050	Hs.128580	ESTs	4.3
458301	AF003834		gb:AF003834 Clontech HI1149x Homo sapiens cDNA	4.3
442277	AW448914	Hs.202391	ESTs	4.3
449463	AI657038	Hs.196109	ESTs	4.3
433426	H69125	Hs.133525	ESTs	4.3
410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fis, clone NT2RM4002	4.3
423040	AA320749	Hs.209464	KIAA1604 protein	4.3
432430	AW079984	Hs.262480	ESTs	4.3
432072	N62937	Hs.269109	ESTs	4.3
452213	AL110237	Hs.28425	Homo sapiens mRNA; cDNA DKFZp566D224 (from c	4.3
403635			predicted exon	4.3
441919	AI553802	Hs.128121	ESTs	4.3
416717	H79559	Hs.297726	ESTs	4.3
430995	NM_005092	Hs.248197	tumor necrosis factor (ligand) superfamily, member 18	4.2
429269	AA449013	Hs.99203	ESTs	4.2
415840	R15955	Hs.21758	ESTs	4.2
451300	AA017066	Hs.237686	EST	4.2
445366	AI221511	Hs.298662	ESTs	4.2
424194	BE245833	Hs.169854	hypothetical protein SP192	4.2
459105	NM_014517	Hs.28423	upstream binding protein 1 (LBP-1a)	4.2
455387	BE069037		gb:QV3-BT0379-161299-040-e12 BT0379 Homo sapie	4.2
410507	AA355288	Hs.271408	ESTs	4.2
453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2) Homo	4.2
450966	AA017245	Hs.32794	ESTs	4.2
432694	AW991585	Hs.276755	ESTs, Weakly similar to F53B1.2 [C.elegans]	4.2
455108	AW856866		gb:RC0-CT0299-291199-031-G02 CT0299 Homo sapie	4.2
443609	AV650231	Hs.282941	ESTs	4.2

427469	AA403084	Hs.269347	ESTs	4.2
417178	N51636		gb:yy87b01.s1 Soares_multiple_sclerosis_2NbHMSP H	4.2
439751	AA196090	Hs.50784	Homo sapiens mRNA full length insert cDNA clone EU	4.2
431982	AW419296	Hs.105754	ESTs	4.1
442641	AI890955	Hs.262983	ESTs	4.1
422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo sapie	4.1
449156	AF103907	Hs.171353	prostate cancer antigen 3	4.1
419668	AI033098	Hs.132777	ESTs	4.1
418236	AW994005	Hs.172572	hypothetical protein FLJ20093	4.1
432663	AI984317	Hs.122589	ESTs	4.1
448313	BE622486	Hs.121688	Homo sapiens cDNA FLJ13463 fis, clone PLACE10034	4.1
411279	AW884776		gb:QV4-OT0067-010300-121-d01 OT0067 Homo sapie	4.1
440652	AI216751	Hs.143977	ESTs	4.1
416608	R11499	Hs.189716	ESTs	4.1
420405	AA743396	Hs.189023	ESTs	4.1
405717			predicted exon	4.1
435267	N23797	Hs.110114	ESTs	4.1
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr virus) recepto	4.1
403560	AI929721	Hs.5120	dynein, cytoplasmic, light polypeptide	4.1
449162	AI632740	Hs.10476	ESTs	4.1
459157	AI904385		gb:CM-BT054-080399-054 BT054 Homo sapiens cDN	4.1
432474	AA584042		gb:nn65e09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA	4.1
455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo sapie	4.0
426456	AA580748	Hs.130658	ESTs	4.0
438597	AA811662	Hs.171497	ESTs	4.0
437934	AW880871	Hs.77496	small nuclear ribonucleoprotein polypeptide G	4.0
459385	BE380047		gb:601159362F2 NIH_MGC_53 Homo sapiens cDNA	4.0
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, sequence 2	4.0
457740	AW500458		gb:UI-HF-BN0-akb-d-07-0-UI.r1 NIH_MGC_50 Homo	4.0
437385	AA757055	Hs.164060	ESTs	4.0
444530	AV650124	Hs.282435	ESTs	4.0
408066	AA046914		gb:zf47h10.r1 Soares retina N2b4HR Homo sapiens cD	4.0
411256	AW834039		gb:QV0-TT0010-091199-053-e09 TT0010 Homo sapie	4.0
433582	BE548749	Hs.148016	ESTs	4.0
438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein [H.sapiens	4.0
414571	BE410746	Hs.22868	protein tyrosine phosphatase, non-receptor type 11	4.0
446190	AI279299	Hs.256564	ESTs	4.0
443542	AI927065	Hs.146040	ESTs	4.0
430444	AW296421	Hs.121035	ESTs	4.0
454573	BE146471		gb:QV0-HT0216-011199-043-c09 HT0216 Homo sapie	4.0
409846	AW501748		gb:UI-HF-BR0p-ajm-b-12-0-UI.r1 NIH_MGC_52 Hom	4.0
456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone HRC02860	4.0
456140	AA169515	Hs.6006	ESTs	4.0
441685	AI459261	Hs.144481	ESTs	4.0
416677	T83470		gb:yd46g06.r1 Soares fetal liver spleen 1NFLS Homo s	4.0
401740			predicted exon	4.0
420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	4.0
442594	AW272467	Hs.254655	Untitled	3.9
426294	AA374185		gb:EST86289 HSC172 cells I Homo sapiens cDNA 5' e	3.9
411922	AW876260		gb:PM4-PT0019-131299-006-E04 PT0019 Homo sapie	3.9
452320	AA042873	Hs.160412	ESTs	3.9
431644	AW972822	Hs.169248	cytochrome c	3.9
409892	AW956113		gb:EST368183 MAGE resequences, MAGD Homo sap	3.9
418132	T92670	Hs.117421	ESTs	3.9
414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (937208) Homo sap	3.9
400196			predicted exon	3.9
416900	M59964	Hs.1048	KIT ligand	3.9
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coil domains, bind	3.9
435957	N39015	Hs.190368	ESTs	3.9
442299	AW467791	Hs.155561	ESTs	3.9
419499	AA808136	Hs.177698	ESTs	3.9
438403	AA806607	Hs.292206	ESTs	3.9
449386	AA001308	Hs.193213	ESTs	3.9
443283	BE568610		gb:601342622F1 NIH_MGC_53 Homo sapiens cDNA	3.9
406481			predicted exon	3.9
453530	AW021633		gb:df26c02.y1 Morton Fetal Cochlea Homo sapiens cDN	3.9
415558	AA885143	Hs.125719	ESTs	3.9
416874	H98752	Hs.42568	ESTs	3.9
454885	AW836922		gb:QV1-LT0036-150200-074-h06 LT0036 Homo sapie	3.9
419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA clon	3.9
440962	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, Secypa Compl	3.9
419401	AW804663		gb:QV4-UM0094-160300-135-d06 UM0094 Homo sap	3.9
406562			predicted exon	3.8
405690	BE409855	Hs.808	heterogeneous nuclear ribonucleoprotein F	3.8
435282	AA677428	Hs.189731	ESTs	3.8
402451			predicted exon	3.8
451577	N69101	Hs.32703	ESTs	3.8
457141	AA521410	Hs.41371	ESTs	3.8
407817	H92553	Hs.40400	ESTs	3.8
412613	AA653507	Hs.285711	Homo sapiens cDNA FLJ13089 fis, clone NT2RP30021	3.8
418355	L42563	Hs.1165	ATPase, H+/K+ transporting, nongastric, alpha polypep	3.8
446357	AW161533	Hs.300866	ESTs	3.8
407448	AJ001865		gb:Homo Sapiens mRNA, partial cDNA sequence for h	3.8
456383	AI148037		gb:qg61e01.r1 Soares_testis_NHT Homo sapiens cDNA	3.8

444651	W58469	Hs.103120	ESTs	3.8
455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo sapie	3.8
442657	BE502631	Hs.130645	ESTs	3.8
429142	AA835639	Hs.104972	ESTs	3.8
429274	AI379772	Hs.99206	ESTs	3.8
437774	AW978199	Hs.291648	ESTs	3.8
427737	AA435988	Hs.178066	ESTs, Weakly similar to AF068289 5 HDCME31P [H.s	3.8
405671			predicted exon	3.8
413627	BE182082	Hs.246973	ESTs	3.8
438858	R37529	Hs.269924	ESTs	3.8
416612	H70565		gb:yr97c04.r1 Soares fetal liver spleen 1NFLS Homo sa	3.8
423045	AW967472	Hs.301511	ESTs, Highly similar to KPT2_HUMAN SERINE/THR	3.8
453361	AA035197	Hs.107375	ESTs	3.7
437243	AA747549	Hs.259122	ESTs	3.7
437987	AW450202	Hs.122963	ESTs	3.7
408781	BE148621	Hs.254602	ESTs	3.7
455895	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo sapie	3.7
431492	AW612343		gb:hg97c10.x1 NCI_CGAP_Kid11 Homo sapiens cDN	3.7
413247	AW963969		gb:EST376042 MAGE resequences, MAGH Homo sap	3.7
422866	NM_002410	Hs.121502	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-g	3.7
431828	AA572994		gb:nm33f12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	3.7
438872	R64197	Hs.23589	ESTs	3.7
438673	AI824717	Hs.123443	ESTs	3.7
416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen 1NFLS Homo sa	3.7
401963			predicted exon	3.7
402867			predicted exon	3.7
408315	AW179148		gb:MR4-ST0067-200899-002-B07 ST0067 Homo sapie	3.7
418320	D86981	Hs.84084	amyloid beta precursor protein (cytoplasmic tail)-bindin	3.7
447199	AI939421	Hs.160900	ESTs	3.7
422590	AA312758	Hs.193945	Homo sapiens cDNA FLJ13962 fis, clone Y79AA10012	3.7
451996	AW514021	Hs.245510	ESTs	3.7
412463	AW953444	Hs.78672	laminin, alpha 4	3.7
440928	AL046575	Hs.130198	ESTs	3.7
441951	W31002	Hs.128195	ESTs	3.7
440705	AA904244	Hs.153205	ESTs	3.7
434231	AF119901	Hs.250568	hypothetical protein PRO2831	3.7
411039	AL135674	Hs.163348	ESTs	3.7
413137	BE066915		gb:PM0-BT0340-231199-001-b07 BT0340 Homo sapie	3.7
417970	AA309234	Hs.57760	Homo sapiens cDNA: FLJ23119 fis, clone LNG07978	3.7
439786	AV652707	Hs.33756	Homo sapiens mRNA full length insert cDNA clone EU	3.7
459595	AL040421		gb:DKFZp434B0714_r1 434 (synonym: htes3) Homo s	3.7
443601	AI078554	Hs.15682	ESTs	3.7
404041			predicted exon	3.6
406122			predicted exon	3.6
404582			predicted exon	3.6
455786	BE090077		gb:RC6-BT0710-300300-021-F02 BT0710 Homo sapie	3.6
411899	AA370573		gb:EST82238 Prostate gland I Homo sapiens cDNA 5' e	3.6
426758	AL036430	Hs.197772	ESTs	3.6
421776	AW301994	Hs.108183	candidate tumor suppressor p33 ING1 homolog	3.6
430169	AA468531	Hs.189047	ESTs	3.6
407695	AI808007	Hs.66450	ESTs	3.6
454564	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapie	3.6
425902	X52509	Hs.161640	tyrosine aminotransferase	3.6
439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN ALU SU	3.6
429066	AA868555	Hs.178222	ESTs	3.6
428690	AI948490	Hs.98765	ESTs	3.6
437302	AA837146	Hs.180275	ESTs	3.6
443973	AI580083	Hs.176154	ESTs	3.6
453993	AW615224	Hs.252839	ESTs	3.6
413623	AA825721	Hs.246973	ESTs	3.6
409196	NM_001874	Hs.169765	carboxypeptidase M	3.6
424916	AW867440	Hs.23096	ESTs	3.6
424769	H06469	Hs.142653	ret finger protein	3.6
400080			predicted exon	3.6
421521	AI638760	Hs.161795	ESTs	3.6
405549			predicted exon	3.6
446114	AI275715	Hs.145926	ESTs	3.6
441392	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERATIN, T	3.6
424025	AI701852	Hs.301296	ESTs	3.5
448527	AI525606		gb:PT1.3_03_G05.r tumor1 Homo sapiens cDNA 5', mR	3.5
437063	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I) binding prot	3.5
449880	AI673006	Hs.231948	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CL	3.5
449311	AI657014		gb:tt49a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA c	3.5
442999	AW662889	Hs.132395	ESTs	3.5
416238	W90448		gb:zh78c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 H	3.5
423209	BE278528	Hs.106823	H.sapiens gene from PAC 42616, similar to syntaxin 7	3.5
409854	AW501833		gb:UI-HF-BR0p-ajo-d-01-0-UI.r1 NIH_MGC_52 Hom	3.5
414941	C14865	Hs.182159	ESTs	3.5
456337	AW751661	Hs.65919	ESTs	3.5
415296	F05086		gb:HSC01A011 normalized infant brain cDNA Homo s	3.5
423338	AB007961	Hs.127338	KIAA0492 protein	3.5
415618	F12954		gb:HSC3GG091 normalized infant brain cDNA Homo s	3.5
405583			predicted exon	3.5
435601	AF217509	Hs.283077	centrosomal P4.1-associated protein; uncharacterized bo	3.5

450867	AA011454	Hs.245122	ESTs	3.5
431339	AA506294	Hs.257266	ESTs	3.5
441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	3.5
431343	AW970603	Hs.300941	Homo sapiens cDNA FLJ11661 fis, clone HEMBA100	3.5
434317	AI674095	Hs.116323	ESTs	3.5
414741	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MAMMA10	3.5
439707	AW297702	Hs.102915	ESTs	3.5
443178	AI631241	Hs.47312	ESTs	3.5
400397	AJ270770	Hs.154485	transcription factor 7-like 2 (T-cell specific, HMG-box)	3.5
455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo sapie	3.5
434362	W27081	Hs.295446	ESTs	3.5
409211	AA078835		gb:zm94h04.s1 Stratagene colon HT29 (937221) Homo	3.5
414390	BE281040		gb:601156234F1 NIH_MGC_21 Homo sapiens cDNA	3.5
457142	AI924353	Hs.290969	EST	3.5
423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	3.5
453363	AI989776	Hs.232623	ESTs	3.5
418913	BE046745		gb:hn39b06.x1 NCI_CGAP_RDF2 Homo sapiens cDN	3.4
440016	AW118114	Hs.137057	ESTs	3.4
405096			predicted exon	3.4
435072	AW592176	Hs.116932	ESTs	3.4
438535	L09078		gb:Homo sapiens mRNA fragment	3.4
424001	W67883	Hs.137476	KIAA1051 protein	3.4
428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.4
410587	AA370706	Hs.11252	ESTs, Weakly similar to Weak similarity with the Ysy6	3.4
454543	AW806895		gb:QV4-ST0023-160400-172-c06 ST0023 Homo sapien	3.4
419515	S81944	Hs.90791	gamma-aminobutyric acid (GABA) A receptor, alpha 6	3.4
410280	AA083558	Hs.261286	ESTs	3.4
425714	AW963278		gb:EST375351 MAGE resequences, MAGH Homo sap	3.4
416895	AW961600		gb:EST373672 MAGE resequences, MAGG Homo sap	3.4
427935	AW503687	Hs.119424	ESTs, Weakly similar to unnamed protein product [H.sa	3.4
411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo sapien	3.4
453339	AW992599	Hs.252797	ESTs	3.4
424696	BE439547	Hs.151903	Homo sapiens clone 24706 mRNA sequence	3.4
436242	AK002187		gb:Homo sapiens cDNA FLJ11325 fis, clone PLACE10	3.4
442837	AI022082	Hs.50492	ESTs	3.4
452807	AA028933	Hs.162434	ESTs	3.4
418110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202 fis, clone HRC01333	3.4
433936	AI208072	Hs.123459	ESTs	3.4
458177	AI744995	Hs.267072	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.4
401896			predicted exon	3.4
406237			predicted exon	3.4
457688	AL110157	Hs.3843	Homo sapiens mRNA; cDNA DKFZp586F2224 (from	3.4
456914	AW363582	Hs.75323	prohibitin	3.4
421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone LNG08361	3.4
419321	N48146	Hs.269069	ESTs	3.4
447876	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase)	3.4
406197			predicted exon	3.4
443005	AI027184	Hs.200918	ESTs	3.4
450078	AI681743		gb:tx38g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	3.4
431301	AA502384	Hs.151529	ESTs	3.4
430202	T85775		gb:yd60g02.r1 Soares fetal liver spleen 1NFLS Homo s	3.4
428559	H24338	Hs.27041	ESTs	3.4
455731	BE072188		gb:QV4-BT0536-211299-055-b09 BT0536 Homo sapie	3.4
420735	AW297440	Hs.88653	ESTs	3.4
430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A receptor, alpha 4	3.3
405836			predicted exon	3.3
449178	AI633748	Hs.197597	ESTs	3.3
453265	U61232	Hs.32675	tubulin-specific chaperone e	3.3
430700	AA768902	Hs.247812	H2A histone family, member K, pseudogene	3.3
424496	AI733451	Hs.129212	ESTs	3.3
446963	AI862668	Hs.176333	ESTs	3.3
422879	AI241409	Hs.188092	ESTs	3.3
419831	AW448930	Hs.5415	ESTs	3.3
449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_1NFLS_S1 H	3.3
406255			predicted exon	3.3
412319	AW936903		gb:RC1-DT0029-030200-012-d02 DT0029 Homo sapie	3.3
401350			predicted exon	3.3
439098	AF085955		gb:Homo sapiens full length insert cDNA clone YR86G	3.3
450589	AI701505	Hs.202526	ESTs	3.3
430749	AJ242956	Hs.25960	v-myc avian myelocytomatosis viral related oncogene, n	3.3
430689	AI695595	Hs.293219	ESTs	3.3
454753	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo sapie	3.3
444479	AA194980	Hs.30818	Homo sapiens cDNA FLJ13681 fis, clone PLACE20000	3.3
413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo sapie	3.3
425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens cDNA 5' end,	3.3
457107	AA418246	Hs.185796	ESTs, Weakly similar to b3418.1 [H.sapiens]	3.3
421480	NM_016158	Hs.104671	erythrocyte transmembrane protein	3.3
444289	BE267060	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	3.3
417725	R25257	Hs.21503	ESTs	3.3
453631	AL046418		gb:DKFZp434N247_r1 434 (synonym: htes3) Homo sa	3.3
450692	H50603	Hs.94037	hypothetical protein FLJ23053	3.3
413357	W47611		gb:zc35e06.r1 Soares_senescent_fibroblasts_NbHSF H	3.3
415327	H22769	Hs.1861	membrane protein, palmitoylated 1 (55kD)	3.3
457569	AW970021	Hs.291120	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	3.3

448601	R61666	Hs.293690	ESTs	3.3
436526	AW993633	Hs.287681	Homo sapiens cDNA: FLJ21685 fis, clone COL09372	3.3
440589	BE397763	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (from	3.3
418768	T39310	Hs.1139	cold shock domain protein A	3.3
426768	AW303337	Hs.270411	ESTs	3.3
400394	AF040257	Hs.283818	Homo sapiens TNF receptor homolog mRNA, partial cd	3.3
433565	AA599763	Hs.112520	ESTs	3.3
424093	AA335025		gb:EST39621 Epididymus Homo sapiens cDNA 5' end,	3.3
449552	AA001742	Hs.83722	ESTs	3.3
431892	AA521315	Hs.194424	ESTs	3.3
405512			predicted exon	3.3
446990	AI354717	Hs.223908	ESTs	3.3
457729	AI821863	Hs.293467	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	3.2
417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	3.2
456420	AW401361	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit,	3.2
403497			predicted exon	3.2
427145	R52635	Hs.25935	ESTs	3.2
406454			predicted exon	3.2
441033	BE562555		gb:601335867F1 NIH_MGC_44 Homo sapiens cDNA	3.2
408444	AW661839	Hs.253204	ESTs	3.2
434739	AA804487	Hs.144130	ESTs	3.2
437060	AA745591	Hs.292063	ESTs	3.2
423092	BE274837	Hs.123637	putative homeodomain transcription factor	3.2
424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-associated glycopr	3.2
443362	AI053464	Hs.166505	ESTs	3.2
437500	AL390150		gb:Homo sapiens mRNA; cDNA DKFZp547L156 (from	3.2
425458	H89317	Hs.182889	ESTs	3.2
439171	AA831133	Hs.294128	ESTs	3.2
407647	AW860158		gb:RC0-CT0379-290100-032-b04 CT0379 Homo sapie	3.2
435608	AW183971	Hs.250896	ESTs	3.2
426743	AA383833	Hs.245022	ESTs	3.2
457525	AW973800		gb:EST385901 MAGE resequences, MAGM Homo sap	3.2
413800	AI129238	Hs.192235	ESTs	3.2
414193	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapiens cDNA	3.2
455565	BE000537		gb:RC3-BN0072-240200-011-d07 BN0072 Homo sapie	3.2
410061	T91029	Hs.15069	ESTs	3.2
450666	T99968	Hs.18799	ESTs	3.2
458529	AV652120	Hs.213232	ESTs	3.2
424751	AA769482	Hs.296320	ESTs	3.2
442225	AI306597	Hs.129192	ESTs	3.2
410990	AW812929		gb:RC3-ST0186-250200-018-c05 ST0186 Homo sapien	3.2
435644	AA700867	Hs.269659	ESTs	3.2
405347			predicted exon	3.2
441202	AI632143	Hs.135853	ESTs	3.2
446694	AV659942	Hs.258132	ESTs	3.2
454652	AW812088		gb:RC4-ST0173-191099-032-a07 ST0173 Homo sapien	3.2
418985	AI042330	Hs.87128	ESTs, Weakly similar to similar to YBS4 YEAST [C.el	3.2
430118	AI377255	Hs.183287	ESTs	3.2
430691	C14187	Hs.103538	ESTs	3.2
416313	H47206	Hs.194109	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CL	3.2
446122	AI362790	Hs.181801	ESTs	3.2
453725	W28543		gb:48c5 Human retina cDNA randomly primed sublibra	3.2
453954	AW118336	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	3.2
428166	AA423849	Hs.79530	M5-14 protein	3.2
447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone CAS05917	3.2
401871			predicted exon	3.2
442160	AI337127	Hs.156325	ESTs	3.2
404708			predicted exon	3.1
412588	AW993055	Hs.44024	ESTs	3.1
431976	AA719001	Hs.291065	ESTs	3.1
408884	AW891024	Hs.281172	ESTs	3.1
433811	AW975015	Hs.123138	ESTs	3.1
431691	AI208511	Hs.292510	ESTs	3.1
418719	AW975590	Hs.161707	ESTs	3.1
431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67 PRO1777 [H	3.1
435699	AI911488	Hs.213724	ESTs	3.1
459344	AW499533	Hs.257976	ESTs	3.1
431729	AW004714	Hs.162033	ESTs	3.1
436771	AW975687	Hs.292979	ESTs	3.1
434480	AW956268	Hs.59395	Homo sapiens clone IMAGE:112574 mRNA sequence	3.1
459547	AI400579	Hs.225186	EST	3.1
427962	AA946582	Hs.133546	Homo sapiens cDNA: FLJ21120 fis, clone CAS05691	3.1
403743			predicted exon	3.1
413560	BE148411		gb:MR0-HT0241-131299-002-f04 HT0241 Homo sapie	3.1
454372	H96643	Hs.283565	FOS-like antigen-1	3.1
450018	AA421642	Hs.24309	hypothetical protein FLJ11106	3.1
428839	AI767756	Hs.82302	ESTs	3.1
407110	AA018042	Hs.95078	ESTs	3.1
436133	T77531	Hs.191124	ESTs	3.1
418872	R94785	Hs.270263	ESTs	3.1
404418			predicted exon	3.1
446877	AI559472	Hs.270720	ESTs	3.1
429053	AA443967	Hs.194114	ESTs	3.1
425189	H16622		gb:ym26c07.r1 Soares infant brain 1NIB Homo sapiens	3.1

404134			predicted exon	3.1
441404	AI638880	Hs.126895	ESTs	3.1
400076			predicted exon	3.1
411876	AW961336	Hs.69705	ESTs, Weakly similar to KIAA0443 [H.sapiens]	3.1
451048	AA013349	Hs.60602	ESTs	3.1
447021	AI356564	Hs.161406	ESTs	3.1
404083			predicted exon	3.0
415833	H05175	Hs.107510	ESTs	3.0
402142			predicted exon	3.0
415820	R53720	Hs.189745	ESTs	3.0
441140	AW016534	Hs.226994	ESTs	3.0
449376	AA001278	Hs.59905	ESTs	3.0
457593	AI738815	Hs.117323	ESTs	3.0
411542	AW850767		gb:IL3-CT0220-031199-025-A05 CT0220 Homo sapien	3.0
403375			predicted exon	3.0
449561	AI022240	Hs.17924	ESTs	3.0
406241			predicted exon	3.0
420306	AA258318	Hs.219226	ESTs	3.0
413161	BE068130		gb:CM2-BT0368-171299-056-a01 BT0368 Homo sapie	3.0
448221	BE622615		gb:601440775T1 NIH_MGC_72 Homo sapiens cDNA	3.0
415920	Z45684		gb:HSCZRD121 normalized infant brain cDNA Homo	3.0
459135	AI902802		gb:RC-BT015-311298-026 BT015 Homo sapiens cDNA	3.0
425357	AA355842		gb:EST64303 Jurkat T-cells VI Homo sapiens cDNA 5'	3.0
454724	AA091228		gb:cchn2152.seq.F Human fetal heart, Lambda ZAP Ex	3.0
429395	AK002071	Hs.201624	hypothetical protein FLJ11209	3.0
427607	AA406119	Hs.270479	ESTs	3.0
443598	AW499970	Hs.14822	ESTs	3.0
437948	AA772920		gb:ae73c09.s1 Stratagene schizo brain S11 Homo sapien	3.0
418105	AW937488	Hs.178000	ESTs	3.0
426763	AL042262	Hs.172101	Human DNA sequence from clone RP1-202I21 on chro	3.0
403473			predicted exon	3.0
427501	AI369280	Hs.131743	ESTs	3.0
453246	NM_000933	Hs.32539	KIAA1264 protein	3.0
404587	M99587	Hs.104134	homeo box (H6 family) 1	3.0
433964	AW241987	Hs.197025	ESTs	3.0
453472	AL037925		gb:DKFZp564M037_r1 564 (synonym: hfbr2) Homo sa	3.0
433183	AF231338	Hs.222024	transcription factor BMAL2	3.0
435899	W89093	Hs.189914	ESTs	3.0
425626	AI537536	Hs.173519	ESTs	3.0
428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, noncatalytic acc	3.0
426593	AW958560		gb:EST370630 MAGE resequences, MAGE Homo sapi	3.0
431899	AA521381	Hs.187726	ESTs	3.0
422406	AF025441	Hs.116206	Opa-interacting protein 5	3.0
448178	AI479482	Hs.170789	ESTs	3.0
404227			predicted exon	3.0
440575	AA889870	Hs.126006	ESTs	3.0
431198	AL047634	Hs.231913	ESTs	3.0
434221	AF119885	Hs.283040	hypothetical protein PRO2543	3.0
459459	AA460445		gb:zx65h11.r1 Soares_total_fetus_Nb2HF8_9w Homo	3.0

TABLE 5B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
407596	1003489_1	R86913 R86901 H25352 R01370 H43764 AW044451 W21298
407647	1007366_1	AW860158 AW862385 AW860159 AW862386 AW862341 AW821869 AW821893 AW062660 AW062656
408066	103649_1	AA046914 AA057231 H38371
408315	1051132_1	AW179148 AW179150
409211	110906_1	AA078835 AA079319 AA078816 AA079026 AA122167 AA111933 AA068989 AA084691 AA068999 AA069038 AA069225 AA650522
409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154667
409846	1156150_1	AW501748 AW502972 AW502513
409854	1156229_1	AW501833 AW502145 AW502581
409892	1157859_1	AW956113 AW503580
410065	1174258_1	AW812744 AW581974 AW812725
410454	1204154_1	AW749041 BE066025 H85202
410495	1205826_1	N95428 W24040 AW751366 H81987
410596	121053_1	AA374186 AW963684 AA086107 AI491986
410667	1214679_1	AW936099 AW936243 AW936097 BE162104 BE162109 AW794263
410758	1219899_1	BE535988 AW801777
410890	1226008_1	AW809575 BE090626 BE090617 AW936551 AW936552 AW936530 AW936550 AW936481
410990	1228649_1	AW812929 AW812779 AW813088
411256	1236790_1	AW834039 AW834040 AW834047 AW845410 BE003128 AW852479
411279	1237516_1	AW884776 AW835737 AW835261 AW835247 AW835246 AW835263 AW835240 AW835258
411280	1237585_1	N50617 N47321 R54159 AW860545 AW835317
411337	1239217_1	AW837349 AW837355 AW882717
411542	1249095_1	AW850767 AW851180 AW851359 AW851223 AW851360 AW851222 AW851108
411543	1249127_1	AW851248 AW851425 AW850805 AW851021 AW850905
411673	1253737_1	BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153665 BE064650 BE064691
411899	126497_1	AA370573 BE160501 BE160500 BE160498 BE160502 BE160497 N72424 AA096462
411922	1265825_1	AW876260 AW876269 AW876340 AW876146 AW876323 AW876320 AW876171 AW876421 AW876227 AW876243
412319	1288602_1	AW936903 AW936907 AW936908 AW936914

412480	129929_1	BE142364 BE142341 AA112025
412732	1323951_1	AW993300 N23107 R22345
413137	1350383_1	BE066915 BE066942
413161	1351262_1	BE068130 BE068135 BE068134 BE068183 BE068184 BE068094
413247	135544_1	AW963969 AW963971 AA127651 AA376726
413357	1364165_1	W47611 BE087851
413516	1374595_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
413560	1376621_1	BE148411 BE148415 H59098
414193	1424706_-2	BE260069
414337	1436706_1	BE386606 BE275195 BE274984
414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
414390	1441570_-1	BE281040
415296	1533528_1	F05086 F05091 R17158
415618	1540651_1	F12954 H10624 R11948 R56523 T75190
415920	1561733_1	Z45684 H09361 R53285
416211	1578993_1	R14625 R17952 H29120 R14650
416238	1580451_1	W90448 H30749
416612	1603885_1	H70565 N77403 H67949
416624	1604694_1	H69044 T47567 H75691 T50292
416677	1608621_1	T83470 T84283 H74054
416895	162874_1	AW961600 AA190217 AA321260
417178	1655565_1	N51636 T51874 T51829
417762	169750_1	AA205976 AA205930
418913	180520_1	BE046745 AI074878 AI817476 AW572513 AA447586 H28330 AA232486 AA365704 BE271167
419401	184454_1	AW804663 AW805017 AA236969
419896	1888662_1	Z99362 Z99363
420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
421418	202288_1	AA806639 AA291008 AA836274 AW978806
422046	210744_1	AI638562 T16929 H13401 F07773 R55836
422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
423403	227942_1	AA325483 AW962169 AW962660
424093	235233_1	AA335025 AA335496 AW966145
424719	242889_1	H90452 AA345767 AW964302 H90399
425189	247825_1	H16622 R17322 AA351959
425357	250578_-1	AA355842
425541	252945_1	AA359119 AW963014 D79884
425714	255333_1	AW963278 AA362266 AA362267
426294	263994_1	AA374185 AW956180 H38344
426528	268722_1	AA380828 AW963760 AA380805 AA380830
426593	269748_1	AW958560 AA382199 AW444933
430202	314322_1	T85775 AW968345 AA468998
430535	319643_1	AW968485 AW968670 AA480922 BE350425
431075	327638_1	BE267477 AA491488 AW836723
431492	333930_1	AW612343 AA922558 AA505925 AA927038 AW972537 AI693564
431828	338201_1	AA572994 AA516249 AA702595
432075	341066_1	AW972934 AA525260 AA525266 AA835021 BE000149 BE000148
432474	348197_1	AA584042 AW973273 AA548798
433371	364430_1	T25451 AA585296 AA585305
433403	36534_-1	AF040247
433767	374014_1	AA609245 AA724581 AW241989 AI377274 T47300
434738	392562_1	AA836265 AA648266 AW974440
436196	41562_1	AK001084 AA078092 AA829049
436242	41641_1	AK002187 R66351
436812	427323_1	AW298067 AA731645 AA810101 AW194180 AI690673 AW978773
437500	43772_1	AL390150 AW959182 AA358923
437948	445966_1	AA772920 D59870 D61151 AI591331
438224	452656_1	AA933999 AA781181
438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
439098	46859_1	AF085955 H69158 H69081
439126	46887_1	AF085984 H95905 H95906
.441033	50807_-1	BE562555
443283	56492_-1	BE568610
445597	644513_1	H65649 AW753545 AI244270
445832	651925_1	AI261545 N59134 AW875371 AW875247
448221	75534_-1	BE622615
448527	766707_1	AI525606 BE549857
448732	77773_-1	BE614063
449311	804513_1	AI657014 AW594035 AI657036 AI638390
449570	81018_1	AA001793 AA001871
450078	823882_1	AI681743 AW897287 AW897205 AW897284
452351	91233_1	AA025647 R45716 AW753786
452453	918300_1	AI902519 AI902518 AI902516
453472	968371_1	AL037925 AL037931 AL037957
453530	97021_1	AW021633 AA036730 AI866854
453631	975024_1	AL046418 N52738 R33840
453725	978760_1	W28543 AL119531
453752	979899_1	AL120800 BE378580
453823	982526_1	AL137967 BE064160 BE064186
454102	1011603_1	AW752363 BE147120 N22640
454487	1216101_1	AW796342 AW796356 BE161430
454543	1223775_1	AW806895 AW866476 AW866465 AW866535 AW866623
454564	1224407_1	AW807573 AW807566 AW807572
454573	1225624_1	BE146471 AW833743 AW833609 AW821469 AW821488 AW821541 AW821531 AW821513 AW821549 AW821384 AW821625 AW821577 AW821547 AW834577

454652	1228071_1	AW812088 AW812105 AW812082
454679	1228929_1	AW813110 AW813113
454724	123128_1	AA091228 H71860 H71073
454753	1233576_1	AW819212 AW819170 BE158474 AW819172 AW819213 AW819200 AW819256 AW819254 AW819178 AW819214 AW819215 AW819233 AW819171
454885	1238874_1	AW836922 AW876719 AW876688 AW836919 AW836997 AW836908 AW836912 AW836993
454940	1245640_1	AW846202 AW846174 AW846532 AW846181 AW846458 AW846206 AW846432 AW846553 AW846533 AW846197 AW846198 AW846189 AW846469 AW846530 AW846560 AW846536 AW846472 AW846470 AW846466 AW846192 AW846479 AW846260 AW846204 AW846139 AW846187 AW846353 AW846462 AW846151 AW846549 AW846538 AW846527 AW846567 AW846531
454994	1248637_1	AW850176 AW850513 AW850412 AW850451
455056	1250934_1	AW853057 AW853039 AW853042 AW853050 AW853114 AW853105 AW853102 AW853111 AW853121 AW853109 AW853126
455067	1252050_1	AW854538 AW854418 AW854412
455108	1253916_1	AW856866 AW856858 AW856856
455387	1287871_1	BE069037 AW936025 BE069178 AW936034
455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
455534	1322942_1	AW991925 AW991919
455565	1329591_1	BE000537 BE180584 BE180540 BE180542 BE180546
455731	1353872_1	BE072188 BE072299 BE072269 BE072317 BE072238
455786	1365510_1	BE090077 BE090079
455790	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
455887	1380836_1	BE154173 BE154098 BE154096
455895	1381386_1	BE154837 BE154879 BE154850 BE154877 BE154835 BE154849 BE154902 BE154905 BE154867 BE154901 BE154904 BE154899
456253	1699178_1	T12198 T19684 T11583 R15526 R15585 R45876 R15562
456383	184252_1	AI148037 AA287178 AA236756
456388	1842839_-1	W28557
457525	351732_1	AW973800 AA557589 AA559886
457740	39528_1	AW500458 AW160900 AF161362 AF150327 AW578393 AW360921 AW360920 AW360902 AW360890 AW732529
458301	543058_1	AF003834 W36292
459135	918516_1	AI902802 AI902783 AI902800
459157	919804_2	AI904385 AI904382

TABLE 5C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400942	7656749	Minus	91593-91757,92720-92843,93962-94079,94824-94997
401004	7229982	Plus	62580-62772
401287	9801612	Minus	42287-42431
401308	9212516	Plus	169019-169649
401350	9931226	Plus	14471-14623
401740	2982169	Plus	148357-148484,148591-148690
401871	8079355	Minus	58158-59585
401896	8569194	Plus	115129-115294
401963	3126783	Plus	51382-51521
402105	8131588	Minus	22856-24055
402109	8131678	Minus	171722-171859,173197-173303
402142	7704985	Minus	29932-30698
402451	9796677	Minus	48137-48343
402867	5596716	Plus	52806-53106,53500-53818
403277	8072597	Minus	27494-27642
403283	8076905	Minus	71124-71996
403375	9255944	Minus	92554-92795
403473	9945095	Minus	54241-54437
403497	6067111	Plus	7221-7441
403531	8076842	Minus	75903-76134
403635	6862664	Minus	157028-157145,161725-161900
403714	7210030	Minus	145556-145873
403743	7652003	Minus	136463-136646
404020	8655966	Minus	174449-174663
404041	8886967	Minus	1334-1503,2483-2585,5230-5337,19656-19804
404044	9558573	Minus	225757-225939
404083	9944029	Minus	16650-17082
404108	8247074	Minus	63603-64942
404134	6981900	Minus	40633-40911
404227	7838233	Minus	93110-93259
404418	7382420	Minus	153339-153481,155099-155294
404451	7638438	Minus	105191-105622
404582	9739220	Plus	53230-53424
404708	9800828	Plus	77522-77658
404868	9454593	Plus	39954-40430
405096	8072599	Plus	140844-140897,148510-148581
405290	3900849	Minus	79582-79765
405347	2979602	Minus	977-1116
405512	9454624	Plus	17802-17966,18573-18697
405549	1552494	Plus	10878-11048
405583	4512287	Plus	56211-56353
405671	2565031	Plus	25805-26923
405717	9588573	Plus	11275-11973
405752	9212305	Plus	91392-91528
405836	5686282	Minus	5031-5217

406122	9144087	Minus	30940-31386
406197	7289992	Minus	47520-47961
406237	7417725	Plus	30032-30501
406241	7417725	Minus	34951-35752
406255	7417729	Plus	2959-3200
406364	9256114	Minus	50715-50833
406454	9588380	Minus	91746-91958
406481	9864741	Minus	91439-91579
406562	7711584	Plus	37316-37426
406605	8272666	Minus	23275-23493,23723-23903

TABLE 6A lists about 68 genes highly down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 5A, except the "average" ovarian cancer level was set to the maximum value amongst various ovarian cancers and the "average" normal ovary level was set to the minimum value from various non-malignant ovary specimens, and the ratio was greater than or equal to 2.5 (i.e. 2.5-fold down-regulated in the highest tumor vs. the lowest normal ovary). This has the overall effect of increasing stringency, and reducing the number of false-positives.

TABLE 6A: ABOUT 68 HIGHLY DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene Title
ratio: ration of normal ovary vs. tumor

Pkey	Ex. Accn	UG ID	Title	ratio
424851	AA676441	Hs.119059	ESTs	7.9
437690	AA804362	Hs.180544	ESTs	4.7
433682	AA642418	Hs.17381	ESTs	4.1
407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cds.	4.1
437787	AI908263	Hs.291625	ESTs	4.0
453282	AK000043	Hs.32922	hypothetical protein FLJ20036	4.0
440987	AA911705	Hs.130229	ESTs	3.8
443131	AI033833	Hs.132689	ESTs	3.8
431075	BE267477		gb:601189542F2 NIH_MGC_7 Homo sapiens cDNA clo	3.6
412637	AA115097	Hs.261313	ESTs	3.6
408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	3.5
420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	3.5
430653	AW902062	Hs.30280	ESTs	3.4
401308			predicted exon	3.4
410758	BE535988		gb:601062418F1 NIH_MGC_10 Homo sapiens cDNA c	3.4
421418	AA806639		gb:ob88g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	3.4
450061	AI797034	Hs.201115	ESTs	3.3
409725	T40760	Hs.90459	EST	3.3
434738	AA836265		gb:od17e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	3.3
431644	AW972822	Hs.169248	cytochrome c	3.3
450938	AW753734	Hs.277215	ESTs	3.2
420497	AW206285	Hs.253548	ESTs	3.2
439426	AI131502	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE C	3.2
407596	R86913		gb:yq30f05.r1 Soares fetal liver spleen 1NFLS Homo sap	3.2
448683	AA167642	Hs.14632	ESTs	3.2
431982	AW419296	Hs.105754	ESTs	3.1
452320	AA042873	Hs.160412	ESTs	3.1
419401	AW804663		gb:QV4-UM0094-160300-135-d06 UM0094 Homo sapim	3.1
402105			predicted exon	3.1
444997	AI204451	Hs.146196	ESTs	3.1
403283			predicted exon	3.0
455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo sapie	3.0
428559	H24338	Hs.27041	ESTs	2.9
419002	T78625	Hs.268594	ESTs	2.9
404868			predicted exon	2.9
409090	W56067	Hs.103105	ESTs	2.9
406605			predicted exon	2.9
441202	AI632143	Hs.135853	ESTs	2.8
422046	AI638562		gb:ts50a10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA cl	2.8
442865	N57659	Hs.114541	ESTs, Weakly similar to neuronal thread protein AD7c-N	2.8
444431	AW513324	Hs.42280	ESTs	2.8
426294	AA374185		gb:EST86289 HSC172 cells I Homo sapiens cDNA 5' en	2.8
412480	BE142364		gb:CM0-HT0143-270999-062-d12 HT0143 Homo sapie	2.8
449858	AW205979	Hs.196065	ESTs	2.8
401464	AF039241	Hs.9028	histone deacetylase 5	2.7
439126	AF085984		gb:Homo sapiens full length insert cDNA clone YT99F0	2.7
403277			predicted exon	2.7
450078	AI681743		gb:tx38g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	2.7
458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKHEAD D	2.7
420620	AA278807	Hs.173343	ESTs	2.7
459054	AW798466	Hs.82396	2',5'-oligoadenylate synthetase 1	2.6
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys), mem	2.6
454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and coiled/coil domains 1(cyt	2.6
454529	Z45439	Hs.270425	ESTs	2.6
446877	AI559472	Hs.270720	ESTs	2.6
412588	AW993055	Hs.44024	ESTs	2.6
449862	AI672277	Hs.199475	ESTs	2.6
446694	AV659942	Hs.258132	ESTs	2.6
424029	AB014594	Hs.137579	KIAA0694 gene product	2.6

454102	AW752363		gb:RC0-CT0201-270999-011-f03 CT0201 Homo sapien	2.6
430922	AW373747	Hs.183337	ESTs	2.6
420289	N55394	Hs.96398	8-oxoguanine DNA glycosylase	2.6
410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF Ho	2.5
412319	AW936903		gb:RC1-DT0029-030200-012-d02 DT0029 Homo sapien	2.5
409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo sapien	2.5
445832	AI261545		gb:qz30a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA	2.5
429755	NM_001364	Hs.215839	discs, large (Drosophila) homolog 2 (chapsyn-110)	2.5
445755	AW294870	Hs.223672	ESTs	2.5

TABLE 6B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
407596	1003489_1	R86913 R86901 H25352 R01370 H43764 AW044451 W21298
409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154667
410495	1205826_1	N95428 W24040 AW751366 H81987
410758	1219899_1	BE535988 AW801777
412319	1288602_1	AW936903 AW936907 AW936908 AW936914
412480	129929_1	BE142364 BE142341 AA112025
419401	184454_1	AW804663 AW805017 AA236969
421418	202288_1	AA806639 AA291008 AA836274 AW978806
422046	210744_1	AI638562 T16929 H13401 F07773 R55836
426294	263994_1	AA374185 AW956180 H38344
431075	327638_1	BE267477 AA491488 AW836723
434738	392562_1	AA836265 AA648266 AW974440
439126	46887_1	AF085984 H95905 H95906
445832	651925_1	AI261545 N59134 AW875371 AW875247
450078	823882_1	AI681743 AW897287 AW897205 AW897284
454102	1011603_1	AW752363 BE147120 N22640
455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191

TABLE 6C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

401308	9212516	Plus	169019-169649
402105	8131588	Minus	22856-24055
403277	8072597	Minus	27494-27642
403283	8076905	Minus	71124-71996
404868	9454593	Plus	39954-40430
406605	8272666	Minus	23275-23493,23723-23903

Table 7A lists about 770 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 7th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 7A: ABOUT 770 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene Title
ratio: ration tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
109680	F09255	Hs.4993	ESTs	23.2
119743	W70242	Hs.58086	ESTs	22.0
132528	AA283006	Hs.50758	chromosome-associated polypeptide C	22.0
129571	X51630	Hs.1145	Wilms tumor 1	20.0
102151	U17280	Hs.3132	steroidogenic acute regulatory protein	19.6
130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	17.5
132624	AA164819	Hs.53631	ESTs	15.9
102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	15.4
101249	L33881	Hs.1904	protein kinase C, iota	14.5
122802	AA460530	Hs.256579	ESTs	14.5
135242	M74093	Hs.9700	cyclin E1	13.8
101804	M86699	Hs.169840	TTK protein kinase	12.2
123005	AA479726	Hs.105577	ESTs	12.0
114965	AA250737	Hs.72472	ESTs	11.5
115536	AA347193	Hs.62180	ESTs	11.4
132191	AA449431	Hs.158688	KIAA0741 gene product	10.9
121853	AA425887	Hs.98502	ESTs	10.9
115881	AA435577	Hs.184942	G protein-coupled receptor 64	10.8
119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical protein	10.5
104301	D45332	Hs.6783	ESTs	10.3
132632	N59764	Hs.5398	guanine-monophosphate synthetase	10.1

105298	AA233459	Hs.26369	ESTs	9.7
108857	AA133250	Hs.62180	ESTs	9.1
113168	T53592	Hs.161586	EST	9.0
115892	AA435946	Hs.50831	ESTs	8.9
125666	AA199856	Hs.118811	ESTs	8.9
102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	8.8
108055	AA043562	Hs.62637	ESTs	8.6
132572	AA448297	Hs.237825	signal recognition particle 72kD	8.6
115909	AA436666	Hs.59761	ESTs	8.5
109166	AA179845	Hs.73625	RAB6 interacting; kinesin-like (rabkinesin6)	8.3
121779	AA422036	Hs.98367	ESTs	8.3
102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	8.0
105317	AA233926	Hs.23635	ESTs	7.8
125250	W87465	Hs.222926	ESTs; Weakly similar to D2092.2 [C.elegans]	7.8
126960	AA317900	Hs.161756	ESTs	7.8
122969	AA478539	Hs.104336	ESTs	7.7
130376	R40873	Hs.155174	KIAA0432 gene product	7.7
123339	AA504253	Hs.101515	ESTs	7.7
134972	M19720	Hs.169252	Human L-myc protein gene; complete cds	7.6
111234	N69287	Hs.21943	ESTs; Weakly similar to ORF YGL221c [S.cerevi	7.5
123689	AA609556	Hs.256562	ESTs	7.5
123494	AA599786	Hs.112110	ESTs	7.4
131985	AA434329	Hs.36563	ESTs	7.4
106738	AA470145	Hs.25130	ESTs	7.4
108768	AA127741	Hs.61345	ESTs	7.3
106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	7.2
123308	AA496211	Hs.103538	ESTs	7.2
106124	AA423987	Hs.7567	ESTs	7.2
111345	N89820	Hs.14559	ESTs	7.1
105200	AA195399	Hs.24641	ESTs	7.1
116416	AA609219	Hs.39982	ESTs	7.1
118846	N80567	Hs.50895	ESTs	7.1
133434	AA278852	Hs.250786	ESTs	7.1
120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [	6.9
115291	AA279943	Hs.122579	ESTs	6.9
111185	N67551	Hs.12844	EGF-like-domain; multiple 6	6.9
108778	AA128548	Hs.90847	general transcription factor IIIC; polypeptid	6.9
132939	U76189	Hs.61152	exostoses (multiple)-like 2	6.9
134520	N21407	Hs.257325	ESTs	6.9
114724	AA131701	Hs.256287	ESTs; Highly similar to SPERM SURFACE PROTEIN	6.8
116296	AA489033	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (from c	6.8
102136	U15552	Hs.85769	acidic 82 kDa protein mRNA	6.7
132725	L41887	Hs.184167	splicing factor; arginine/serine-rich 7 (35kD	6.5
109648	F04600	Hs.7154	ESTs	6.4
116401	AA599963	Hs.59698	ESTs	6.4
127563	AI367707	Hs.150587	ESTs	6.4
104252	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM	6.4
120438	AA243441	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	6.2
131978	D80008	Hs.36232	KIAA0186 gene product	6.2
134621	L02547	Hs.172865	cleavage stimulation factor; 3' pre-RNA; subu	6.2
120571	AA280738	Hs.128679	ESTs	6.2
102627	U66561	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.1
100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	6.1
118204	N59859	Hs.48443	ESTs	6.0
131386	AA096412	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	6.0
129097	S50223		HKR-T1=Kruppel-like zinc finger protein [huma	5.9
131228	AA279157	Hs.24485	chondroitin sulfate proteoglycan 6 (bamacan)	5.9
106369	AA443828	Hs.25324	ESTs	5.9
108255	AA063157	Hs.172608	ESTs	5.8
125370	AA256743	Hs.151791	KIAA0092 gene product	5.8
130010	N52966	Hs.142838	ESTs	5.8
131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37kD)	5.7
116238	AA479362	Hs.47144	DKFZP586N0819 protein	5.7
102221	U24576		LIM domain only 4	5.6
130757	R00641	Hs.18925	ESTs; Weakly similar to cDNA EST yk339a7.5 co	5.6
131278	U81523	Hs.25195	endometrial bleeding associated factor (left-	5.6
101383	M14113	Hs.79345	coagulation factor VIIIc; procoagulant compon	5.5
131836	AA610086	Hs.32990	DKFZP566F084 protein	5.5
129628	U26727	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	5.5
106523	AA453441	Hs.31511	ESTs	5.5
111772	R28287	Hs.237146	ESTs	5.5
101255	L34600	Hs.149894	mitochondrial translational initiation factor	5.5
106895	AA489665	Hs.25245	ESTs	5.5
104943	AA065217	Hs.169674	ESTs	5.5
129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	5.4
102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)-like	5.4
106553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	5.4
112305	R54822	Hs.26244	ESTs	5.3
123972	C14762	Hs.70337	immunoglobulin superfamily; member 4	5.3
102676	U72514	Hs.12045	putative protein	5.3
106459	AA449741	Hs.4029	glioma-amplified sequence-41	5.2
107865	AA026104	Hs.61252	ESTs	5.2
121121	AA399371	Hs.189095	ESTs; Weakly similar to zinc finger protein S	5.2
127162	N76398	Hs.21187	ESTs	5.2

131646	AA171895	Hs.30057	Homo sapiens clone 24749 and 24750 mRNA seque	5.2
121770	AA421714	Hs.11469	KIAA0896 protein	5.2
122512	AA449311	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	5.1
105870	AA399623	Hs.23505	ESTs	5.1
100341	D63506	Hs.8813	syntaxin binding protein 3	5.1
116848	H65187	Hs.39001	ESTs	5.1
120821	AA347419	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	5.1
130690	AA084286	Hs.139033	paternally expressed gene 3	5.1
122661	AA454936	Hs.245541	ESTs	5.1
123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [	5.1
108810	AA130596	Hs.71331	ESTs; Weakly similar to POTENT HEAT-STABLE PR	5.0
110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	5.0
120619	AA284372	Hs.111471	ESTs	5.0
122792	AA460225	Hs.99519	ESTs	5.0
129912	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [H.s	5.0
102823	U90914	Hs.5057	carboxypeptidase D	4.9
129890	M13699	Hs.111461	ceruloplasmin (ferroxidase)	4.9
101084	L05425		Homo sapiens autoantigen mRNA; complete cds	4.9
134859	D87716	Hs.90315	KIAA0007 protein	4.9
115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	4.9
105516	AA257971	Hs.21214	ESTs	4.9
114932	AA242751	Hs.16218	KIAA0903 protein	4.9
106672	AA461300	Hs.30643	ESTs	4.8
106126	AA424006	Hs.22972	ESTs; Moderately similar to H5AR [M.musculus]	4.8
110695	H93463	Hs.124777	ESTs	4.8
102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer; nonpo	4.8
133282	U52960	Hs.250855	SRB7 (suppressor of RNA polymerase B; yeast)	4.8
119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio	4.7
120695	AA291468		ESTs	4.7
128651	AA446990	Hs.103135	ESTs	4.7
103152	X66533	Hs.77890	guanylate cyclase 1; soluble; beta 3	4.7
108699	AA121514	Hs.70832	ESTs	4.7
115094	AA255921	Hs.88095	ESTs	4.7
121429	AA406293	Hs.193498	ESTs	4.7
123203	AA489671	Hs.89709	glutamate-cysteine ligase (gamma-glutamylcyst	4.7
126802	AA947601	Hs.97056	ESTs	4.7
130527	C17384	Hs.184227	F-box protein 21	4.7
134470	X54942	Hs.83758	CDC28 protein kinase 2	4.7
100449	D87470	Hs.75400	KIAA0280 protein	4.7
110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	4.7
115901	AA436403	Hs.86909	ESTs; Moderately similar to Frizzled-6 [H.sap	4.7
109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; complete	4.6
116195	AA465148	Hs.72402	ESTs	4.6
132122	U65092	Hs.40403	Cbp/p300-interacting transactivator; with Glu	4.6
108990	AA152296	Hs.72045	ESTs	4.6
109055	AA160529	Hs.48524	ESTs	4.6
115937	AA443269	Hs.30991	KIAA0957 protein	4.6
133520	X74331	Hs.74519	primase; polypeptide 2A (58kD)	4.6
131200	AA609427	Hs.210706	ESTs; Moderately similar to !!!! ALU SUBFAMIL	4.6
121369	AA405657	Hs.128791	Human DNA sequence from clone 967N21 on chrom	4.5
132880	AA444369	Hs.177537	ESTs	4.5
127386	AI457411	Hs.106728	ESTs	4.5
120067	W93592	Hs.47343	ESTs	4.5
122986	AA479063	Hs.102947	ESTs	4.5
135286	AA401269	Hs.97849	ESTs	4.5
130155	L33404	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	4.5
106103	AA421104	Hs.12094	ESTs	4.5
102654	U68494	Hs.24385	Human hbc647 mRNA sequence	4.4
107876	AA025315	Hs.61184	Novel human gene mapping to chomosome X	4.4
109454	AA232255	Hs.46912	ESTs	4.4
125960	D63307	Hs.145968	ESTs	4.4
126892	AI160190	Hs.76127	hect (homologous to the E6-AP (UBE3A) carboxy	4.4
100269	D38550	Hs.1189	E2F transcription factor 3	4.4
134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	4.3
100502	HG1496-HT1496		Adrenal-Specific Protein Pg2	4.3
105542	AA261858	Hs.8241	ESTs; Weakly similar to heat shock protein hs	4.3
109787	F10610	Hs.34853	inhibitor of DNA binding 4; dominant negative	4.3
110759	N21671	Hs.19025	ESTs	4.3
129970	AA478975	Hs.200434	ESTs	4.3
134666	AA482319	Hs.8752	putative type II membrane protein	4.3
117693	N40939	Hs.44162	ESTs; Weakly similar to cDNA EST yk342h12.5 c	4.3
111008	N53388	Hs.7222	ESTs	4.3
120977	AA398155	Hs.97600	ESTs	4.2
105808	AA393808	Hs.21490	KIAA0438 gene product	4.2
121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [	4.2
100893	HG4557-HT4962		Small Nuclear Ribonucleoprotein U1, 1snrp	4.2
107176	AA621762	Hs.7576	ESTs	4.2
118976	N93629	Hs.93391	ESTs	4.2
130703	N63295	Hs.18103	ESTs	4.2
106540	AA454607	Hs.38114	ESTs; Weakly similar to coded for by C. elega	4.2
119367	T78324	Hs.90905	ESTs	4.2
133633	D21262	Hs.75337	nucleolar phosphoprotein p130	4.2
105520	AA258068	Hs.33085	WD repeat domain 3	4.2
114264	Z40074	Hs.27595	ESTs	4.1

131046	X02530	Hs.2248	IP10; 'small inducible cytokine subfamily B (	4.1
105220	AA210695	Hs.17212	ESTs	4.1
103111	X63187	Hs.2719	epididymis-specific; whey-acidic protein type	4.1
125640	R37700	Hs.208261	ESTs	4.1
110561	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CONJUGATING	4.1
118092	N54915	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from c	4.1
134891	F03517	Hs.90787	ESTs	4.1
112364	R59312	Hs.197642	ESTs; Weakly similar to DNA-DIRECTED RNA POLY	4.1
120699	AA291716	Hs.97258	ESTs	4.1
106272	AA432074	Hs.32538	ESTs	4.1
112041	R43300	Hs.22929	ESTs	4.1
131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix-loop	4.1
116134	AA460246	Hs.50441	ESTs; Highly similar to CGI-04 protein [H.sap	4.1
107638	AA009528	Hs.42743	ESTs; Weakly similar to predicted using Genef	4.0
131941	D62657	Hs.35086	ubiquitin-specific protease 1	4.0
106154	AA425304	Hs.6994	ESTs	4.0
105546	AA262032	Hs.26089	ESTs; Weakly similar to 62D9.a [D.melanogaste	4.0
106319	AA436606	Hs.7392	ESTs; Weakly similar to Gu protein [H.sapiens	4.0
121816	AA424814	Hs.187509	ESTs	4.0
122851	AA463627	Hs.99598	ESTs	4.0
123337	AA504153	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevi	4.0
128643	N40212	Hs.102958	ESTs	4.0
129011	S72869	Hs.107932	DNA segment; single copy; probe pH4 (transfor	4.0
130895	AA609828	Hs.21015	ESTs; Highly similar to tetracycline transpor	4.0
132323	AA436102	Hs.256559	ESTs	4.0
134255	J05032	Hs.80758	aspartyl-tRNA synthetase	4.0
102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (beta)	4.0
102123	U14518	Hs.1594	centromere protein A (17kD)	4.0
102813	U90651	Hs.151461	embryonic ectoderm development protein	3.9
113970	W86748	Hs.8109	ESTs	3.9
107145	AA621108	Hs.173001	ESTs	3.9
114212	Z39338	Hs.21201	DKFZP566B0846 protein	3.9
106614	AA458934	Hs.179912	ESTs	3.9
132742	AA490862	Hs.55901	ESTs; Weakly similar to C43H8.1 [C.elegans]	3.9
120948	AA397822	Hs.104650	ESTs; Highly similar to similar to mago nashi	3.9
129337	R63542	Hs.110488	KIAA0990 protein	3.9
103835	AA172215	Hs.93748	ESTs; Moderately similar to TRANSCRIPTION FAC	3.9
133330	U42360	Hs.71119	Putative prostate cancer tumor suppressor	3.9
133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homologou	3.9
133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	3.9
133350	AA135468	Hs.71573	ESTs	3.9
115623	AA401475	Hs.39733	postsynaptic protein CRIPT	3.9
101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	3.9
102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	3.9
134248	AA292677	Hs.80624	ESTs	3.9
102380	U40434	Hs.155981	mesothelin	3.9
116157	AA461063	Hs.44298	ESTs; Highly similar to HSPC011 [H.sapiens]	3.8
106691	AA463453	Hs.23259	ESTs; Weakly similar to ACTIN; CYTOPLASMIC 2	3.8
115844	AA430124	Hs.234607	ESTs	3.8
107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.cerevi	3.8
106498	AA452141	Hs.7171	ESTs	3.8
134405	J04177	Hs.82772	collagen; type XI; alpha 1	3.8
106260	AA431448	Hs.5250	ESTs; Weakly similar to BACR37P7.g [D.melanog	3.8
109864	H02554	Hs.30323	ESTs	3.8
124648	N91948	Hs.125034	ESTs	3.8
134719	L07515	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.8
113702	T97307	Hs.161720	ESTs; Moderately similar to !!!! ALU SUBFAMIL	3.8
128639	N91246	Hs.102897	ESTs	3.8
111299	N73808	Hs.24936	ESTs	3.7
129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	3.7
119741	W70205	Hs.43670	kinesin family member 3A	3.7
105012	AA116036	Hs.9329	chromosome 20 open reading frame 1	3.7
128734	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	3.7
130567	L07493	Hs.1608	replication protein A3 (14kD)	3.7
114253	Z39909	Hs.14831	ESTs	3.7
103169	X68560	Hs.44450	Sp3 transcription factor	3.7
111269	N70711	Hs.18885	ESTs; Highly similar to CGI-116 protein [H.sa	3.7
112876	T03488	Hs.4842	ESTs	3.7
118261	N62780	Hs.94122	ESTs	3.7
130385	AA126474	Hs.155223	stanniocalcin 2	3.7
129300	C20976	Hs.110165	ESTs; Highly similar to ribosomal protein L26	3.7
134388	M15841	Hs.82575	small nuclear ribonucleoprotein polypeptide B	3.7
106968	AA504631	Hs.26813	ESTs; Weakly similar to hypothetical 43.2 kDa	3.7
100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	3.7
100418	D86978	Hs.84790	KIAA0225 protein	3.7
101484	M24594	Hs.20315	interferon-induced protein 56	3.7
102547	U57911	Hs.46638	chromosome 11 open reading frame 8	3.7
103587	Z29083	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.7
130600	AA478601	Hs.258737	ESTs	3.7
128733	AA328993	Hs.104558	ESTs	3.7
134375	AA412720	Hs.82389	ESTs; Highly similar to CGI-118 protein [H.sa	3.7
134098	X06323	Hs.79086	ribosomal protein; mitochondrial; L3	3.6
101188	L20320	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.6
132149	T10822	Hs.4095	ESTs	3.6

116200	AA465358	Hs.118793	ESTs; Highly similar to p621 [H.sapiens]	3.6
121920	AA428300	Hs.161841	ESTs	3.6
128609	AA234365	Hs.102456	survival of motor neuron protein interacting	3.6
101078	L04510	Hs.792	ADP-ribosylation factor domain protein 1; 64k	3.6
108693	AA121289	Hs.49597	ESTs; Highly similar to retinoic acid-induced	3.6
109139	AA176121	Hs.59757	zinc finger protein 281	3.6
111870	R37778	Hs.18685	ESTs; Weakly similar to hypothetical protein	3.6
113848	W60080	Hs.27099	DKFZP564J0863 protein	3.6
127947	AI432475	Hs.146327	ESTs	3.6
128056	AI379480	Hs.125449	ESTs; Weakly similar to MaxiK channel beta 2	3.6
129914	U22377	Hs.13321	rearranged L-myc fusion sequence	3.6
132148	AA283988	Hs.4094	ESTs	3.6
134644	S83308	Hs.87224	SRY (sex-determining region Y)-box 5	3.6
115047	AA252627	Hs.22554	homeo box B5	3.6
102398	U42359		Human N33 protein form 1 (N33) gene, exon 1 a	3.6
127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	3.6
105545	AA262030	Hs.5152	ESTs; Weakly similar to katanin p80 subunit [	3.6
101483	M24486	Hs.76768	procollagen-proline; 2-oxoglutarate 4-dioxyge	3.6
105709	AA291268	Hs.26761	DKFZP586L0724 protein	3.6
122636	AA454103	Hs.110031	ESTs	3.6
124792	R44357	Hs.132784	ESTs; Weakly similar to cDNA EST EMBL:T01421	3.6
103621	Z47727	Hs.150675	polymerase (RNA) II (DNA directed) polypeptid	3.5
105427	AA251330	Hs.28248	ESTs	3.5
121553	AA412488	Hs.48820	ESTs	3.5
115167	AA258421	Hs.43728	hypothetical protein	3.5
134570	U66615	Hs.172280	SWI/SNF related; matrix associated; actin dep	3.5
110787	N24716	Hs.12244	ESTs; Weakly similar to C44B9.1 [C.elegans]	3.5
131621	U77665	Hs.139120	ribonuclease P (30kD)	3.5
132813	N72116	Hs.57435	solute carrier family 11 (proton-coupled diva	3.5
116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMP	3.5
131965	W90146	Hs.35962	ESTs	3.5
115221	AA262942	Hs.79741	ESTs	3.5
116093	AA456020	Hs.50848	ESTs; Weakly similar to KIAA0862 protein [H.s	3.5
123507	AA600176	Hs.112345	ESTs	3.5
129801	F11087	Hs.239666	ESTs	3.5
115084	AA255566	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	3.5
123442	AA598803	Hs.111496	ESTs	3.5
115061	AA253217	Hs.41271	ESTs	3.5
100146	D13645	Hs.2471	KIAA0020 gene product	3.5
115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	3.5
115360	AA281950	Hs.5057	carboxypeptidase D	3.5
130261	D83767	Hs.153678	reproduction 8	3.4
100824	HG4058-HT4328		Oncogene Aml1-Evi-1, Fusion Activated	3.4
102287	U31814	Hs.3352	histone deacetylase 2	3.4
102788	U86602	Hs.74407	nucleolar protein p40	3.4
118836	N79820	Hs.50854	ESTs	3.4
102423	U44754	Hs.179312	small nuclear RNA activating complex; polypep	3.4
106300	AA435840	Hs.19114	high-mobility group (nonhistone chromosomal)	3.4
106156	AA425354	Hs.4210	ESTs	3.4
106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	3.4
107868	AA025234	Hs.61260	ESTs	3.4
108187	AA056538	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	3.4
116123	AA459282	Hs.43756	ESTs	3.4
119501	W37721	Hs.151363	ESTs	3.4
129121	AA127459	Hs.108788	ESTs; Weakly similar to zeste [D.melanogaster	3.4
131638	D87120	Hs.29882	predicted osteoblast protein	3.4
132962	N34893	Hs.6153	ESTs; Highly similar to CGI-48 protein [H.sap	3.4
133767	D63875	Hs.173288	KIAA0155 gene product	3.4
111823	R35253	Hs.24944	ESTs	3.4
134372	D63877	Hs.82324	KIAA0157 protein	3.4
130938	AA013250	Hs.21398	ESTs; Moderately similar to PUTATIVE GLUCOSAM	3.4
115169	AA258427	Hs.58427	ESTs	3.4
123978	C20653	Hs.170278	ESTs	3.4
108807	AA129968	Hs.49376	ESTs; Weakly similar to PROTEIN PHOSPHATASE P	3.4
132581	R42266	Hs.52256	ESTs; Weakly similar to beta-TrCP protein E3R	3.4
134654	W23625	Hs.8739	ESTs; Weakly similar to ORF YGR200c [S.cerevi	3.4
105730	AA292701	Hs.5364	DKFZP564I052 protein	3.4
111295	N73275	Hs.21275	ESTs; Weakly similar to ubiquitin-conjugating	3.3
102009	U02680	Hs.82643	protein tyrosine kinase 9	3.3
114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.s	3.3
130604	X03635	Hs.1657	estrogen receptor 1	3.3
100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polype	3.3
121748	AA421171	Hs.234545	ESTs	3.3
106698	AA463745	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDEN	3.3
134353	S77154	Hs.82120	nuclear receptor subfamily 4; group A; member	3.3
134154	AA211320	Hs.79404	neuron-specific protein	3.3
133142	F03321	Hs.65874	ESTs	3.3
124461	N50641	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (from c	3.3
104903	AA055534	Hs.124134	ESTs	3.3
106772	AA478106	Hs.12692	ESTs; Weakly similar to protein phosphatase-1	3.3
109704	F09687	Hs.12876	ESTs	3.3
111131	N64267	Hs.10177	ESTs	3.3
115019	AA251906	Hs.48473	ESTs	3.3
116019	AA450312	Hs.237480	Homo sapiens mRNA; cDNA DKFZp434E102 (from cl	3.3

118528	N67889	Hs.49397	ESTs	3.3
124027	F03625	Hs.107537	ESTs	3.3
131699	R68657	Hs.90421	ESTs; Moderately similar to !!!! ALU SUBFAMIL	3.3
111044	N55443	Hs.23625	ESTs	3.3
103768	AA089997	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEMBRANE	3.3
131882	N49091	Hs.3385	ESTs; Highly similar to CGI-134 protein [H.sa	3.3
123673	AA609471	Hs.112712	ESTs	3.3
132936	AB002305	Hs.6111	KIAA0307 gene product	3.3
103023	X53793	Hs.117950	multifunctional polypeptide similar to SAICAR	3.3
120572	AA280794	Hs.258787	ESTs	3.3
132384	AA479933	Hs.46967	Human DNA sequence from clone 167A19 on chrom	3.3
105658	AA282914	Hs.10176	ESTs	3.2
105086	AA147719	Hs.159441	ESTs	3.2
118695	N71781	Hs.50081	Homo sapiens mRNA full length insert cDNA clo	3.2
112092	R44538	Hs.140889	ESTs	3.2
125154	W38419	Hs.24936	ESTs	3.2
108040	AA041551	Hs.48644	ESTs	3.2
133453	M68941	Hs.73826	protein tyrosine phosphatase; non-receptor ty	3.2
124006	D60302	Hs.108977	ESTs	3.2
116083	AA455653	Hs.44581	ESTs; Weakly similar to HEAT SHOCK 70 KD PROT	3.2
106753	AA476944	Hs.7331	ESTs	3.2
102621	U66075	Hs.50924	GATA-binding protein 6	3.2
103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypeptide G	3.2
128926	AA481403	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [H.s	3.2
101167	L15309	Hs.193677	zinc finger protein 141 (clone pHZ-44)	3.2
104055	AA393755	Hs.117211	ESTs; Highly similar to CGI-62 protein [H.sap	3.2
112917	T10196	Hs.4263	ESTs; Weakly similar to /prediction	3.2
120358	AA213459	Hs.100932	transcription factor 17	3.2
121857	AA426017	Hs.62694	ESTs; Highly similar to DNA-REPAIR PROTEIN CO	3.2
122124	AA434257	Hs.186679	ESTs; Moderately similar to !!!! ALU SUBFAMIL	3.2
132231	H99131	Hs.42635	ESTs	3.2
134272	X76040	Hs.223014	protease; serine; 15	3.2
115860	AA431719	Hs.61809	ESTs	3.2
115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.melano	3.2
134125	R38102	Hs.50421	KIAA0203 gene product	3.2
129160	AA131252	Hs.109007	ESTs	3.2
121710	AA419011	Hs.96744	DKFZP586D0823 protein	3.2
102242	U27185	Hs.32943	retinoic acid receptor responder (tazarotene	3.2
104956	AA074880	Hs.120975	ESTs; Weakly similar to hypothetical protein	3.2
113047	T25867	Hs.7549	ESTs	3.2
115017	AA251880	Hs.179982	tumor protein p53-binding protein	3.2
133780	M14219	Hs.76152	decorin	3.1
129453	AA421213	Hs.111632	Lsm3 protein	3.1
130353	X86018	Hs.172210	MUF1 protein	3.1
106036	AA412505	Hs.10653	ESTs	3.1
102234	U26312	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamma)	3.1
106133	AA424346	Hs.107573	sialyltransferase	3.1
116803	H47357		ESTs; Moderately similar to weak similarity t	3.1
106721	AA465194	Hs.6670	ESTs	3.1
107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein [H.sa	3.1
133228	N90029	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA;	3.1
104733	AA019498	Hs.23071	ESTs	3.1
103879	AA228148	Hs.50252	ESTs; Weakly similar to putative [C.elegans]	3.1
103038	X54941	Hs.77550	CDC28 protein kinase 1	3.1
135154	AA126433	Hs.173242	sorting nexin 4	3.1
114860	AA235112	Hs.106227	ESTs; Moderately similar to similar to murine	3.1
102437	U46569	Hs.221986	aquaporin 5	3.1
100352	D64159		Homo sapiens mRNA for 3-7 gene product, partl	3.1
103631	Z48570		H.sapiens Sp17 gene	3.1
104238	AB002364	Hs.27916	a disintegrin-like and metalloprotease (repro	3.1
108613	AA100967	Hs.69165	ESTs	3.1
115915	AA436884	Hs.48926	ESTs	3.1
120640	AA286945	Hs.163933	ESTs	3.1
124068	H03099	Hs.101619	ESTs	3.1
130376	U91931	Hs.155172	adaptor-related protein complex 3; beta 1 sub	3.1
131632	AA443671	Hs.29826	ESTs	3.1
131523	H88801	Hs.201676	M phase phosphoprotein 10 (U3 small nucleolar	3.1
115827	AA427890	Hs.44426	ESTs; Weakly similar to PHOSPHOLIPID HYDROPER	3.1
108828	AA131584	Hs.71435	DKFZP564O0463 protein	3.1
112198	R49483	Hs.22159	ESTs; Weakly similar to ZINC FINGER PROTEIN H	3.1
123960	AA621785	Hs.170008	methylmalonate-semialdehyde dehydrogenase	3.1
131538	Z29331	Hs.28505	ubiquitin-conjugating enzyme E2H (homologous	3.1
105616	AA280670	Hs.24968	ESTs	3.1
101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (zeta	3.1
100280	D42085	Hs.155314	KIAA0095 gene product	3.1
132744	X54326	Hs.55921	glutamyl-prolyl-tRNA synthetase	3.1
103105	X61970	Hs.76913	proteasome (prosome; macropain) subunit; alph	3.1
106984	AA521201	Hs.7129	ESTs	3.1
105127	AA158132	Hs.11817	ESTs; Weakly similar to contains similarity t	3.1
102302	U33052	Hs.69171	protein kinase C-like 2	3.1
117708	N45114	Hs.46476	ESTs	3.1
111314	N74574	Hs.33922	H.sapiens novel gene from PAC 117P20; chromos	3.0
132902	AA490969	Hs.168147	ESTs	3.0
130356	X84373	Hs.155017	nuclear receptor interacting protein 1	3.0

128420	AI088155	Hs.14146	ESTs; Weakly similar to unknown [H.sapiens]	3.0
108746	AA126974	Hs.43388	ESTs	3.0
127236	AI341818	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	3.0
114208	Z39301	Hs.7859	ESTs	3.0
107071	AA609053	Hs.35198	ESTs	3.0
104957	AA074919	Hs.10026	ESTs; Weakly similar to ORF YJL063c [S.cerevi	3.0
124073	H05394	Hs.127376	KIAA0266 gene product	3.0
130869	AA128100	Hs.2057	uridine monophosphate synthetase (orotate pho	3.0
101232	L28997	Hs.242894	ADP-ribosylation factor-like 1	3.0
104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapiens]	3.0
126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-relate	3.0
128584	M11433	Hs.101850	retinol-binding protein 1; cellular	3.0
100405	D86425	Hs.82733	nidogen 2	3.0
101335	L49054		Homo sapiens t(3;5)(q25.1;p34) fusion gene NP	3.0
108761	AA127514	Hs.61603	ESTs	3.0
111346	N89829	Hs.13259	ESTs	3.0
114988	AA251089	Hs.94576	ESTs; Weakly similar to phosducin; retinal [H	3.0
116008	AA449338	Hs.48589	ESTs; Weakly similar to finger protein HZF6;	3.0
116545	D20313	Hs.74899	ESTs	3.0
117873	N49967	Hs.46624	ESTs	3.0
121463	AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 protein [H.s	3.0
128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapiens]	3.0
131185	M25753	Hs.23960	cyclin B1	3.0
134380	D38073	Hs.179565	minichromosome maintenance deficient (S. cere	3.0
105740	AA293206	Hs.10852	ESTs	3.0
130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture antig	3.0
134423	W96151	Hs.83006	ESTs; Highly similar to CGI-139 protein [H.sa	3.0
104896	AA054228	Hs.23165	ESTs	3.0
134407	X72964	Hs.82794	caltractin (20kD calcium-binding protein)	3.0
106378	AA445994	Hs.21331	ESTs	3.0
112283	R53545	Hs.20952	Homo sapiens clone 24411 mRNA sequence	3.0
109018	AA156960	Hs.114992	ESTs	3.0
114239	Z39742	Hs.222478	ESTs	3.0
114969	AA250775	Hs.87747	ESTs	3.0
116408	AA608752	Hs.71969	Homo sapiens mRNA; cDNA DKFZp564P0823 (from c	3.0
115286	AA279803	Hs.82204	ESTs	2.9
105809	AA393827	Hs.20104	ESTs	2.9
113811	W44928	Hs.4878	ESTs	2.9
107248	D59894	Hs.34782	ESTs	2.9
134489	U09284	Hs.112378	LIM and senescent cell antigen-like domains 1	2.9
134064	D87685	Hs.78893	KIAA0244 protein	2.9
127370	AI024352	Hs.70337	immunoglobulin superfamily; member 4	2.9
113277	T65797	Hs.11774	protein (peptidyl-prolyl cis/trans isomerase)	2.9
132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.9
109010	AA156460	Hs.44229	dual specificity phosphatase 12	2.9
130095	F01831	Hs.14838	ESTs	2.9
106618	AA459249	Hs.8715	ESTs; Weakly similar to Similarity with snail	2.9
103427	X97303		H.sapiens mRNA for Ptg-12 protein	2.9
133980	D00760	Hs.181309	proteasome (prosome; macropain) subunit; alph	2.9
111353	N90430	Hs.6616	ESTs	2.9
105344	AA235303	Hs.8645	ESTs	2.9
134498	M63180	Hs.84131	threonyl-tRNA synthetase	2.9
117910	N50828	Hs.12940	zinc-fingers and homeoboxes 1	2.9
118903	N90774	Hs.132207	ESTs; Moderately similar to !!!! ALU SUBFAMIL	2.9
121713	AA419198	Hs.105577	ESTs	2.9
129080	H19307	Hs.108507	ESTs	2.9
129404	AA172056	Hs.111128	ESTs	2.9
129457	X55330	Hs.207776	aspartylglucosaminidase	2.9
130352	D87450	Hs.154978	KIAA0261 protein	2.9
133415	X69699	Hs.73149	paired box gene 8	2.9
120649	AA287115	Hs.99697	ESTs	2.9
131257	AA256042	Hs.24908	ESTs	2.9
134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	2.9
116734	F13789	Hs.93796	DKFZP586D2223 protein	2.9
105028	AA126719	Hs.25282	ESTs	2.9
114986	AA251010	Hs.87807	ESTs	2.9
105651	AA282481	Hs.18439	ESTs	2.9
101714	M68874		Human phosphatidylcholine 2-acylhydrolase (cP	2.9
123398	AA521265	Hs.105514	ESTs	2.9
106007	AA411462	Hs.11042	ESTs; Weakly similar to veli 1 [H.sapiens]	2.9
109450	AA232183	Hs.173042	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.9
104685	AA010530	Hs.9599	Human BAC clone GS025M02 from 7q21-q22	2.9
108677	AA115629	Hs.118531	ESTs	2.9
116028	AA452112	Hs.42644	thioredoxin-like	2.9
105404	AA243303	Hs.21187	ESTs	2.9
132365	AA598694	Hs.46541	Homo sapiens PAC clone DJ0894A10 from 7q32-q3	2.9
119638	W52480	Hs.56148	ESTs; Moderately similar to NY-REN-58 antigen	2.9
124637	N80716	Hs.75798	Human DNA sequence from clone 1183I21 on chro	2.9
130588	AA287735	Hs.16411	Human DNA sequence from clone 1189B24 on chro	2.9
105640	AA281623	Hs.7525	ESTs; Weakly similar to KIAA0742 protein [H.s	2.9
131818	Z39297	Hs.3281	neuronal pentraxin II	2.9
119298	T23820	Hs.155478	cyclin T2	2.9
128742	D00763	Hs.251531	proteasome (prosome; macropain) subunit; alph	2.9
115089	AA255876	Hs.86919	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.9

100468	D89289	Hs.118722	fucosyltransferase 8 (alpha (1;6) fucosyltran	2.8
132920	L06133	Hs.606	ATPase; Cu++ transporting; alpha polypeptide	2.8
113490	T88700	Hs.173374	ESTs	2.8
133451	Y00764	Hs.73818	ubiquinol-cytochrome c reductase hinge protei	2.8
128770	H98645	Hs.143460	protein kinase C; nu	2.8
129122	N62515	Hs.108790	ESTs	2.8
104827	AA035630	Hs.8551	PRP4/STK/WD splicing factor	2.8
111348	N90041	Hs.9585	ESTs	2.8
130987	R45698	Hs.21893	ESTs; Weakly similar to cAMP inducible 2 prot	2.8
102139	U15932	Hs.2128	dual specificity phosphatase 5	2.8
114902	AA236359	Hs.39504	ESTs	2.8
106094	AA419461	Hs.18127	ESTs	2.8
126438	N93125	Hs.137300	ESTs	2.8
107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	2.8
104491	N71513	Hs.39328	ESTs	2.8
105043	AA132239	Hs.11810	ESTs; Weakly similar to CD4.2 [C.elegans]	2.8
106855	AA486182	Hs.17975	ESTs	2.8
109695	F09530	Hs.180591	ESTs; Weakly similar to R06F6.5b [C.elegans]	2.8
120455	AA251083	Hs.104347	ESTs	2.8
130861	N23393	Hs.20509	ESTs	2.8
131649	AA481254	Hs.30120	ESTs	2.8
128517	AA280617	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapien	2.8
100486	HG1112-HT1112		Ras-Like Protein Tc4	2.8
116729	F13700	Hs.115823	ribonuclease P; 40kD subunit	2.8
101851	M94250	Hs.82045	midkine (neurite growth-promoting factor 2)	2.8
115465	AA286941	Hs.43691	ESTs	2.8
100137	D13627	Hs.15071	chaperonin containing TCP1; subunit 8 (theta)	2.8
125837	H05323	Hs.146401	endothelial monocyte-activating polypeptide	2.8
131562	U90551	Hs.28777	H2A histone family; member L	2.8
129445	AA306121	Hs.111515	ESTs; Weakly similar to predicted using Genef	2.8
129239	D31544	Hs.109701	ESTs; Moderately similar to weak similarity t	2.8
106507	AA452584	Hs.91585	protein phosphatase 1; regulatory (inhibitor)	2.8
101664	M60752	Hs.121017	H2A histone family; member A	2.8
129426	AA412087	Hs.168272	EST; Highly similar to protein inhibitor of a	2.8
103437	X98260	Hs.82254	M-phase phosphoprotein 11	2.8
129821	F11019	Hs.12696	cortactin SH3 domain-binding protein	2.8
130160	Z39228	Hs.151344	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransfe	2.8
104257	AF006265	Hs.9222	estrogen receptor-binding fragment-associated	2.8
116204	AA465701	Hs.108646	ESTs	2.8
125914	AA262925	Hs.180034	cleavage stimulation factor; 3' pre-RNA; subu	2.8
131510	AA207114	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	2.8
106291	AA435551	Hs.30824	ESTs	2.8
122761	AA459296	Hs.105039	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.8
107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-inducing f	2.8
108535	AA084505	Hs.226440	Homo sapiens clone 24881 mRNA sequence	2.8
116226	AA478729	Hs.76450	ESTs	2.8
120266	AA173939	Hs.193902	ESTs; Weakly similar to inner centromere prot	2.8
128654	H20689	Hs.103180	actin-like 6	2.8
116726	F13681	Hs.42309	ESTs	2.7
132640	U33821		Tax1 (human T-cell leukemia virus type I) bin	2.7
133273	AA147725	Hs.69469	dendritic cell protein	2.7
108846	AA132983	Hs.44155	DKFZP586G1517 protein	2.7
105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (from c	2.7
129164	AA282183	Hs.109045	ESTs	2.7
133618	U78524	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding prot	2.7
120521	AA258785	Hs.107476	ATP synthase; H+ transporting; mitochondrial	2.7
116429	AA609710	Hs.82837	Human chromosome 3p21.1 gene sequence	2.7
110984	N52006	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	2.7
100372	D79997	Hs.184339	KIAA0175 gene product	2.7
125134	W19228	Hs.100748	ESTs	2.7
129254	AA453624	Hs.1098	deoxynucleotidyltransferase; terminal	2.7
102339	U37022	Hs.95577	cyclin-dependent kinase 4	2.7
106589	AA456646	Hs.28661	ESTs	2.7
119118	R44122	Hs.42743	ESTs; Weakly similar to predicted using Genef	2.7
105973	AA406320	Hs.21201	DKFZP566B0846 protein	2.7
106317	AA436568	Hs.172140	ESTs	2.7
115551	AA365527	Hs.177861	ESTs; Highly similar to CGI-110 protein [H.sa	2.7
103789	AA096178	Hs.70337	immunoglobulin superfamily; member 4	2.7
105079	AA143190	Hs.12677	ESTs; Highly similar to CGI-147 protein [H.sa	2.7
109299	AA205649	Hs.86371	zinc finger protein 254	2.7
122089	AA432136	Hs.98682	ESTs	2.7
129108	L20321	Hs.1087	serine/threonine kinase 2	2.7
129385	D82675	Hs.110950	Homo sapiens clone 25007 mRNA sequence	2.7
131412	U34044	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selenium d	2.7
104052	AA393164	Hs.97644	mammaglobin 2	2.7
116254	AA481146	Hs.41086	ESTs; Weakly similar to OXYSTEROL-BINDING PRO	2.7
106878	AA488872	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (from c	2.7
114652	AA101416	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED SPLICI	2.7
106831	AA482014	Hs.29463	centrin; EF-hand protein; 3 (CDC31 yeast homo	2.7
101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypeptide E	2.7
124428	N36881	Hs.82202	ribosomal protein L17	2.7
114471	AA028074	Hs.103387	ESTs	2.7
102051	U07550	Hs.1197	heat shock 10kD protein 1 (chaperonin 10)	2.7
106916	AA490814	Hs.24170	ESTs; Weakly similar to ribosomal S1 protein	2.7

116142	AA460649	Hs.39457	ESTs	2.7
109912	H05509	Hs.24639	ESTs	2.7
103193	X70476	Hs.75724	coatomer protein complex; subunit beta 2 (bet	2.7
102046	U07151	Hs.182215	ADP-ribosylation factor-like 3	2.7
104567	R64534	Hs.101469	ESTs	2.7
112996	T23539	Hs.7165	zinc finger protein 259	2.7
118138	N57773	Hs.93560	ESTs; Weakly similar to trg [R.norvegicus]	2.7
123095	AA485724	Hs.192119	ESTs	2.7
124315	H94892	Hs.6906	v-ral simian leukemia viral oncogene homolog	2.7
124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (from cl	2.7
132834	H77546	Hs.57898	ESTs; Highly similar to NY-REN-49 antigen [H.	2.7
107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	2.7
130648	AA075427	Hs.17296	ESTs; Weakly similar to /prediction	2.7
106685	AA461551	Hs.16251	ESTs; Highly similar to 73 kDA subunit of cle	2.6
133848	AA093287	Hs.76728	ESTs	2.6
134880	AA092376	Hs.90606	15 kDa selenoprotein	2.6
128871	AA400271	Hs.106778	Homo sapiens mRNA for putative Ca2+-transport	2.6
106846	AA485223	Hs.34892	ESTs	2.6
119892	W84548	Hs.94896	ESTs	2.6
132309	AA460917	Hs.2780	jun D proto-oncogene	2.6
132923	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	2.6
114365	Z41688	Hs.18653	ESTs	2.6
114162	Z38909	Hs.22265	ESTs	2.6
133370	AA156897	Hs.72157	DKFZP564I1922 protein	2.6
106818	AA480890	Hs.3542	ESTs	2.6
133501	W16684	Hs.74284	ESTs; Moderately similar to Similar to S.cere	2.6
100530	HG1869-HT1904		Male Enhanced Antigen	2.6
130553	AA430032	Hs.252587	pituitary tumor-transforming 1	2.6
108917	AA137078	Hs.173648	ESTs	2.6
122249	AA436679	Hs.258543	ESTs; Highly similar to CGI-07 protein [H.sap	2.6
119598	W45531	Hs.94642	ESTs	2.6
119902	W84865	Hs.40094	Human DNA sequence from clone 167A19 on chrom	2.6
133272	AA465016	Hs.69423	kallikrein 10	2.6
132575	AA045365	Hs.5188	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.6
130459	AA460264	Hs.155983	KIAA0677 gene product	2.6
133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (beta)	2.6
131130	T19399	Hs.23255	nucleoporin 155kD	2.6
112043	R43317	Hs.26312	glioma amplified on chromosome 1 protein (leu	2.6
116146	AA460701	Hs.193200	ESTs	2.6
122378	AA446100	Hs.103617	ESTs	2.6
103134	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
133395	AA491296	Hs.72805	ESTs	2.6
115652	AA405098	Hs.38178	ESTs	2.6
104975	AA086071	Hs.50758	chromosome-associated polypeptide C	2.6
134691	M59979	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	2.6
112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	2.6
100092	AF000231	Hs.75618	RAB11A; member RAS oncogene family	2.6
102635	U66838	Hs.79378	cyclin A1	2.6
104490	N71503	Hs.43087	ESTs; Weakly similar to dysferlin [H.sapiens]	2.6
106813	AA479922	Hs.181022	ESTs	2.6
106872	AA487907	Hs.18282	ESTs; Highly similar to unknown [H.sapiens]	2.6
107022	AA599041	Hs.28866	programmed cell death 10	2.6
107113	AA610073	Hs.23900	ESTs; Weakly similar to oligophrenin-1 like p	2.6
113281	T66300	Hs.112356	Homo sapiens mRNA for lipoyltransferase; comp	2.6
115586	AA399218	Hs.92423	ESTs	2.6
115779	AA424183	Hs.70945	ESTs	2.6
122895	AA469946	Hs.105325	ESTs	2.6
124726	R15740	Hs.104576	carbohydrate (keratan sulfate Gal-6) sulfotra	2.6
129775	R94659	Hs.12420	ESTs	2.6
131991	AA251909	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	2.6
132518	D57975	Hs.5064	ESTs	2.6
134612	AA451712	Hs.171581	ESTs; Highly similar to ubiquitin C-terminal	2.6
130313	AA620323	Hs.154320	ubiquitin-activating enzyme E1C (homologous t	2.6
131971	R70167	Hs.3611	ESTs	2.6
133175	AA134767	Hs.66666	ESTs	2.6
102083	U10323	Hs.75117	interleukin enhancer binding factor 2; 45kD	2.6
125670	AI432621	Hs.82685	CD47 antigen (Rh-related antigen; integrin-as	2.6
121822	AA425107	Hs.97016	ESTs; Moderately similar to SH3 domain-bindin	2.6
106719	AA465171	Hs.236844	ESTs	2.6
130029	AA236412	Hs.236510	ESTs; Moderately similar to PFT27 [M.musculus	2.6
124328	H97781	Hs.14415	ESTs; Highly similar to CGI-108 protein [H.sa	2.6
105387	AA236951	Hs.108636	chromosome 1 open reading frame 9	2.6
103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit; alph	2.6
116294	AA489000	Hs.93748	ESTs; Moderately similar to TRANSCRIPTION FAC	2.6
135339	D59269	Hs.127842	Homo sapiens mRNA full length insert cDNA clo	2.6
125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 2	2.6
102504	U52077	Hs.247948	Human mariner1 transposase gene; complete con	2.6
131076	H44386	Hs.22666	ESTs	2.6
114096	Z38342	Hs.27007	chromosome condensation 1-like	2.6
120402	AA234339	Hs.50282	GTP-binding protein ragB	2.6
102125	U14550	Hs.107573	sialyltransferase	2.6
134653	AA452818	Hs.87385	ESTs	2.6
101959	S80343	Hs.180832	arginyl-tRNA synthetase	2.6
116766	H13260	Hs.95097	ESTs	2.6

104954	AA074514	Hs.26213	ESTs; Weakly similar to protein [H.sapiens]	2.5
108771	AA127924	Hs.71034	ESTs	2.5
116439	AA610068	Hs.43913	PIBF1 gene product	2.5
133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	2.5
132792	AA401903	Hs.242985	hemoglobin; gamma G	2.5
129620	AA010686	Hs.239720	ESTs; Weakly similar to KIAA0691 protein [H.s	2.5
120296	AA191353	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.s	2.5
115615	AA401186	Hs.48617	ESTs	2.5
102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A) expre	2.5
106288	AA435536	Hs.24336	ESTs	2.5
107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	2.5
104525	R16007	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	2.5
128917	AA204876	Hs.206097	oncogene TC21	2.5
102299	U32907	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.5
115363	AA282071	Hs.152759	activator of S phase kinase	2.5
130399	AA449417	Hs.155356	Homo sapiens mRNA for putative glucosyltransf	2.5
130752	D50927	Hs.18895	tousled-like kinase 1	2.5
132724	AA417962	Hs.55498	geranylgeranyl diphosphate synthase 1	2.5
106743	AA476352	Hs.21938	ESTs; Weakly similar to KIAA0704 protein [H.s	2.5
128949	AA190993	Hs.8850	a disintegrin and metalloproteinase domain 12	2.5
125685	AI040346	Hs.4943	hepatocellular carcinoma associated protein;	2.5
105826	AA398243	Hs.21806	ESTs; Moderately similar to similar to NEDD-4	2.5
110841	N31610	Hs.18645	ESTs; Weakly similar to partial CDS [C.elegan	2.5
111987	R42036	Hs.6763	KIAA0942 protein	2.5
132669	AA188378	Hs.54602	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.5
100398	D84557	Hs.155462	minichromosome maintenance deficient (mis5; S	2.5
130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subunit [	2.5
114481	AA033562	Hs.151572	ESTs	2.5
113404	T82323	Hs.70337	immunoglobulin superfamily; member 4	2.5
100260	D38491	Hs.174135	KIAA0117 protein	2.5
103563	Z22534	Hs.150402	activin A receptor; type I	2.5
104573	R68952	Hs.29780	ESTs	2.5
105025	AA126336	Hs.22744	ESTs; Weakly similar to ZINC FINGER PROTEIN 1	2.5
105524	AA258158	Hs.22153	ESTs; Weakly similar to KIAA0352 [H.sapiens]	2.5
106157	AA425367	Hs.32094	ESTs	2.5
107243	D59489	Hs.34727	ESTs	2.5
109920	H05733	Hs.30558	ESTs	2.5
109981	H09552	Hs.26090	ESTs; Weakly similar to T20B12.1 [C.elegans]	2.5
114518	AA046407	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like 1	2.5
114768	AA149007	Hs.182339	Ets homologous factor	2.5
118906	N91000	Hs.94433	ESTs	2.5
119025	N98926	Hs.55209	ESTs; Weakly similar to DMR-N9 PROTEIN [H.sap	2.5
131712	N29502	Hs.30991	KIAA0957 protein	2.5
132233	X04706	Hs.93574	homeo box D3	2.5
132740	AA227751	Hs.55896	ESTs	2.5
115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the beta t	2.5
128820	F10338	Hs.106309	Friend of GATA2	2.5
124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	2.5
128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypeptide F	2.5
121361	AA405494	Hs.183052	ESTs	2.5
134133	X93920	Hs.180383	dual specificity phosphatase 6	2.5
102502	U51678	Hs.78050	small acidic protein	2.5
115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity to Ye	2.5
132874	AA425776	Hs.58609	ESTs	2.5
109646	F04543	Hs.5028	DKFZP564O0423 protein	2.5
111197	N68093	Hs.22909	ESTs	2.5
102968	X16396	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD	2.5
124911	R88992	Hs.123645	ESTs	2.5
106628	AA459657	Hs.12311	Homo sapiens clone 23570 mRNA sequence	2.5
116988	H82527		ys69e12.s1 Soares retina N2b4HR Homo sapiens	2.5
131075	Y00757	Hs.2265	secretory granule; neuroendocrine protein 1 (	2.5
133578	X78627	Hs.75066	translin	2.5
100420	D86983	Hs.118893	p53-responsive gene 2	2.5
130743	W87710	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from cl	2.5
122465	AA448164	Hs.99153	ESTs; Highly similar to CGI-73 protein [H.sap	2.5
115117	AA256492	Hs.49007	poly(A) polymerase	2.5
124582	N68477	Hs.108408	ESTs; Highly similar to CGI-78 protein [H.sap	2.5
104771	AA025911	Hs.24994	ESTs; Highly similar to CGI-53 protein [H.sap	2.5
108059	AA043944	Hs.62663	ESTs	2.5
105628	AA281251	Hs.35696	ESTs; Weakly similar to putative zinc finger	2.5
109261	AA195255	Hs.61779	ESTs	2.5
119789	W73140	Hs.50915	kallikrein 5	2.5
130512	AA045304	Hs.181271	ESTs; Highly similar to CGI-120 protein [H.sa	2.5
134402	U25165	Hs.82712	fragile X mental retardation; autosomal homol	2.5
104769	AA025887	Hs.114774	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.5
125787	AA744748	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDEN	2.5
131775	AA459555	Hs.31921	KIAA0648 protein	2.5

TABLE 7B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
101335	46413_1	L49054 N87447 AA248791 AA452193 AI015525 AI762070 AA781526 AW183498 AA625682 AI268713 AA400391 AI193725 AW590304 W56360 AA936067 AI990398 AA406183 AA628888 AA844206 AA621117 AI141092 AI808150 BE379750 AI351482 AA093527 AA405119 AA400562 AW368723 AA463811 AW242927 R50034 W56334 F21257 AA164314 BE074125 AA470924 AI307439 W16738 AA026647 T35999 T19178 AA164313 AI744010 AI015466 AI014921
100906	4312_1	AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 AI795876 AA644165 T36030 AW392852 AA446421 AW881866 AI469428 BE548103 T96204 R94457 N78225 AI564549 AW004984 AW780423 AW675448 AW087890 AA971454 AA305698 AA879433 AA535069 AI394371 AA928053 AI378367 N59764 AI364000 AI431285 T81090 AW674657 AW674987 AA897396 AW673412 BE063175 AW674408 AI202011 R00723 AI753769 AI460161 AW079585 AW275744 AI873729 D25791 BE537646 T81139 R00722
102221	3861_1	NM_006769 U24576 AW161961 AW160473 AW160465 AW160472 AW161069 AI824831 AW162635 AI990356 AW162477 AW162571 AI520836 AW162352 AW162351 AW162752 AI962216 AI537346 AA853902 H17667 BE045346 BE559802 BE255391 AA985217 AA235051 AI129757 AW366451 T34489 D56106 D56351 AI936579 AW023219 AW889335 AW889120 AW889232 AW889175 BE093702 AW889349 AA147546 AI952998 AA912579 AI143356 AW902211 R64717 AW157236 AI815242 D45274 AW263991 AA442920 AA129965 AL035713 AI923255 AI949082 AI142826 AI684160 AI701987 AI678954 AI827349 BE463635 AW628092 AW302281 AA493203 BE348856 BE536419 AW193969 AW673561 AW592609 AI224044 H43943 AA091912 R49632 R48353 AI568409 R48256 AI198046 H27986 H43899 AI678759 AI680310 AI624220 H17052 AA156410 N56062 AI699430 AA664529 T09406 T10459 AA627506 AI379584 N83831 N88633 AW022651 AA971281 AA248036 AI039197 AI914689 AA973825 AL047305 AA129966 AI798369 AW264348 AI445879 AI658759 N67924 AI933507 AI216121 AI333174 T10972 AI375028 AI186756 AI273778 AA610487 AI797946 AA853903 AA903939 AI338587 AI278494 AW627595 AA904019
101714	30725_1	M68874 AL022147 M72393 AL049797 BE439441 T27650 AI766240 AW150345 AW778943 AI627464 BE439479 AA587049 AI277900 AI984983 AI630935
116803	55078_4	H47357 W33034 H55976 H55975 R67830 AA527091 F24482 AW841585 R66514
116988	185904_1	AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526
132640	179_1	AW162087 AA224538 AA471218 AA088655 AA375275 BE440052 AF090891 AA324435 AF063549 AI110675 AA322223 AW953306 AA233590 AW949864 AW949859 AA383721 AA081878 U33821 NM_006024 AA350900 AA081588 AI148087 AF268075 AA088185 AI142478 AA081824 AI887930 AA070570 BE185248 AI459825 BE257794 AA420459 AA420859 AA777997 AA081219 AW815721 AW854758 AA157932 BE018208 AW378974 AL041212 AI247564 AW581897 AI002897 BE543242 AI811690 AW852076 AW852270 AA360969 AA094943 AA090680 AW601554 AA099673 AA662226 AA356814 AA330174 AA187544 C02751 AA315460 BE168358 AW080447 AI813764 AI624222 AW156901 AI954032 AW473780 AI861975 AA173643 AW511541 AI951492 BE301686 AA669760 BE182212 AA081009 T69431 AI186207 AA604124 AA707346 AA173953 AI016700 AI125916 AA358962 AI673719 T90593 T90497 T10776 AW513002 AW304292 AA724885 AW474759 AI811621 AW068925 AA666305 AI580161 AI128023 AW471151 AA534849 AA666358 AI078833 AI139223 AI244874 AI381658 AW263441 AI432440 AW802882 N66401 AA224251 AI167469 AI141060 AA099214 AI537130 AL120428 AA948655 D53110 AA076099 AA938617 AA826543 AI357914 AA565098 AA807994 AI288812 AA632832 AA157933 AA639802 AA634268 AA282337 AA551431 AA557374 AA256923 AA872943 AA009665 H89626 AA810386 T92925 T36145 AA632190 AA130436 AI686635 AA130437 AW392904 AW392839 AW392848 AW392836 AA729737 AA070450 AW392890 W04825 AA771848 AA084634 AA481985 AI263840 AI801006 AA235380 AI954229 AI559330 AI208724 AA887638 T25894 AA041269 W44443 AI581770 W46171 AA878485 W46535 AA197336 AA894945 AA394224 AI766834 AI582590 AI033007 AA481889 AW190598 AW392855 R27279 AA398137 AI248407 AI241386 AI991753 AI826585 AA865699 AI096806 AI833030 AA041279 AW888745 AI703279 N70572 AI912553 BE549931 AI240422 AW376187 AW591692 AA975905 AW614967 AA009666 W44332 AA664659 T06561 BE468150 AI650695 AA587920 AI473310 AI032991 AA256499 AW104241 BE163782 AI984973 BE163613 AI263906 AA628191 AA282072 BE163769 BE163775 AI492939 AI473315 D56907 AA587930 H89480 AI362373 AA598483 D56595 AI167590 C16223 AI935415 D62555 D62884 D63130 AI760286 AI650286 AW173598 AI499145 AI122566 AW903408 AI810569 AA854936 BE049510 D62065 D61900 D62101 R27475 AI469835 AI669086 N80399 N48922 N48746 AA481381 R22858 H13912 AC004549 AW602500 AW768788
103427	43892_1	BE514383 AA071273 AW247987 AW673286 BE312102 AW749824 BE071985 AW577383 BE071945 BE072005 AW577355 BE071965 AW239231 BE072000 BE071960 AW577360 AW749830 AW373020 X97303 AW999522 BE000192 BE562219 BE266655 BE264970
103631	152_34	R64730 AF214731 T19173 BE258318 AF161446 BE542228 BE383856 BE206748 BE543260 AA640735 AA788907 BE251313 BE221852 AW855357 AA224407 AW855346 BE150454 AW070651 BE326867 AW051698 AI829278 AI470927 AW855345 AI804942 AI971004 BE046620 AI863664 AA808492 AI915971 BE046949 AW590711 AI468066 BE409685 AA332653 BE385394 AA852623 BE255591 BE254968 AA211871 BE255493 BE257727 BE255389 BE257491 BE262528 BE261296 BE313277 BE261714 BE314316 Z28434 AA315545 BE008562 BE012093 BE161393 T31969 AA305848 AW955238 BE619156 AI191748 AA323396 AW361760 AA216118 BE264939 AA325954 AW580281 AA302597 AW888908 AW888893 BE312970 AA134402 H52679 AA478191 T34090 AW961505 Z24771 AA179552 R57244 BE315207 AW583121 AI372747 T33143 AW377460 T33141 R14922 AW352414 H93249 AW405576 T33102 R89545 N46625 H08434 BE165062 AW367891 H93121 H47325 T30931 AW402852 H47410 Z20368 T18928 T30758 H93254 AW389725 R96628 AI372407 R88995 AI815980 AW157278 AW607664 AW163288 AA133492 AA099328 AA157348 AI816063 AW449556 AA157252 AW608980 H66576 AW821127 T32030 AW856058 AA032188 Z42120 R18582 AW402392 BE408021 AA280989 AA039427 AA035354 AW328008 T94186 R97481 AA181444 AA774697 BE613141 AW630221 H13066 AI124578 AW754481 BE262112 AW839942 H60108 AW364002 AW363800 BE547161 BE082634 AA642471 BE619719 BE082719 W28879 AW794944 C01685 AI291127 AW166099 AI936102 AI478929 R70284 AA872914 W31065 N54216 AI568741 H56262 NM_017425 Z48570 AI831777 T75007 AA354867 AA427988 AI922844 AA733170 AW821145 BE081547 AW881571 AW881573 AW055249 AA204724 AI417415 AI127303 AI355013 AI039527 AW593259 AA576745 AI457317 AW593236 H93126 BE396072 AL134941 AW629175 AI424011 AA115732 AA179986 AI334944 AW367922 AW152304 AA806752 AI312418 AW935023 BE301136 AA032258 AI829922 AI372406 BE177074 AW513743 AI151526 AA975643 AA478034 AI814920 AW080063 AI032624 BE177107 AA319768 AW935098 AI017620 AA974477 D51441 C14225 AL043583 D80145 AI690771 AW009711 AW881570 AI220431 N51090 AI143003 AA961480 AA039351 AI094885 AI096520 AA179553 AA593974 AI373929 AA677252 AA687374 AA886867 AA312863 AI150654 AI138450 AA133209 H99368 AI565632 AW070496 AI539748 H59455 AI811537 H52680 T74907 AI499657 R96670 AA854796 AA427863 AA224345 AA889899 AI347782 AA931056 AI076059 AI360841 AI797975 AI362268 AI200968 BE350785 R97433 N98499 AA134403 AA035355 AW263162 AI369607 D80144 AI376627 AI520801 AA365942 AI707705 AI123495 T33101 H08716 AA804238 AA922201 AA723522 AW183592 AI445884 F34614 AW022342 AA363998 AA568793 AA152475 D31233 AA852622 AA099862 AI129147 AA922699 AA782664 T33142 T30009 T32913 AI676138 AI914657 N34899 AI372746 AI265911 AI352444 AA443158 AA910603 AI420273 AA868050 AI277700 C14224 AW082087 R41447 Z38385 AI911845 AI961888 R91976 F04560 AA661955 AI857675 AA369666 AA424207 N79953 AA382958 AA894626 AI884964 AA846989 AA215454 AI742580 AI339437 AI806879 AI091373 AA782558 AI026868 AW590904 AW204599 BE348235 AI819318 AA122324 AA939221 AW139711 AA131608 AW613548 AA122286 AI309179 AA437247 AW339322 AI671306 AW439848 AA131701 AI078075 N64624 AA812881 AI140547
129097	25953_1	BE243933 AA355449 T29766 F08396 N83324 NM_006963 S50223 AI207648 AA258092 AA113952 AI311718 AI128612 AW607449 M77172 AI951311 X52346 AA903307 AI569810 N55421 W77876 R37223 R83788 AA031666 H47092 AA133451 AA311095 AA906963 H87667 N56058 AA393593 W24864 H10710 F06925 F07239 AW386140 AA325018 AA235950 AW373176 N57158 AA258093 N39467 R21609 BE089979 R34173 AW889005 AA745644 AI693852 AA424914 AA744771 W72632 AI291213 AA524318 AI472134 AI911230 AA528418 AA115745 AA775720 AI671134 AA975044 AW298117 AA321015 N26288 AW952194 AI743379 AI204233 AI801026 AA830690 AI146980 AW104611 AI338576 R21507 AI367623 BE244484 AI269308 AA031667 AI884346 AA731989 AA988943 AA235951 AA807887 AA642645 AI246489 N29739 AI216718 AI383349 AI038618 AI351476 AA806031 AI914178 H10711 AI095573 H89220 AW470854 AA729015 R83353 AA782239 R34295 H87165 AW419059 AI653689 Z40349 H89114 AW074506 AA397785 AA888377 AI911228 F03193 AI468783 AA702615 AI830829 AA748323 R37224 AA424915 AA731647 H47183
120695	9683_3	AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA425910 AI017004 AI241295 AA402816 AA291468

100352	37786_1	AL133887 D64159 AF112218 AI766633 AL039303 AL133888 BE620604 AW976259 AW262792 AW591383 AI365413 N36652 AA807027 AI472041 BE620065
101084	13883_1	AW409934 AW245855 AU077157 AW163245 AW161434 AW250083 AA316055 BE621134 AA171883 BE272494 L05425 BE250310 NM_013285 BE311494 AA858436 AA308223 AW362598 AA373618 BE394454 AA126101 AA581348 AA303227 AA058438 AA126544 AL135350 AW996947 AA403201 AA446682 W79685 AW246249 AW577783 AW002316 AA320025 AW753913 AI798554 AW070650 BE250413 AW250835 BE076336 AI925558 AI907634 AW804193 AW804270 AA902387 AW804232 AW804255 AW607751 AI909114 AW157242 AA934590 AI628921 AI470650 AW409935 AW172793 AA401208 AW162279 AA888018 BE206452 AI826742 AA857353 AA483614 AA126418 AA722289 AA780182 AW768894 AW183614 AW156969 AI244063 AA863491 AI376281 AA582490 AA846248 AI474094 AW246802 AA446557 AA126000 AI699045 AI702310 AI253092 AA171554 AA831455 AW118384 AI954511 AI760439 AI867001 AA493881 W81287 AA515590 AA659297 AA635139 AA659293 AA766044 AA196109 N32569 AI907635
100502	26409_1	U15979 X17544 W52755 NM_003836 Z12172 AW370136 BE262564 T49116 AA333753 BE262238 BE313737 H38153 AW583056 R28890 BE259532 D16897 AA885610 AA911293 AA319627 R94472 R29022 AA443405 R96397 W04904 W01746 W01204 N74203 N58621 AA701996 AW418723 N53220 AA602813 AA576129 AA593786 AA911577 AA575957 AI149135 AW573058 AA772985 AI188918 AI372065 AA575838 W60010 AI004576 AI131265 AA319845 T50070 AI335742 AA235245 W32706 AA447372 R96355 N59573 AA904616 AI291224 BE467454 T49117 AI268620 AA928248 AA449494 AA318817 T49929 R94473 H38154 AI076649 AW935307 AW605112 AW935433 AW935342 AW935310 AW935345 AI298308 AW935395 AW935384 AI184857 AA319871 T29465 C21134 Z19785 AA329107 T52079 AW935346 C06234 AI951555 T49928 AA371745 AA369296 AA346673 R82547 T50006
102398	entrez_U42359	U42359

Table 8A lists about 54 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 3rd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 4th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 8A: ABOUT 54 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene Title
ratio: ration tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	12.1
101249	L33881	Hs.1904	protein kinase C; iota	11.8
132528	AA283006	Hs.50758	chromosome-associated polypeptide C	11.5
102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.0
115536	AA347193	Hs.62180	ESTs	10.0
129571	X51630	Hs.1145	Wilms tumor 1	9.3
105298	AA233459	Hs.26369	ESTs	7.8
121779	AA422036	Hs.98367	ESTs	7.3
104301	D45332	Hs.6783	ESTs	6.9
132191	AA449431	Hs.158688	KIAA0741 gene product	6.7
102136	U15552	Hs.85769	acidic 82 kDa protein mRNA	6.6
101804	M86699	Hs.169840	TTK protein kinase	6.5
132572	AA448297	Hs.237825	signal recognition particle 72kD	5.9
106738	AA470145	Hs.25130	ESTs	5.8
108857	AA133250	Hs.62180	ESTs	5.8
115291	AA279943	Hs.122579	ESTs	5.8
132632	N59764	Hs.5398	guanine-monophosphate synthetase	5.8
116401	AA599963	Hs.59698	ESTs	5.7
132725	L41887	Hs.184167	splicing factor, arginine/serine-rich 7 (35kD	5.7
129097	S50223		HKR-T1=Kruppel-like zinc finger protein [huma	5.6
134520	N21407	Hs.257325	ESTs	5.5
108778	AA128548	Hs.90847	general transcription factor IIIC; polypeptid	5.4
131228	AA279157	Hs.24485	chondroitin sulfate proteoglycan 6 (bamacan)	5.2
116238	AA479362	Hs.47144	DKFZP586N0819 protein	5.2
108055	AA043562	Hs.62637	ESTs	5.1
132939	U76189	Hs.61152	exostoses (multiple)-like 2	5.1
115909	AA436666	Hs.59761	ESTs	5.0
120438	AA243441	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	5.0
123494	AA599786	Hs.112110	ESTs	5.0
109648	F04600	Hs.7154	ESTs	4.9
132624	AA164819	Hs.53631	ESTs	4.9
111234	N69287	Hs.21943	ESTs; Weakly similar to ORF YGL221c [S.cerevi	4.9
135242	M74093	Hs.9700	cyclin E1	4.9
123005	AA479726	Hs.105577	ESTs	4.8
116296	AA489033	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (from c	4.7
100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	4.6
111345	N89820	Hs.14559	ESTs	4.6
102627	U66561	Hs.158174	zinc finger protein 184 (Kruppel-like)	4.5
106459	AA449741	Hs.4029	glioma-amplified sequence-41	4.5
102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)-like	4.5
129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	4.5
130376	R40873	Hs.155174	KIAA0432 gene product	4.4
120619	AA284372	Hs.111471	ESTs	4.4
122802	AA460530	Hs.256579	ESTs	4.4
116416	AA609219	Hs.39982	ESTs	4.3
115094	AA255921	Hs.88095	ESTs	4.2
126802	AA947601	Hs.97056	ESTs	4.2
126892	AI160190	Hs.76127	hect (homologous to the E6-AP (UBE3A) carboxy	4.2
105516	AA257971	Hs.21214	ESTs	4.1
131985	AA434329	Hs.36563	ESTs	4.1

114965	AA250737	Hs.72472	ESTs	4.0
120821	AA347419	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	4.0
134621	L02547	Hs.172865	cleavage stimulation factor, 3' pre-RNA; subu	4.0
134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	4.0

TABLE 8B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
101249	2520_1	L18964 NM_002740 L33881 AA095249 BE080871 AW605320 M85571 AA179776 AA160650 AW117327 BE467131 AW088338 AW937631 AW087514 AI480090 AI873147 T57875 AI217404 AA827196 AI279471 AA969093 AA815168 AA988896 AI754623 T28044 AW950302 AW950294 AI032193 AI953696 AI630583 AA062633 BE541355 AA180493 AW015748 AA255651
100661	23182_1	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655
116401	95855_1	AW893940 AW978851 AA034240 AI686323 AI767653 AA829515 AA053933 AA737691 W92607 AW261869 AA835698 AA447216 AI623248 Z21891 AA835700 AA599963 T20152 AA533167
116416	373989_1	AW753676 R11789 AW001886 AA609219 AW780420 AI860557 AI280331 AI334300 AI288870 AA669343 N29918 BE537790 AA934687 H79075 N42970 R63752
132191	54683_4	AA507576 AI610269 AI380079 R40309 AI203932 AI342128 AI342578 R43110 AW583269 AI375234 AI092708 R52802 AI028462 AI016062 AI189144 AI016691 W45515 AA551452 AA449431 T10046 AA424059 N62822 AW197701 AA465242 AI418989 AI942433 AI891115 BE302316 AI743979 AI283341 AW340338 AA774643 AW104778 AI078020 N21487 H97562 AA970063 BE327945 F03880 F03885 AA970699 AI298468 AI380330 AI247787 AA770467 AI200154 AI089863 AI089890 AI695738 W88524 AI471010 AA700191 AA778937 BE440182 R79225 AA338236 AA548984 AA907692 N21250 AW904736 AI909337 AA987772 AW959228 AI149372 N29644 AI039967 AA677529 AI694291 R85811 N28672 AA465598 AA321185 AW130492 AI824479 AI682992
130941	2774_1	NM_000869 D49394 BE252349 AW249320 AW249140 AW250535 S82612 AJ003079 AJ005205 AW178407 AA811360 AW976407 AW976408 AW248903 AA731733 AA804189 AA703169 AI435492 AI076288 AA912176 AW248713 AA743457 R08170 C06167 R02351
115909	47548_1	AW872527 AA453863 AA442475 AF086541 AA365801 AI692575 AW131631 AA732993 W96131 AA436666 AA453779 AA365504 AW959717 AA975337 AA365503 AI632902 AA659686 AA665087 C00396 AA988869
108778	18565_1	AF133123 NM_012086 AA128292 S81493 AL137453 BE614053 AA307628 BE009521 BE085659 BE085542 BE085598 AL120654 R13165 AA429306 R13465 R55236 AW994182 W00838 AW994417 AW994404 AW994426 AW994321 AA516147 AA345603 AW953009 BE315104 AI126654 AA626457 AA291327 H67983 H66271 H67976 AW270955 AA758221 AI023487 AI921811 AI953370 AF085850 R70992 N25129 AW295143 AI433661 AW608361 AA873402 AI217453 AI953358 AA262143 AA928495 AI475268 AI167211 AW385961 AA259045 AI762630 AA428238 AI001932 AI735550 AI951370 AA766807 S81492 AA918976 AI040967 R70939 AA469065 T70340 AA477615 AA478070 AI017743 AI608833 AI635824 AI186039 AA741312 AI040184 H67656 AA258221 AA731316 AI381293 AW298473 R55237 R37375 AI768014 AA128548 AI206773 AI879827 R64193
102136	17647_1	AA300576 U15552 NM_014597 AA223318 AA171806 BE269461 AW578439 AW604388 AW953513 AA772816 AW604383 AW577851 BE169672 AW117711 AW366303 AW366302 AW366308 AW366304 AW366300 AI908432 AW591937 AI358420 AW272622 C75067 AI926471 AW002266 BE064947 BE064722 T10372 AW838681 AI811119 AW262098 AA588547 AI916666 AI440083 AI078150 F24260 AA512919 AI953413 AI064798 AI420425 AA191324 BE503222 AI632721 AA180035 AA558329 W44843 T10610 W38442 BE542869 AI125024 BE279566 AW747936 AI589491 AA559096 AI090265 AA548959 AA223220 AW515936 AW368395 AW368407 BE540776 AI039762 AI584020 AA171691
108857	61_1	AK001468 AA190315 AA374980 AW961179 AA307782 AA315295 AA347194 AW953073 AW368190 AW368192 AA280772 AA251247 N85676 AI215522 AI216389 N87835 R12261 R57094 AI660045 AA347193 R16712 AW119006 N55905 N87768 AW900167 AI341261 AI818674 D20285 AI475165 AA300756 R40626 AI122827 AA133250 AI952488 AA970372 AA889845 AW069517 AI524385 AA190314 AI673359 AA971105 AI351088 AI872789 AI919056 AI611216 AK001472 BE568761 AA581004
102305	18424_1	AL043202 U33286 NM_001316 AF053641 AL048759 N99830 AA263091 AW408174 N90467 R84306 AA317882 BE613644 AA307378 T10722 AA207207 AA315560 AA113938 AW386317 AW386316 L44546 AW386335 AA243317 AA713588 AA192541 AA649035 BE300737 AW752491 AW902334 AW993922 BE003403 AA251521 AA382754 AA339152 AA382619 H58600 H67810 T70379 T82109 D81644 D60375 H59003 BE075732 AA471242 H17790 F11801 T84903 R78076 BE614356 R16380 R16395 AA876127 W95535 AA164768 AI279876 H02142 C18698 AA365866 AW954410 AI539769 T39128 AL121103 AA192466 AA213367 AI963800 BE090601 Z20096 BE566508 AI969470 BE044090 T65536 AA837311 AA075484 AA075621 AA778294 AA587266 T69722 AA446118 X85624 AI334209 AI587101 AI281280 AA568602 AA946837 C75603 AA236997 AA459274 AI150191 AA165156 AI198839 AA789258 AI139373 AA236574 AI127770 AA678954 AI140786 AA113939 AI187231 AI754062 AI753243 AA934719 AW439362 H02038 C17463 AI400951 AA227539 N66040 R89384 AA872668 AI344110 W95420 AA164700 C05669 BE094097 AI826398 H58956 T17222 AW139044 AI271344 T16445 R42323 C75565 AA165228 AI025443 AA165229 C21496 AI826239 AI868711 AA582354 AA524392 R01549 R01641 Z21083 AA528463 T39127 AA989472 F09450 AA084485 BE004378 AW974353 AA137250 AI278406 AW609291 AA137249 AA142866 AA639198 AW609271 AW149760 AI025112 AA236620 AA937248 U90736 AW005487 AW674427 BE397971 AW609285 T65602 T99684 T97378 AW609366 T85647 AI572235 T99083 AA199583 AW303874 T35523 AA586445 Z39669 AA459503 N95643 AW821210 AW813461 AW582064 AW609293 AW609320 AW609270 AW582085 AW582071 AW609318 AW813451 AW813456 AW582079 AW609276 AW609280 AW609290 AW582101 AW582102 AW609263 AW609317 AW609256 AW609305 AW582063 F06655 AW605343 AA446426 BE090595 AW969578 T79852 AI082505 N63239 AI973168 AI086182 AA846711 AI874213 AA730605 AI927257 AA912624 D60376 T10180 AA705847 AI018123 AA493197 T67083 R77739 AA953087 R00885 AI370606 R01642 AA862914 N57843 AW023353 H77483 H68082 R42337 H58601 T97267
109648	708849_1	H17800 AI362549 AI671064 T23526 F03426 F04694 F04600 AI635856 Z38715 F02039 AW022635
132528	11027_8	T78736 AA284422 AA283006
101804	26687_1	M86699 NM_003318 AL133475 AA122377 Z21415 R57092 AA806569 AA811904 BE538323 R41558 AA421620 AI337292 AA470077 AW795371 AA543024 AI677941 AI472200 AI215042 AA732384 AA837143 AA804229 AI907533 AI742701 AA121159 AI973225 AI620839
132572	31281_1	AI929659 AA227827 AF069765 AW408768 NM_006947 AF077019 AA220974 H07969 C14621 D52294 BE512960 BE614138 BE258539 BE251981 AA355433 AA481126 AW403053 BE542282 AI929818 AL120605 AW753079 AW391834 BE018603 BE395262 W21406 AW663259 AW975690 W93905 W96519 AI863832 AA443177 AA730942 T99558 T86581 W19444 N55583 AI701020 AI928986 AI857864 AI590849 AW081819 AA714970 AI122630 W04887 AW662427 AA602680 W93645 AA582946 AW008812 AA311187 AA463631 AI421918 AI400518 AI921404 AA143770 AA587675 BE302192 AA813080 AI493386 AW327435 AW340871 AI143616 AA687231 AA218961 AI362249 AI378345 N74716 AW969249 AA468581 AA516399 AI274726 AI131244 AI572604 AI929236 AW327971 R65637 N90309 H07877 W96486 AI358806 T90801 AI383246 AI740957 T86758 AI471248 AI864233 AA910590 AI079094 AW805781 AA709025 AW196707 AW327436 AI903790 AI873956 T99348 AI924643 AW103910 AI802993 AI080390 T99098 D19794 AW327972 AI935904 AI288575 AW360875 AA779784 N93574 AW769295 W32639 AA363094 N89012 W39751 AI291329 AI291371 AA829411 AI985219 AI422775 AA918940 AA363108 AA192633 AF086131 AA373679 AA165043 AA355705 AI243507 AI027796 AA573461 AA757260 AI370979 AA574149 AA558276 N70650 AI478948 R35393 AA448435 AA334659 AW879356 AA436527 AW972044 W25165 AA521219 AI094141 AI302096 AW578551 AW578534 AW390535 AI131472 N50381 AA736938 AI089112 AA863053 AI359793 AA962268 T27353 D82590 AA448297 AI277168 AI368457 AA872737 AA330346 AA308346 AA342341 AA355159 T85701 BE162893 T99703
131985	113870_1	AA503020 AI858190 AI686571 AW615203 AW073686 AW172459 AI828762 AW150534 AI859795 AA411046 AI539195 AA404609 AI638559 AA434329 AA171844 AI684143 AA953518 AW470108 AI870700 AA706376 AI539668 AI683712 AA075579 AI682137 AA291512 AA554431 H51315 AA404225 AA075632 AA172293 H51911
132624	42095_1	AA326108 W74020 AW612698 AI750909 AA487800 AJ270695 AA044941 H20708 AA296750 AA018401 AA378581 AW964159 AA018887 R68533 AA525338 AA526640 H84308 AA278942 AA164818 AA847110 T82335 N25519 AA021474 N31381 N36297 AA838191 AA318932

		AA961206 N41430 N41439 AW630477 W37595 BE394538 AA365256 N47771 N34873 AA988105 AI242138 AW148523 AI978761 N50882 AA527448 AW086200 AI750910 N50868 AA709437 N51946 AI222179 AA732883 H96742 AW615360 N53720 W37490 R87362 AA613273 H98999 AI469022 AI368442 AI460122 N20486 N24087 AA164819 N24878 AW471270 AW590458 R68240 AA594434 N20400 AI419626 AW500664 AI033658 AA593215 AA907408 AA713508 AI422627 H85551 AA923571 D62680 AW627456 H96206 AA016289 AA485896 N25691
132632	4312_1	AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 AI795876 AA644165 T36030 AW392852 AA446421 AW881866 AI469428 BE548103 T96204 R94457 N78225 AI564549 AW004984 AW780423 AW675448 AW087890 AA971454 AA305698 AA879433 AA535069 AI394371 AA928053 AI378367 N59764 AI364000 AI431285 T81090 AW674657 AW674987 AA897396 AW673412 BE063175 AW674408 AI202011 R00723 AI753769 AI460161 AW079585 AW275744 AI873729 D25791 BE537646 T81139 R00722
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102627	25245_1	AL021918 AA160639 U66561 AA321623 U52098 AL119453 AA455712 N80080 N46550 W07223 N75923 W05057 AI811577 AA455657 AI275409 AI139121 AI927568 AI927562 AI139471 AA160473 N78795 AI719983 AI718928 AA723097 AI335776 N39140 N59184 AI587600 AI864812 AA732097 N74667 AA832398 H89600 D19825 AI554833
132725	29101_1	NM_006276 NM_006276 L41887 L22253 BE379909 BE567870 BE274265 BE539518 AW239523 AW239271 AI093618 BE504485 AA580279 AA494481 BE440161 AW780428 BE543960 D55986 AA852399 AI630020 W77996 AA278193 R10505 AI963201 AI739336 BE174301 AA662222 AA664912 AA244152 AW611553 BE503285 AA211023 AA383016 AI698174 AW195381 AA948229 AI768495 AI690437 N30025 AI718952 AI953572 BE464509 AA777315 AI337221 AW070910 AI953848 AW674561 H54177 AW510890 AW078699 AI436178 AA630759 BE502074 AA278769 AI499038 AW469072 AA778071 AW236753 AI933033 AI690458 AI276691 AW768235 AI952118 AA425156 AA610579 W73953 AA244153 W86034 AI948872 AI952678 AW087811 AI333591 AI869883 AI926911 W48865 AL048024 AA214485 AI972522 AI151368 W48738 AA214467 AA334640 AI678170 AA927525 AA581588 W96283 AA365470 AI471919 AW611488 AA211834 AI365198 AI698365 AW002238 AA507624 W96150 AA446490 AL048025 AA852400 AA362221 AI338376 R35083 AA290812 R10397 AA975988 AW236462 Z43032 H16969 F13487 D19858 AA452207 BE085942 AA344396 AW949533 AA279472 AW902406 AW070440 BE395195 H00835 AA300750 AA729303 AA420591 AA385025 AA420542 R69155 AA420592 AA281747 N88502 AI458206 AI700996 AW418607 AW341202 AI825692 W00640 AA214405 AA044744 AI950617 BE467493 AW474113 AA446310 BE328705 AI911573 AW243968 AI628622 AW173020 AW079958 AI140387 AW051969 AW299438 AI127170 AW769164 AI422435 AI307116 BE549519 AI371116 AA281748 AA701073 AA679948 BE551197 N50345 AW338776 BE326601 AI142892 AW470687 AI989568 AA911241 AW294822 AI174414 AA804366 AI004725 AW271994 AI559313 AI270102 AI351542 AW768904 AA765964 AI961708 AI149231 AA995907 AI094280 AI185753 H01219 AW768846 AA747500 AA970106 AI601238 AA513452 AW612802 BE075163 R39171 AI565328 AI375559 F10356 AA284625 BE241509 AI702889 AW193010 AA649847 AW439150 AA721407 AA810333 AA706384 AI049887 BE569015 BE622280 BE566618 AW967342 R69269
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134161	16074_1	AA634543 AI682259 AF117108 BE396917 NM_006547 U97188 U76705 BE560799 BE396918 BE269531 BE560268 BE560346 AA836048 AL023775 BE545535 AA427803 C18804 D58801 AA303353 U46218 BE539704 AA187966 AA252545 AA261821 D63197 AI824109 AI088047 AI424833 AI807368 AI250857 AA741476 AI146832 AA169615 AI809821 AI274288 AW136704 AI206172 AA917039 AA243584 AI808611 AW674709 AA935733 AW450092 AA905172 AA471196 AA302256 AW673348 AI352044 AW511295 AA247134 W81035 AA722962 AW662471 R64432 AW044616 AI086619 AW628546 AW043682 AA425750 AI743038 AI368723 AA187143 AI376987 AI803976 AI275537 AW471358 AW104877 AA195464 W81072 AW197351 AA932674 AI393420 AI434998 R63822 AW085083 AI240272 W87006 AA011347 H58428 AI497895 R23223
132939	11857_1	AB009284 AF000416 AA022636 BE082610 AW367997 AA491410 AA337477 AA336421 W38526 AA625283 AA773685 AA490078 T66134 AA847838 AA022647 AW054726 AI918001 AA431966 AI263596 AI804298 AW469314 U76189 AA779001 AA625945 AL042357 AI674730 AA410350 AK001450 AV654353 AA058443 D81618 AA853665 W31930 AA334445 AW955767 N47777 AA883784 AA428916 AI652062 AA329703 AI417923 AI435031 AA708791 AI989636 AI220345 AI239913 AI220102 AI435875 AI076731 AI377049 AI039173 AW972638 N90076 AW263652 BE440048 BE440013 AA577463 AI038774 AW204992 AA846580 AA501952 AA342058 AA508525 D61670 W31725 AI689499 AI955969 AA526628 AI282717 T66198
111345	6692_1	AW263155 AA314512 AW408152 AA360413 BE206274 AK001402 AA307665 AW954678 W39078 AW369236 AW369115 AW369096 AW753235 AW369072 AW361194 AW369125 AW364187 H94225 T79502 AA131908 BE071359 AW368503 AW801517 AW801322 AI674163 AA861077 AI738568 AI830199 AW118577 AI478895 AI688497 H92996 AW083479 AW970625 AW613124 AI632234 AI654210 AI696847 AI923423 AA131909 AA806630 AA806158 AW592520 R96509 AA813923 AA502823 AW467889 AA960972 AA994566 AI280346 AA884588 AA653563 AI200023 N89820 AW768792 C00145 R96554 T79416
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134520	13358_3	BE091005 BE541579 AW387738 AW386083 H13769 AW377820 AW369180 AW753239 AW672695 BE379572 AW021732 AW891450 AW891416 BE091358 N50375 BE091354 BE091365 BE091361 BE091363 BE091350 AA353863 AA845510 N21407 AW770981 AI361577 AA526557 AA525443 AW893622 AA630898 AI418983 BE172016 AA550754 AA664574 C16147 AA355902 AW958586 N51590 C20995 BE544186 AI337578 AA090549 AI807374 AW450654 BE067578 AA446781 AA447058 T10807 AA457082 AI267703 AI880220 BE568979 AW380506 BE150744 AW380468 AW380546 BE150713 D60029 H88099 BE546301 BE150731 AW368467 BE091348
135242	5782_1	AI583187 M73812 AW339829 M74093 BE252510 BE252518 BE536901 U40788 W95578 BE018493 BE544205 N83637 AI671049 AW439693 AW300786 AW374970 AA592960 AI215885 AI215884 BE302101 AI186210 AW771831 T54213 AW452924 AA834019 W95471 AA628312 AW304866 AA570076 AI559873 T54121
134621	27351_1	AA037145 L02547 NM_001324 AW411516 AA314711 AA143605 BE394455 AA325731 AA093227 AA083307 BE299438 BE295669 AA370886 AA338272 AA166862 BE304837 BE298306 R60507 AW238966 N72750 AW505406 AW994153 AA309742 AA309929 BE090721 AW904189 AW904214 AA363564 R94127 AA352101 R28249 AA206337 AW577208 AA385473 AA355463 AA400696 AA075587 W72815 AA554033 AA075530 AA620555 AA554034 T27804 AW950014 AI570740 AI268538 AA704423 AW411517 AI278646 AW339924 AI668917 AI796034 AA994601 R94082 AW027137 AA400652 AW299746 W72816 AA988494 AA146582 AW087489 AA992763 AW516454 AA992759 AW270444 AA227188 AI208929 AA167720 AI052527 AA865660 AA569368 AI888464 AI670003 AA827620 AA507543 AI888385 R88418 AW959083 AI341077 AI825719 BE552285 AA738076 AW085903 R28242
126802	116467_4	AW805510 AW805503 AW805500 AW805819 AW517040 AW473670 AW516701 T30141 AA894497 BE349504 AI272007 AI985274 BE501962 AW102975 AI801727 AW197918 T24046 AA947601 AW900958
126892	38252_1	AF121856 BE242657 U83194 AA226732 AI160190 AA948725 AI079958 AW513369 W39443 AW408479 W06854 AA094683 AI985095 AA316647 H96313 N78438 R81582 H95034 R79674 AA488552 W25292 W31697 W19918 T30640 R08686 H78637 AA165100 Z41909

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105298	8689_1	BE387790 BE276849 BE246825 BE246900 AA380487 AA332996 AW408727 AK000294 AI636887 AW197272 AW590657 AW594006 AI768979 AI751632 AA580098 AA313261 AA300475 AA133237 AA233499 BE242126 BE242597 BE242254 AA314374 AW961210 AW939345 AA173535 AA305779 R99373 AA128304 AA447246 AA476365 T34973 BE264878 N25149 Z24939 BE263038 AA128317 Z46082 H23504 AW378551 AA088533 AA442625 H15235 H79172 AA344697 AA344742 AL040280 BE173256 BE173129 T59749 AA088410 BE242311 AA173576 AA455337 AA129715 AA582953 AW612637 AA917038 AW340019 AW006315 AW593024 H05915 AW294592 AI146814 AW195659 AW440271 AI209090 AI288689 H98630 H15174 AI214454 AI569471 AA085808 AW188361 AI751631 AW440477 AW300860 AA516088 AI365108 AI305805 AI264064 AI246276 AA442611 AA807059 AA233459 AA875987 AI374653 AA972665 AA947515 AA436867 AI216423 AI657181 AI680306 AA436854 AI537153 AA883723 Z28659 AA705973 Z40741 AA463884 AI216025 AI564986 AA476316 AI432566 AI571662 AA447126 AW293675 AI675617 AW009004 H23498
120438	166102_1	AW015242 AA831493 AI292346 AI076966 AI191561 AA243441 AI183309 AA252613 AI038422 AI306531 AW051480 AI348605 AA195119 AI817119 AI091896 AA738440 AA195013 AA976687 AA459659 AI246250 BE219252 AI703457 AA243291 AA243401 AA989100 AA931640 AA459782
105516	9334_1	AK001269 AL354613 AA147472 AA490803 BE207628 AW816113 AA085574 AW503392 AA299910 AW750305 BE079539 BE079484 BE512838 AK001593 AW968772 AW967440 AW206280 AA251270 AI627886 AA303599 AA147473 BE206616 AA490611 AA715039 AW590866 AW590447 AI864512 AA204731 AA894490 BE001136 AA612785 AA237035 AA149960 Z44257 R12986 AA448446 AI734041 AA422167 BE220551 R66041 R32927 R32942 AA258773 AW386142 R53730 N54624 AW880296 AA253485 AW954441 H98989 AW614348 AI654838 AA779793 AW237213 N66635 AI186812 AA947479 BE158011 AI859480 AW805579 N52010 AA806305 AI628445 AW270990 AA778165 AA149949 AI650728 AA749108 AA687257 AI261661 AA747442 AA481351 AA206339 AA903407 AW473306 AI688930 AA262281 AA448310 AA748820 AI347430 BE465692 R32839 AW510564 AA436408 AA257971 AA253362 AA938330 AA513150 AA976840 AA687117 AI281547 AA046243 R32825 AI631554 AW139818 AI244536 R52946 AW235443 R40183 AA299909 AA811958 AI302918 Z40213 BE158047 BE158060 AA767245 AW748159 AW500735 AA094074
129097	25953_1	BE243933 AA355449 T29766 F08396 N83324 NM_006963 S50223 AI207648 AA258092 AA113952 AI311718 AI128612 AW607449 M77172 AI951311 X52346 AA903307 AI569810 N55421 W77876 R37223 R83788 AA031666 H47092 AA133451 AA311095 AA906963 H87667 N56058 AA393593 W24864 H10710 F06925 F07239 AW386140 AA325018 AA235950 AW373176 N57158 AA258093 N39467 R21609 BE089979 R34173 AW889005 AA745644 AI693852 AA424914 AA744771 W72632 AI291213 AA524318 AI472134 AI911230 AA528418 AA115745 AA775720 AI671134 AA975044 AW298117 AA321015 N26288 AW952194 AI743379 AI204233 AI801026 AA830690 AI146980 AW104611 AI338576 R21507 AI367623 BE244484 AI269308 AA031667 AI884346 AA731989 AA988943 AA235951 AA807887 AA642645 AI246489 N29739 AI216718 AI383349 AI038618 AI351476 AA806031 AI914178 H10711 AI095573 H89220 AW470854 AA729015 R83353 AA782239 R34295 H87165 AW419059 AI653689 Z40349 H89114 AW074506 AA397785 AA888377 AI911228 F03193 AI468783 AA702615 AI830829 AA748323 R37224 AA424915 AA731647 H47183
120619	169895_1	AW965339 AL045632 AA333229 AI806195 AA284372 AA206108 AA682533 AW449514 AA804785 AI215473 AI357263 AI651208 AI651753
129229	20927_1	AF013758 NM_006451 AI538709 AA209236 AA300293 AA367274 AA126598 AA324825 AW955225 F11436 AW374740 AW374714 AW374774 AW751514 W74780 AI909015 AW997079 AW997067 AW379344 AW363397 W38589 AA043823 BE169280 AI909016 AW994851 AI740638 AW148560 AW368339 AI858333 AA314718 AW954872 AW468734 AI681980 AW519045 AW055171 AA579286 AW069164 AW615004 AA345052 AI446735 AI142106 AA662683 AW002813 AI418280 AW613203 AI613333 AI354480 AI929755 AI146977 W74674 AW799610 AI798529 AI589422 AA043957 AI223043 AA157016 AI446759 D56729 AI587471 F30716 AA812125 AI537301 AA653347 D11966 AI434383 AA598533 AI287254 AW139140 AW051033 AA601911 AI702506 AA737460 T30221 AI129081 N90213 AA805225 AI798518 BE001071 T10841 W20199 AW664594 AW195667 D60123 D61496 AW468018 AI720097 N90553 AA829375 AW513266 H92758 AA585324 C14767 AI922391 D60124 D60666 AW071558 BE044120 AA728821 AA211941
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106459	3897_1	AA789081 AW408328 NM_006530 U61384 AA449641 AW138216 AA448598 AJ245746 AI365301 N44728 AA255743 AA360783 BE550380 AW593925 AI962309 AA322097 AW964625 AI695988 AW672827 BE543256 AK001413 AW603395 AA651700 AA449053 AA465540 AW083185 T62128 Z78373 AW673713 AW468061 BE350755 AW673958 AW675504 AA995709 AW574841 AA835883 AI248439 AA548364 T62072 N33193 AA814046 AI376210 AI340020 AA449766 AA703407 AA427613 AI470108 AI298757 AA507602 AI658941 AA449478 AA633165 AA449741 AA831821 AA903673 AA682588 AW673075
115094	190995_1	AA255920 AI817197 AA255921 AI612925 AW874669 AA493440
129571	1726_1	X51630 M80232 X61631 S75264 AA172249 AA134066 AA130278 AA130187 AA130291 AA031554 AI246677 Z21455 AI745434 AW273544 AW088613 AW471307 AI745483 AI399854 AI683952 AA031555 AA298075 AI935945 T29809 AA172099 AA356120
121779	287665_1	AW513143 AA422036 AI821669 AW514232 AA477828 AW772009 AW439799 AW089884
106738	174703_1	AW149266 R49246 AW237401 AA938113 AW665871 AI969698 AI950812 AW874276 AI571939 AA741222 AI869822 AW104061 AI569994 AW972559 AA506012 AI553704 AA470145 AI332421 AA218990 AW131361 AI709076 AW392488 AW392477 AI970981 AW392476 D61949 H44981 BE172698
123005	75629_1	AW369771 AW748174 AA290801 AA419198 AA044331 AA127909 AW995442 AI480343 AA044582 AW956159 AA373451 AA127965 AL134913 AW994956 BE622314 BE006298 BE006312 BE006305 BE006317 BE006303 AA043906 AA234175 AA479726
108055	100690_1	AJ404672 AJ289819 AW976000 AA043561 AW450885 AW452879 AA043562 AA788832 AI564338 AI564330 AI368875 AA643607 AA994375 AA810342 AI367704
115291	22325_1	BE545072 AI540751 AA301103 AI916675 N85422 BE563965 AA327978 AI816094 AK001515 BE501319 AA279943 BE138895 AA343765 AW963051 AW082308 AI823992 AI653752 AI589007 AI816135 AI566535 BE501307 AW272765 AW242239 AA766315 AI014927 AA578848 AI354483 AI476548 AI038579 AA973322 AA992180 AW472921 BE504789 AI392988 AA506076 AA769228 AI370562 AL137710 BE005656 AW965920
130376	24827_-4	R40873
115536	61_1	AK001468 AA190315 AA374980 AW961179 AA307782 AA315295 AA347194 AW953073 AW368190 AW368192 AA280772 AA251247 N85676 AI215522 AI216389 N87835 R12261 R57094 AI660045 AA347193 R16712 AW119006 N55905 N87768 AW900167 AI341261 AI818674 D20285 AI475165 AA300756 R40626 AI122827 AA133250 AI952488 AA970372 AA889845 AW069517 AI524385 AA190314 AI673359 AA971105 AI351088 AI872789 AI919056 AI611216 AK001472 BE568761 AA581004
114965	153955_1	AI733881 AA165164 AI826437 AI972791 AA165165 BE219575 AI732586 AI821571 AA250737 AW136875 AI984273 AI249271
131228	8262_1	AW207469 AL079814 AA354351 AF020043 AW291396 BE550484 NM_005445 BE046917 AW594249 AI651554 AI631515 AW771344 AI969758 AI699982 AA247175 AI244676 D44780 AW593978 AI638479 AI373676 AW089547 AL121432 AA554698 AI016991 AI087260 AW449939 AF067163 W40482 AW316558 AI537184 AW381979 W40150 AI810562 AA573151 AI630288 AI675561 AI674420 AW840733 AW022653 AA114219 AJ005015 AL046587 AA878141 AW271896 AW085287 AA150465 BE536295 AA463412 BE093222 AA213739 AA485586 AI825913 AA706307 AI337348 R31995 AI819641 R32095 AW976653 AA742375 AA142957 AI808214 AW468303 AI205987 AI206347 AI769095 BE501640 AA113866 AI093931 AI752855 AA612743 AA463411 AA279157 AI123791 AA213570 AI207305 AW627814 R31945 R32040
116238	10772_1	AV660717 NM_015437 AL050285 R95774 AI867094 AA443833 AI367670 AA609046 AI440298 AI613139 AI291826 AW028954 AI123242 AI824715 AW079750 AA479362 AW150151 AI952267 AA814094 AI168431 AI566595 AI521422 AI920793 AW051241 N70051 AI689429

		AI783813 AI769315 AI743691 AI915645 AA479473 C21435 N50944 N50902 AW978102 H23837 BE087538 AA316516
122802	287993_1	AI687303 AW571681 AI554465 AI684252 AI581056 AA604098 AI628160 AI859843 AA424021 AA460530 BE042778 AW273200 AW273223 AW167288 AW083347 AI654306 AW517496 AW104708 AW273214 BE139512 AW189487 AW130822 AW167419 AI289485 AW150010 H88004 AI743745 AW088710
123494	21202_1	AW179019 AW179011 AF135160 NM_014050 AF078860 BE018005 AK000285 AF151038 BE245156 AW179007 AA345114 BE619758 BE619209 W25509 AA314339 AA336674 AA337956 AW954843 AW390412 N46796 AA316235 AA314286 R15686 BE535633 N57134 N46483 AW368462 AA923517 AA665223 AI418513 AA837523 AI359320 AI309273 AI522278 N40939 AA904977 AA938272 N30240 AA887965 AI671972 AI028109 AA094652 AA883262 AA887781 AI744447 AW592944 AI077790 AW860883 AW148667 N89861 AA557195 AI191824 AI433166 AI719760 AA453089 AA630656 AA300976 AA639620 AW675033 AA284393 AW886987 AI476335 AI332939 BE301513 AA452920 AW674302 AI925483 AW170412 AI698717 AI375985 BE220535 AI688151 AW514809 AW062346 AA599786 BE350848 AI560848 AI023075 AA864875 AA166871 AI807947 AW514579 AI978602 AI860340 AA830886 AI374788 AI283592 AA683152 AA743159 AI379932 AI432056 AI128904 AW150433 N38909
116296	11967_2	AW149502 Z43342 AW002826 AL049382 AA442545 AW971471 BE220243 AW968952 AA043607 AW299245 AA659892 AI038768 H26330 BE463534 AI628252 AA836139 AI277291 AA489033 AA741239 AI209064 AI300253 AI275761 Z39417 C01835

Table 9A lists about 382 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult ovaries was greater than or equal to 10. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult ovaries level was set to the arithmetic mean amongst various non-malignant ovaries. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues (see Table 7A) was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 382 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
ratio: ratio tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
134454	L33930	Hs.173996	CD24 antigen (small cell lung carcinoma clust	86.2
102927	X12876	Hs.65114	keratin 18	84.7
115909	AA436666	Hs.59761	ESTs	72.3
123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [	66.8
115674	AA406542	Hs.71520	ESTs	65.4
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin; bone	63.1
101839	M93036	Hs.692	membrane component; chromosomal 4; surface ma	56.8
115221	AA262942	Hs.79741	ESTs	56.1
108059	AA043944	Hs.62663	ESTs	52.3
121853	AA425887	Hs.98502	ESTs	47.8
133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	47.0
103546	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	46.5
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-lik	45.5
102979	X17042	Hs.1908	proteoglycan 1; secretory granule	44.6
130967	AA134138	Hs.182579	Homo sapiens leucine aminopeptidase mRNA; com	44.5
102009	U02680	Hs.82643	protein tyrosine kinase 9	40.4
126960	AA317900	Hs.161756	ESTs	39.6
103111	X63187	Hs.2719	epididymis-specific; whey-acidic protein type	39.1
133829	AA453783	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from c	39.0
111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapiens]	38.9
102803	U89916	Hs.26126	claudin 10	38.8
104943	AA065217	Hs.169674	ESTs	38.7
106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (from cl	38.4
120655	AA287347	Hs.238205	ESTs	38.1
102968	X16396	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD	36.3
104052	AA393164	Hs.97644	mammaglobin 2	36.0
109166	AA179845	Hs.73625	RAB6 interacting; kinesin-like (rabkinesin6)	35.9
101332	L47276		Homo sapiens (cell line HL-6) alpha topoisome	35.0
106167	AA425906	Hs.7956	ESTs	34.5
101042	J05428	Hs.10319	UDP glycosyltransferase 2 family; polypeptide	34.3
125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from c	33.7
101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin; uteri	32.3
126410	R51912	Hs.12409	somatostatin	32.1
134326	U16306	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	32.0
125739	AA428557	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	31.6
132254	L20826	Hs.430	plastin 1 (I isoform)	31.4
112610	R79392	Hs.23643	ESTs	30.9
101441	M21005	Hs.100000	S100 calcium-binding protein A8 (calgranulin	30.6
116345	AA496981	Hs.199067	HER3 receptor tyrosine kinase (c-erbB3; ERBB3	30.1
108860	AA133334	Hs.129911	ESTs	29.8
133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	29.2
107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	28.9
106210	AA428239	Hs.10338	ESTs	28.9
134711	X04011	Hs.88974	cytochrome b-245; beta polypeptide (chronic g	28.0
125769	AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	27.5
107222	D51235	Hs.82689	tumor rejection antigen (gp96) 1	27.4
102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; importin a	26.9
134691	M59979	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	26.8
105588	AA279215	Hs.10867	ESTs	26.3
130718	N70196	Hs.18376	ESTs	26.3
111185	N67551	Hs.12844	EGF-like-domain; multiple 6	25.6
131965	W90146	Hs.35962	ESTs	25.6
132903	AA235404	Hs.5985	Homo sapiens clone 25186 mRNA sequence	25.6
114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride chann	25.5

101185	L19872	Hs.170087	aryl hydrocarbon receptor	25.2
128742	D00763	Hs.251531	proteasome (prosome; macropain) subunit; alph	25.1
116724	F13665	Hs.65641	ESTs	24.9
111929	R40057	Hs.112360	prominin (mouse)-like 1	24.9
102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	24.8
131210	AA430047	Hs.24248	ESTs	24.7
101714	M68874		Human phosphatidylcholine 2-acylhydrolase (cP	24.6
100154	D14657	Hs.81892	KIAA0101 gene product	24.6
134656	X14787	Hs.87409	thrombospondin 1	24.3
100294	D49396	Hs.75454	antioxidant protein 1	23.9
104080	AA402971	Hs.57771	kallikrein 11	23.7
107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-inducing f	23.7
115697	AA411502	Hs.63325	ESTs; Weakly similar to airway trypsin-like p	23.7
130350	U02020	Hs.239138	pre-B-cell colony-enhancing factor	23.7
105870	AA399623	Hs.23505	ESTs	23.6
118528	N67889	Hs.49397	ESTs	23.4
105309	AA233790	Hs.4104	ESTs; Weakly similar to cDNA EST yk386g7.5 co	23.2
109680	F09255	Hs.4993	ESTs	23.2
131501	AA121127	Hs.181307	H3 histone; family 3A	23.2
100824	HG4058-HT4328		Oncogene Aml1-Evi-1, Fusion Activated	23.1
111890	R38678	Hs.12365	ESTs	23.0
101543	M31166	Hs.2050	pentaxin-related gene; rapidly induced by IL-	22.8
102095	U11313	Hs.75760	sterol carrier protein 2	22.8
114988	AA251089	Hs.94576	ESTs; Weakly similar to phosducin; retinal [H	22.8
120695	AA291468		ESTs	22.8
130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	22.8
106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine aminotr	22.7
109141	AA176428	Hs.193380	ESTs	22.6
102345	U37283	Hs.58882	Microfibril-associated glycoprotein-2	22.6
115652	AA405098	Hs.38178	ESTs	22.4
100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polype	22.3
105463	AA253370	Hs.32646	ESTs	22.2
132624	AA164819	Hs.53631	ESTs	22.2
119743	W70242	Hs.58086	ESTs	22.0
132528	AA283006	Hs.50758	chromosome-associated polypeptide C	22.0
107174	AA621714	Hs.25338	ESTs	21.8
134495	D63477	Hs.84087	KIAA0143 protein	21.8
131985	AA434329	Hs.36563	ESTs	21.5
105832	AA398346	Hs.21898	ESTs	21.2
126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-relate	21.2
114846	AA234929	Hs.44343	ESTs	20.9
109703	F09684	Hs.24792	ESTs; Weakly similar to ORF YOR283w [S.cerevi	20.9
135154	AA126433	Hs.173242	sorting nexin 4	20.8
131185	M25753	Hs.23960	cyclin B1	20.7
105616	AA280670	Hs.24968	ESTs	20.5
131148	C00038	Hs.23579	ESTs	20.2
129337	R63542	Hs.110488	KIAA0990 protein	20.2
133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	20.1
127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	19.9
133711	J04130	Hs.75703	small inducible cytokine A4 (homologous to mo	19.8
131818	Z39297	Hs.3281	neuronal pentraxin II	19.7
125303	Z39821	Hs.107295	ESTs	19.6
109112	AA169379	Hs.72865	ESTs	19.5
105376	AA236559	Hs.8768	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ	19.2
103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	19.1
100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	19.1
129571	X51630	Hs.1145	Wilms tumor 1	19.0
115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the beta l	18.9
131562	U90551	Hs.28777	H2A histone family; member L	18.9
131272	AA423884	Hs.139033	paternally expressed gene 3	18.9
130343	AA490262	Hs.15485	ESTs; Weakly similar to APICAL-LIKE PROTEIN [	18.8
103245	X76648	Hs.28988	glutaredoxin (thioltransferase)	18.7
101809	M86849		Homo sapiens connexin 26 (GJB2) mRNA, complet	18.6
105344	AA235303	Hs.8645	ESTs	18.4
135225	AA455988	Hs.9667	butyrobetaine (gamma); 2-oxoglutarate dioxyge	18.4
116786	H25836	Hs.83429	tumor necrosis factor (ligand) superfamily; m	18.3
131510	AA207114	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	18.2
124059	F13673	Hs.99769	ESTs	18.0
103352	X89398	Hs.78853	uracil-DNA glycosylase	17.9
132742	AA490862	Hs.55901	ESTs; Weakly similar to C43H8.1 [C.elegans]	17.9
135242	M74093	Hs.9700	cyclin E1	17.9
123494	AA599786	Hs.112110	ESTs	17.8
129168	T90621	Hs.109052	chromosome 14 open reading frame 2	17.7
128517	AA280617	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapien	17.6
130160	Z39228	Hs.151344	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransfe	17.6
103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	17.5
119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio	17.5
122946	AA477445	Hs.105341	ESTs	17.5
125819	AA044840	Hs.251871	CTP synthase	17.5
131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix-loop	17.5
115061	AA253217	Hs.41271	ESTs	17.3
113702	T97307	Hs.161720	ESTs; Moderately similar to !!!! ALU SUBFAMIL	17.3
115291	AA279943	Hs.122579	ESTs	17.3
102567	U59863	Hs.146847	TRAF family member-associated NFKB activator	17.2

129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	17.2
129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	17.2
110769	N22222		yw34b06.s1 Morton Fetal Cochlea Homo sapiens	17.1
113182	T55234	Hs.9676	Human DNA sequence from clone 30M3 on chromos	17.0
115892	AA435946	Hs.50831	ESTs	17.0
123114	AA486407	Hs.105235	ESTs; Moderately similar to KIAA0454 protein	17.0
123442	AA598803	Hs.111496	ESTs	17.0
123339	AA504253	Hs.101515	ESTs	16.9
123689	AA609556	Hs.256562	ESTs	16.9
131941	D62657	Hs.35086	ubiquitin-specific protease 1	16.8
120649	AA287115	Hs.99697	ESTs	16.8
102139	U15932	Hs.2128	dual specificity phosphatase 5	16.8
115522	AA331393	Hs.47378	ESTs	16.7
135243	AA215333	Hs.97101	putative G protein-coupled receptor	16.6
131257	AA256042	Hs.24908	ESTs	16.5
109508	AA233892	Hs.55902	ESTs; Weakly similar to !!!! ALU SUBFAMILY SX	16.3
132701	AA279359	Hs.55220	BCL2-associated athanogene 2	16.3
134449	L34155	Hs.83450	laminin; alpha 3 (nicein (150kD); kalinin (16	16.3
126180	R18070	Hs.3712	ubiquinol-cytochrome c reductase; Rieske iron	16.3
106124	AA423987	Hs.7567	ESTs	16.2
115363	AA282071	Hs.152759	activator of S phase kinase	16.2
117588	N34895	Hs.44648	ESTs	16.1
131245	AA620599	Hs.24766	DKFZP564E1962 protein	16.1
101674	M61916	Hs.82124	laminin; beta 1	16.0
126819	AA305536	Hs.161489	ESTs	16.0
134039	S78569	Hs.78672	laminin; alpha 4	16.0
130648	AA075427	Hs.17296	ESTs; Weakly similar to /prediction	15.9
102823	U90914	Hs.5057	carboxypeptidase D	15.8
128470	AA447504	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from cl	15.8
115844	AA430124	Hs.234607	ESTs	15.7
132543	AA417152	Hs.5101	protein regulator of cytokinesis 1	15.7
130155	L33404	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	15.7
101008	J04162	Hs.763	Fc fragment of IgG; low affinity IIIa; recept	15.7
120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [	15.6
116844	H64938	Hs.38331	ESTs	15.6
106753	AA476944	Hs.7331	ESTs	15.6
114767	AA148885	Hs.154443	minichromosome maintenance deficient (S. cere	15.5
114768	AA149007	Hs.182339	Ets homologous factor	15.5
127370	AI024352	Hs.70337	immunoglobulin superfamily; member 4	15.5
101507	M27492	Hs.82112	interleukin 1 receptor; type I	15.4
102519	U52969	Hs.80296	Purkinje cell protein 4	15.4
102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	15.4
111244	N69556	Hs.24724	MFH-amplified sequences with leucine-rich tan	15.4
120404	AA234921	Hs.96427	KIAA1013 protein	15.3
130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltran	15.2
129519	AA298786	Hs.112242	ESTs	15.1
106553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	15.0
109502	AA233837	Hs.44755	ESTs; Weakly similar to membrane glycoprotein	14.9
115967	AA446887	Hs.42911	ESTs	14.9
104636	AA004415	Hs.106106	ESTs	14.9
134133	X93920	Hs.180383	dual specificity phosphatase 6	14.9
134444	X04470	Hs.251754	secretory leukocyte protease inhibitor (antil	14.8
132998	Y00062	Hs.170121	protein tyrosine phosphatase; receptor type;	14.8
131997	D82399	Hs.136644	Homo sapiens clone 23714 mRNA sequence	14.6
134056	R27358	Hs.7886	ESTs; Weakly similar to Pelle associated prot	14.6
101249	L33881	Hs.1904	protein kinase C; iota	14.5
105298	AA233459	Hs.26369	ESTs	14.5
107119	AA620307	Hs.27379	ESTs	14.5
115839	AA429038	Hs.40541	ESTs	14.5
122802	AA460530	Hs.256579	ESTs	14.5
129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosyltransf	14.3
130269	AA284694	Hs.168352	nucleoporin-like protein 1	14.3
134374	D62633	Hs.8236	ESTs	14.3
106370	AA443841	Hs.18676	sprouty (Drosophila) homolog 2	14.2
130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture antig	14.1
132923	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	14.1
107968	AA034020	Hs.61539	ESTs	14.1
125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 2	14.1
107148	AA621131	Hs.5889	ESTs; Weakly similar to W01A11.2 gene product	14.1
110788	N24730	Hs.15420	ESTs	14.0
109481	AA233342	Hs.90680	ESTs; Weakly similar to WD40 protein Ciao 1 [	13.9
105646	AA282147	Hs.5888	ESTs	13.9
106030	AA412251	Hs.12802	development and differentiation enhancing fac	13.8
132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma 1 su	13.7
133230	S82240	Hs.6838	ras homolog gene family; member E	13.7
124803	R45480	Hs.164866	cyclin K	13.6
121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [	13.6
105200	AA195399	Hs.24641	ESTs	13.5
105627	AA281245	Hs.23317	ESTs	13.5
114986	AA251010	Hs.87807	ESTs	13.5
118036	N52844	Hs.196008	ESTs	13.5
134672	N79749	Hs.87627	ESTs; Weakly similar to cDNA EST EMBL:T00542	13.5
110915	N46252	Hs.29724	ESTs	13.3
117984	N51919	Hs.47368	ESTs	13.3

132550	AA029597	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	13.3
124315	H94892	Hs.6906	v-ral simian leukemia viral oncogene homolog	13.2
102547	U57911	Hs.46638	chromosome 11 open reading frame 8	13.2
125134	W19228	Hs.100748	ESTs	13.2
111806	R33468	Hs.24651	ESTs	13.1
106983	AA521195	Hs.10887	similar to lysosome-associated membrane glyco	13.0
106498	AA452141	Hs.7171	ESTs	13.0
110787	N24716	Hs.12244	ESTs; Weakly similar to C44B9.1 [C.elegans]	13.0
122860	AA464414	Hs.112159	ESTs	13.0
131535	AA504642	Hs.28436	ESTs; Weakly similar to coded for by C. elega	13.0
116188	AA464728	Hs.184598	ESTs	13.0
107243	D59489	Hs.34727	ESTs	12.9
129300	C20976	Hs.110165	ESTs; Highly similar to ribosomal protein L26	12.9
134487	R38185	Hs.83954	Homo sapiens unknown mRNA	12.8
102348	U37519	Hs.87539	aldehyde dehydrogenase 8	12.8
131839	H80622	Hs.33010	KIAA0633 protein	12.8
119620	W47620	Hs.56009	2'-5'oligoadenylate synthetase 3	12.8
120802	AA343533	Hs.128777	ESTs; Weakly similar to predicted using Genef	12.7
102250	U28014	Hs.74122	caspase 4; apoptosis-related cysteine proteas	12.7
105539	AA258873	Hs.25242	ESTs	12.7
114965	AA250737	Hs.72472	ESTs	12.7
118001	N52151	Hs.47447	ESTs	12.7
100448	D87469	Hs.57652	EGF-like-domain; multiple 2	12.6
130920	D50975	Hs.75525	calreticulin	12.6
131075	Y00757	Hs.2265	secretory granule; neuroendocrine protein 1 (	12.6
105496	AA256323	Hs.25264	DKFZP434N126 protein	12.5
109235	AA193592	Hs.42300	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ	12.5
118215	N62195	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthas	12.5
134388	M15841	Hs.82575	small nuclear ribonucleoprotein polypeptide B	12.5
106897	AA489790	Hs.167496	RAN binding protein 6	12.4
133050	S67325	Hs.63788	propionyl Coenzyme A carboxylase; beta polype	12.4
109683	F09308	Hs.27607	ESTs	12.3
121463	AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 protein [H.s	12.3
102876	X03663	Hs.174142	colony stimulating factor 1 receptor; formerl	12.2
101804	M86699	Hs.169840	TTK protein kinase	12.2
129017	H13108	Hs.107968	ESTs	12.1
105812	AA394126	Hs.20814	ESTs; Highly similar to CGI-27 protein [H.sap	12.1
106459	AA449741	Hs.4029	glioma-amplified sequence-41	12.0
107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RecA ho	12.0
107080	AA609210	Hs.19221	ESTs	12.0
110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	12.0
112253	R51818	Hs.104222	Homo sapiens mRNA; cDNA DKFZp566L034 (from cl	12.0
116760	H11054	Hs.155342	protein kinase C; delta	12.0
120314	AA194166	Hs.221040	KIAA1038 protein	12.0
123005	AA479726	Hs.105577	ESTs	12.0
132572	AA448297	Hs.237825	signal recognition particle 72kD	12.0
110561	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CONJUGATING	12.0
101923	S75256		HNL=neutrophil lipocalin [human, ovarian canc	11.9
134992	H05625	Hs.92414	ESTs	11.8
105516	AA257971	Hs.21214	ESTs	11.8
105248	AA226968	Hs.22826	ESTs	11.7
109130	AA172040	Hs.20161	ESTs; Weakly similar to IgE receptor beta sub	11.7
115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	11.7
116135	AA460314	Hs.94179	ESTs	11.7
116284	AA487252	Hs.237809	ESTs; Weakly similar to hypothetical protein	11.7
132384	AA479933	Hs.46967	Human DNA sequence from clone 167A19 on chrom	11.7
134753	Y09216	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	11.7
125136	W31479	Hs.129051	ESTs	11.7
133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homologou	11.6
117395	N26330	Hs.93701	ESTs	11.5
127007	AA299360		EST11857 Uterus tumor I Homo sapiens cDNA 5'	11.5
130567	L07493	Hs.1608	replication protein A3 (14kD)	11.5
135073	AA452000	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	11.5
115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	11.4
115536	AA347193	Hs.62180	ESTs	11.4
133240	D31161	Hs.68613	ESTs	11.3
106521	AA453431	Hs.14732	malic enzyme 1; NADP(+)-dependent; cytosolic	11.3
107674	AA011027	Hs.41143	KIAA0581 protein	11.3
114149	Z38814	Hs.27196	ESTs	11.3
132478	H20906	Hs.49500	KIAA0746 protein	11.2
104252	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM	11.2
102436	U46499	Hs.790	microsomal glutathione S-transferase 1	11.2
106726	AA465339	Hs.7141	ESTs	11.2
100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	11.2
110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	11.2
130417	U58522	Hs.155485	huntingtin-interacting protein 2	11.2
132906	AA142857	Hs.234896	ESTs; Highly similar to geminin [H.sapiens]	11.2
107853	AA024427	Hs.59461	DKFZP434C245 protein	11.2
103467	Y00451	Hs.78712	aminolevulinate; delta-; synthase 1	11.1
100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	11.1
102654	U68494	Hs.24385	Human hbc647 mRNA sequence	11.1
103172	X68742	Hs.116774	integrin; alpha 1	11.1
106856	AA486183	Hs.15839	ESTs; Weakly similar to similar to oxysterol-	11.1
108255	AA063157	Hs.172608	ESTs	11.1

124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (from cl	11.1
129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	11.1
128845	AA455658	Hs.10649	basement membrane-induced gene	11.1
129025	AA420992	Hs.103441	ESTs; Weakly similar to testicular tektin B1-	11.0
107638	AA009528	Hs.42743	ESTs; Weakly similar to predicted using Genef	11.0
134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	11.0
115262	AA279112	Hs.88594	ESTs	11.0
102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	10.9
106614	AA458934	Hs.179912	ESTs	10.9
107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein [H.sa	10.9
115764	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) homolog	10.9
121770	AA421714	Hs.11469	KIAA0896 protein	10.9
132191	AA449431	Hs.158688	KIAA0741 gene product	10.9
133214	Y10659	Hs.250911	interleukin 13 receptor; alpha 1	10.9
133914	N32811	Hs.77542	ESTs	10.8
101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	10.8
102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.8
104147	AA451992	Hs.226799	ESTs; Highly similar to HSPC039 protein [H.sa	10.8
106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	10.8
115881	AA435577	Hs.184942	G protein-coupled receptor 64	10.8
129950	M31516	Hs.1369	decay accelerating factor for complement (CD5	10.8
132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	10.8
133784	AA214305	Hs.76173	ESTs	10.8
134248	AA292677	Hs.80624	ESTs	10.8
105565	AA278302	Hs.18349	ESTs; Weakly similar to partial CDS [C.elegan	10.8
127999	AA837495	Hs.69851	ESTs; Weakly similar to Wiskott-Aldrich syndr	10.8
108040	AA041551	Hs.48644	ESTs	10.7
130367	Z38501	Hs.8768	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ	10.7
108539	AA084677	Hs.54558	ESTs; Weakly similar to protein B [H.sapiens]	10.7
111345	N89820	Hs.14559	ESTs	10.7
115583	AA398913	Hs.45231	LDOC1 protein	10.7
128965	T17440	Hs.107418	ESTs	10.7
101396	M15796	Hs.78996	proliferating cell nuclear antigen	10.6
132164	U84573	Hs.41270	procollagen-lysine; 2-oxoglutarate 5-dioxygen	10.6
101275	L37936	Hs.3273	Ts translation elongation factor; mitochondri	10.6
104660	AA007160	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from cl	10.6
108609	AA100694	Hs.69499	Human DNA sequence from BAC 15E1 on chromosom	10.6
112041	R43300	Hs.22929	ESTs	10.6
114208	Z39301	Hs.7859	ESTs	10.6
118537	N67974	Hs.75431	fibrinogen; gamma polypeptide	10.6
106919	AA490885	Hs.21766	ESTs	10.6
115984	AA447687	Hs.91109	ESTs	10.6
105538	AA258860	Hs.32597	ring finger protein (C3H2C3 type) 6	10.6
102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	10.5
116710	F10577	Hs.70312	ESTs	10.5
119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical protein	10.5
112996	T23539	Hs.7165	zinc finger protein 259	10.5
103029	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulating ac	10.5
101255	L34600	Hs.149894	mitochondrial translational initiation factor	10.4
107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta subun	10.4
125617	AI287461	Hs.164950	ESTs	10.4
131475	Z39053	Hs.27263	ESTs	10.4
132073	N67408	Hs.38516	ESTs	10.4
101469	M22877	Hs.169248	Human somatic cytochrome c (HCS) gene; comple	10.3
102437	U46569	Hs.221986	aquaporin 5	10.3
104301	D45332	Hs.6783	ESTs	10.3
127236	AI341818	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	10.3
101465	M22612	Hs.241395	protease; serine; 1 (trypsin 1)	10.3
113805	W42957	Hs.250617	ESTs	10.2
133536	Y00264	Hs.177486	amyloid beta (A4) precursor protein (protease	10.2
109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; complete	10.2
113523	T90037	Hs.16686	ESTs	10.2
116195	AA465148	Hs.72402	ESTs	10.2
134542	X57025	Hs.85112	insulin-like growth factor 1 (somatomedin C)	10.2
125298	Z39255	Hs.235350	YDD19 protein	10.2
119367	T78324	Hs.90905	ESTs	10.2
134470	X54942	Hs.83758	CDC28 protein kinase 2	10.2
134288	AA430008	Hs.8117	ESTs	10.1
105127	AA158132	Hs.11817	ESTs; Weakly similar to contains similarity t	10.1
110627	H70485	Hs.35225	ESTs; Weakly similar to MBNL protein [H.sapie	10.1
115188	AA261819	Hs.88367	ESTs	10.1
132632	N59764	Hs.5398	guanine-monophosphate synthetase	10.1
124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	10.1
100079	AB002365	Hs.23311	KIAA0367 protein	10.0
113987	W87494	Hs.9641	ESTs; Moderately similar to COMPLEMENT C1Q SU	10.0
117280	N22107	Hs.172241	ESTs	10.0

TABLE 9B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
100661	23182_1	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655

101332	25130_1	J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 AI471482 AI970337 AA737616 AI827444 AW003286 AI742333 AI344044 AI765634 AI948838 AW235336 AW172827 AA095289 BE046383 AI734240 W16699 AI660329 AI289433 AA933778 AW469242 AA468838 AA806983 AA625873 W78031 BE206307 AA550803 AI743147 AI990075 AA948274 AA129533 AI635399 AA605313 AI624669 AW594319 AI221834 AI337434 AA307706 BE550282 AI760467 AI630636 AI221521 AW674314 AW078889 AI933732 AI686969 AI186928 AW074595 AI127486 AL079644 AI910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427 AW383395 H09977 AA306247 AA352501 AW403639 F05421 AA224473 AA305321 H93904 AA089612 AW391543 AW402915 AW173382 AW402701 AW403113 R94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 AI375913 BE384156 W24652 AA746288 AA568223 BE090591 H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 AI453437 AW263710 AI076594 AA583483 AW873194 AW575166 AI128799 AI803319 AL042776 AW074313 AI887722 AI032284 AA447521 AI123885 N29334 AI354911 AW090687 AA236763 AA435535 AA236910 AA047124 AA236734 AW514610 H93467 AA962007 AI446783 AA127259 AI613495 AI686720 AI587374 AA936731 AA702453 AI859757 AA216786 AI251819 AI469227 AA806022 AI092324 N71868 AA968782 AA236919 AA809450 AA227220 AA765284 AI192007 AA768810 AA805794 AA729280 AA806238 AW768817 N71879 AI050686 AA505822 AA668974 AI688160 BE045915 AW466315 AA731314 AA649568 AA834316 AW591901 AW063876 AW294770 AI300266 AI336094 AI560380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01675 AI457474 AW466316 AA550969 AA630788
100824	5_36	AI393237 AI521317 AI761348 AF025841 D43968 AW994987 L34598 AF025841 D89789 D89788 D89790 AW998932 AI971742 AI310238 X90976 AW139668 AW674280 AI365552 AA877452 AV657554 C75229 AA376077 AI798056 AW609213 W25586 H30149 BE075089 BE075190 AW580858 H99598 AA425238 AA133916 AW363478 BE158121 BE158127 AW467960 BE158135 BE158126 BE158145 N92860 AA847246 AI961688 AI361423 AA878154 AA043767 AI863712 AI559226 AW339007 AI371266 AI368901 AA046624 AA134739 AW449154 AA130232 AI458720 AA962511 AI700627 R70437 AW004008 AA045229 AI671572 H99599 AA043768 AI685454 AI871685 N29937 X90977 AA524240 AI142114 AI825750 AI567805 AI631365 AI347893 AA134740 F20669 AA046707 AW793216 AW963298 AW959380 AA363265 AI784593 AI268201 R69451 AV657618 AI695588
101714	30725_1	M68874 AL022147 M72393 AL049797 BE439441 T27650 AI766240 AW150345 AW778943 AI627464 BE439479 AA587049 AI277900 AI984983 AI630935
101809	32963_1	M86849 AA315280 NM_004004 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930 AW384563 AW384544 AW384566 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW271245 AW378298 AW384497 AI598114 AW264544 AI018136 AW021810 AA961504 AW086214 AW771489 AW192483 AI290266 AW192488 AW384490 AW007451 AW890895 AA554460 AA613715 AW020066 AI783695 AI589498 AI917637 AW264471 AW384491 AI816732 AW368530 AW368521 AW368463 AA461087 AI341438 AI970613 AI040737 AI418400 AA947181 AA962716 AI280695 AW769275 AW023591 AI160977 AA055400 N71882 AA490466 AW243772 AW316636 AI076554 AW511702 N69323 H88912 AA257017 AI952506 H88913 AI912481 AA600714 BE465701 N64149 C00523 N64240 AA677120
101923	30543_1	X99133 X83006 W38398 AA401137 AA298242 AA366738 AA308126 AW583781 AA298668 AW845024 BE140204 AW845005 U47734 AA837575 NM_005564 AA329732 AA421943 BE171567 S75256 AI750047 AI762213 AA100735 AW612993 AI474120 AW062884 AI940001 AW062852 AW062899 BE182639 AW778875 AA528093 AW517424 AI939989 AA076188 BE182636 AA169569 AA167439 AI283967 AA167783 AA076140 AI749649 AA166792 AI708618 AA400973 AA514773 AA514789 AA164458 AA167440 AA074845 AA421944 AA514874 AA079557 AA102361 AA587027 AA642930 AA878029 AA164459 AW176400 AW475086 AA857522 AA148193 AA838234 AA593897 AI284506 AW193324 AA148194 AW583341 AI669077 AW264913 AA074902 AI680515 AA169874 AA169614 AA079651 AW591737 AW190644 AA076565 AA662747 AA075896 AA535642 N27757 AI306666 AA074727 N79823 AA524360 AI826800 AA173827 BE140374 BE004062 AW265060 BE184103 AI199258 AA857853 AA299459 AA837890 AI626104 AA503624 BE183618 BE183717 AA573267 AI833071 AW270590 AA506601 BE004010 AA837854 AI675895 AI810491 AI184883 AW664712 AA076046 AA515574 AW352267 AI797418 AA172395 AI749194 AI559933 AA502597 AA321220 AI866124 AI695633 AA494293 AW085635 AA165649 AA165663
127007	19921_1	AB037771 BE005079 AA394189 AW959650 AA299360 AA398081 W37627 AW750817 AW630138 AI522058 BE326323 AA374890 AW418534 AW997510 AW995214 AW959649 AA504426 D79223 D79621 AI276062 AI973155 AA653470 AA337887 AI382521 AW084427 D57078 W37628 AI610506 Z30230 AI567034 AA766091 H25097 H25078 AW991507 AA319736
110769	229824_1	BE000831 AA541787 AW173038 AA327931 AW117510 AW664665 AI066624 AI478955 AI863075 AI073744 AA490170 R46651 AI075653 F02865 N22222 AW972956
120695	9683_3	AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA425910 AI017004 AI241295 AA402816 AA291468

Table 10A lists about 733 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" ovarian cancer level was set to the about the 80th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to the 90th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 10A: ABOUT 733 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
ratio: ratio tumor vs normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	56.1
418179	X51630	Hs.1145	Wilms tumor 1	33.5
400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic protein receptor	30.0
452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
415511	AI732617	Hs.182362	ESTs	28.1
422956	BE545072	Hs.122579	ESTs	28.1
410929	H47233	Hs.30643	ESTs	27.4
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	25.2
449034	AI624049	Hs.277523	gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	23.7
427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	22.7
428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1	21.9
448243	AW369771	Hs.77496	ESTs	21.3
430691	C14187	Hs.103538	ESTs	21.2
444783	AK001468	Hs.62180	ESTs	20.8
407638	AJ404672	Hs.288693	EST	20.1
423739	AA398155	Hs.97600	ESTs	19.7
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	19.0
451110	AI955040	Hs.301584	ESTs	18.8
426427	M86699	Hs.169840	TTK protein kinase	18.7

428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED	18.3
419854	AW664873	Hs.87836	Homo sapiens PAC clone RP5-1087M19 from 7q11.	18.3
439706	AW872527	Hs.59761	ESTs	18.3
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	17.4
410247	AF181721	Hs.61345	RU2S	17.0
428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-	16.9
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	16.6
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	16.2
423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein, parti	15.9
428187	AI687303	Hs.285529	ESTs	15.9
438817	AI023799	Hs.163242	ESTs	15.9
424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untr	15.9
407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation	15.7
412723	AA648459	Hs.179912	ESTs	15.3
424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	15.2
443646	AI085198	Hs.298699	ESTs	15.1
424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	14.8
428976	AL037824	Hs.194695	ras homolog gene family, member I	14.6
418738	AW388633	Hs.6682	solute carrier family 7, member 11	14.3
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	14.2
436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p	14.1
427356	AW023482	Hs.97849	ESTs	13.9
418601	AA279490	Hs.86368	calmegin	13.8
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7
428532	AF157326	Hs.184786	TBP-interacting protein	13.6
402408			0	13.6
447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	13.4
451807	W52854	Hs.27099	DKFZP564J0863 protein	13.4
423575	C18863	Hs.163443	ESTs	13.2
443211	AI128388	Hs.143655	ESTs	13.2
437872	AK002015	Hs.5887	RNA binding motif protein 7	13.0
451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (from c	12.7
442655	AW027457	Hs.30323	ESTs	12.5
452096	BE394901	Hs.226785	ESTs	12.4
414972	BE263782	Hs.77695	KIAA0008 gene product	12.3
435039	AW043921	Hs.130526	ESTs	12.3
447033	AI357412	Hs.157601	EST - not in UniGene	12.3
433764	AW753676	Hs.39982	ESTs	12.2
442611	BE077155	Hs.177537	ESTs	12.0
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, parti	11.9
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.8
421478	AI683243	Hs.97258	ESTs	11.8
426635	BE395109	Hs.129327	ESTs	11.8
415989	AI267700	Hs.111128	ESTs	11.7
433159	AB035898	Hs.150587	kinesin-like protein 2	11.5
452249	BE394412	Hs.61252	ESTs	11.4
418506	AA084248	Hs.85339	G protein-coupled receptor 39	11.3
442353	BE379594	Hs.49136	ESTs	11.3
447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
450480	X82125	Hs.25040	zinc finger protein 239	11.3
425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-relate	11.2
433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
445258	AI635931	Hs.147613	ESTs	11.1
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	11.0
429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-bind	10.9
404567			0	10.8
423811	AW299598	Hs.50895	homeo box C4	10.7
452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapiens]	10.6
441627	AA947552	Hs.58086	ESTs	10.3
443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMAN GLUCOS	10.3
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	10.2
427469	AA403084	Hs.269347	ESTs	10.1
415227	AW821113	Hs.72402	ESTs	10.1
445413	AA151342	Hs.12677	CGI-147 protein	10.0
425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	10.0
421451	AA291377	Hs.50831	ESTs	10.0
410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine h	9.8
427878	C05766	Hs.181022	CGI-07 protein	9.7
408460	AA054726	Hs.285574	ESTs	9.7
422972	N59319	Hs.145404	ESTs	9.7
443715	AI583187	Hs.9700	cyclin E1	9.7
440901	AA909358	Hs.128612	ESTs	9.6
453160	AI263307	Hs.146228	ESTs	9.6
415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN	9.5
425282	AW163518	Hs.155485	huntingtin interacting protein 2	9.5
400250			0	9.5
410568	AW162948	Hs.64542	pre-mRNA cleavage factor Im (68kD)	9.3
442957	AI949952	Hs.49397	ESTs	9.3
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	9.3
434401	AI864131	Hs.71119	Putative prostate cancer tumor suppressor	9.2
453628	AW243307	Hs.170187	ESTs	9.1

452055	AI377431	Hs.293772	ESTs	9.1
424086	AI351010	Hs.102267	lysyl oxidase	9.1
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	9.1
416208	AW291168	Hs.41295	ESTs	9.0
407168	R45175	Hs.117183	gb:yg40f01.s1 Soares infant brain 1NIB Homo s	9.0
445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	8.9
409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone OVARC10	8.9
433527	AW235613	Hs.133020	ESTs	8.9
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	8.8
423020	AA383092	Hs.1608	replication protein A3 (14kD)	8.7
425665	AK001050	Hs.159066	ESTs	8.6
443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	8.6
449433	AI672096	Hs.9012	ESTs	8.6
453878	AW964440	Hs.19025	ESTs	8.6
450505	NM_004572	Hs.25051	plakophilin 2	8.6
407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	8.5
414315	Z24878		gb:HSB65D052 STRATAGENE Human skeletal muscle	8.5
425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	8.5
435181	AA669339	Hs.28838	KIAA1571 protein	8.5
436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HEMBA10	8.5
418384	AW149266	Hs.25130	ESTs	8.4
453370	AI470523	Hs.182356	ESTs, Moderately similar to translation initi	8.4
409041	AB033025	Hs.50081	KIAA1199 protein	8.4
447078	AW885727	Hs.301570	ESTs	8.4
448674	W31178	Hs.154140	ESTs	8.3
433393	AF038564	Hs.98074	atrophin-1 interacting protein 4	8.3
433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNTHETASE	8.3
421155	H87879	Hs.102267	lysyl oxidase	8.2
438394	BE379623	Hs.27693	CGI-124 protein	8.2
400298	AA032279	Hs.61635	STEAP1	8.1
409092	AI735283	Hs.172608	ESTs	8.1
440250	AA876179	Hs.134650	ESTs	8.1
409143	AW025980	Hs.138965	ESTs	8.1
407771	AL138272	Hs.62713	ESTs	8.1
419088	AI538323	Hs.77496	ESTs	8.1
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	7.9
431750	AA514986	Hs.283705	ESTs	7.9
435635	AF220050	Hs.181385	uncharacterized hematopoietic stem/progenitor	7.9
441826	AW503603	Hs.129915	phosphotriesterase related	7.9
417728	AW138437	Hs.24790	KIAA1573 protein	7.8
418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	7.8
421039	NM_003478	Hs.101299	cullin 5	7.8
446999	AA151520	Hs.279525	hypothetical protein PRO2605	7.8
429609	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM	7.8
415139	AW975942	Hs.48524	ESTs	7.7
450192	AA263143	Hs.24596	RAD51-interacting protein	7.7
423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (from c	7.7
436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	7.7
450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	7.5
426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA, subu	7.5
433330	AW207084	Hs.132816	ESTs	7.5
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clo	7.5
427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE066	7.5
422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	7.5
436476	AA326108	Hs.53631	ESTs	7.5
412170	D16532	Hs.73729	very low density lipoprotein receptor	7.4
428954	AF100781	Hs.194678	WNT1 inducible signaling pathway protein 3	7.4
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.4
439262	AA832333	Hs.124399	ESTs	7.4
435420	AI928513	Hs.59203	ESTs	7.3
422892	AA988176	Hs.121553	hypothetical protein FLJ20641	7.3
457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	7.3
411571	AA122393	Hs.70811	hypothetical protein FLJ20516	7.2
409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled diva	7.2
418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitial collag	7.2
420900	AL045633	Hs.44269	ESTs	7.2
424001	W67883	Hs.137476	KIAA1051 protein	7.2
400301	X03635	Hs.1657	Estrogen receptor 1	7.1
400238			0	7.1
413573	AI733859	Hs.149089	ESTs	7.1
428071	AF212848	Hs.182339	transcription factor ESE-3B	7.1
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	7.1
453062	AW207538	Hs.61603	ESTs	7.1
456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical protein	7.1
442500	AI819068	Hs.209122	ESTs	7.1
446142	AI754693	Hs.145968	ESTs	7.0
417791	AW965339	Hs.111471	ESTs	7.0
418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	7.0
451797	AW663858	Hs.56120	ESTs	7.0
452909	NM_015368	Hs.30985	pannexin 1	7.0
453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypept	7.0
436281	AW411194	Hs.120051	ESTs	7.0
449897	AW819642	Hs.24135	transmembrane protein vezatin; hypothetical p	6.9
414142	AW368397	Hs.150042	ESTs	6.9

448776	BE302464	Hs.30057	transporter similar to yeast MRS2	6.9
419423	D26488	Hs.90315	KIAA0007 protein	6.9
420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from cl	6.8
452971	AI873878	Hs.91789	ESTs	6.8
413597	AW302885	Hs.117183	ESTs	6.8
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	6.8
437478	AL390172	Hs.118811	ESTs	6.7
425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	6.7
421184	NM_003616	Hs.102456	survival of motor neuron protein interacting	6.7
410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
446608	N75217	Hs.257846	ESTs	6.6
438167	R28363	Hs.24286	ESTs	6.6
445459	AI478629	Hs.158465	ESTs	6.6
452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	6.6
410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	6.6
410292	AA843087	Hs.124194	ESTs	6.5
415716	N59294	Hs.301141	Homo sapiens cDNA FLJ11689 fis, clone HEMBA10	6.5
424770	AA425562		gb:zw46e05.r1 Soares_total_fetus_Nb2HF8_9w Ho	6.5
438122	AI620270	Hs.129837	ESTs	6.5
439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	6.5
444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiety X	6.5
450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.5
418203	X54942	Hs.83758	CDC28 protein kinase 2	6.5
439901	N73885	Hs.124169	ESTs	6.5
428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	6.4
404552			0	6.4
404599			0	6.4
419503	AA243642	Hs.137422	ESTs	6.4
420149	AA255920	Hs.88095	ESTs	6.4
440411	N30256	Hs.156971	ESTs, Weakly similar to Weak similarity with	6.4
449108	AI140683	Hs.98328	ESTs	6.4
452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and metallopr	6.4
453619	H87648	Hs.33922	H.sapiens novel gene from PAC 117P20, chromos	6.4
410273	BE326877	Hs.281523	ESTs	6.3
434486	AA678816	Hs.117142	ESTs	6.3
454036	AA374756	Hs.93560	ESTs, Weakly similar to unnamed protein produ	6.3
403381			0	6.2
421308	AA687322	Hs.192843	ESTs	6.2
419346	AI830417		gb:wh94d12.x1 NCI_CGAP_CLL1 Homo sapiens cDNA	6.2
446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone HEP038	6.2
453047	AW023798	Hs.286025	ESTs	6.2
442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosolic,	6.1
410102	AW248508	Hs.279727	ESTs;	6.1
410004	AI298027	Hs.299115	ESTs	6.1
413335	AI613318	Hs.48442	ESTs	6.1
424945	AI221919	Hs.173438	hypothetical protein FLJ10582	6.1
427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	6.1
451229	AW967707	Hs.48473	ESTs	6.1
452641	AW952893	Hs.237825	signal recognition particle 72kD	6.1
433172	AB037841	Hs.102652	hypothetical protein ASH1	6.1
425465	L18964	Hs.1904	protein kinase C, iota	6.1
437117	AL049256	Hs.122593	ESTs	6.0
423440	R25234	Hs.143434	contactin 1	6.0
430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.0
433252	AB040957	Hs.151343	KIAA1524 protein	6.0
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	6.0
436954	AA740151	Hs.130425	ESTs	5.9
436032	AA150797	Hs.109276	latexin protein	5.9
424590	AW966399	Hs.46821	hypothetical protein FLJ20086	5.9
444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bindi	5.9
418379	AA218940	Hs.137516	fidgetin-like 1	5.9
438081	H49546	Hs.298964	ESTs	5.8
443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.8
450459	AI697193	Hs.299254	ESTs	5.8
433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3) mRNA	5.8
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced ge	5.8
417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	5.7
429181	AW979104	Hs.294009	ESTs	5.7
454933	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo sapi	5.7
456553	AA721325	Hs.189058	ESTs, Weakly similar to cAMP-regulated guanin	5.7
430371	D87466	Hs.240112	KIAA0276 protein	5.7
425371	D49441	Hs.155981	mesothelin	5.7
424513	BE385864	Hs.149894	mitochondrial translational initiation factor	5.6
432015	AL157504	Hs.159115	ESTs	5.6
438109	AI076621	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN ALU SU	5.6
407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	5.6
407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypeptide	5.6
416565	AW000960	Hs.44970	ESTs	5.6
417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	5.5
419752	AA249573	Hs.152618	ESTs	5.5
422093	AF151852	Hs.111449	CGI-94 protein	5.5
424583	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	5.5
430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 20kD	5.5
452534	AW083022	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	5.5

453279	AW893940	Hs.59698	ESTs	5.5
424188	AW954552	Hs.142634	zinc finger protein	5.5
453884	AA355925	Hs.36232	KIAA0186 gene product	5.5
424641	AB001106	Hs.151413	glia maturation factor, beta	5.5
444478	W07318	Hs.240	M-phase phosphoprotein 1	5.5
427975	AI536065	Hs.122460	ESTs	5.5
424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	5.5
442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fis, clone Y79AA10	5.5
417995	AW974175	Hs.188751	ESTs	5.4
418946	AI798841	Hs.132103	ESTs	5.4
419963	AA743276	Hs.301052	ESTs	5.4
420362	U79734	Hs.97206	huntingtin interacting protein 1	5.4
422670	AA371612	Hs.115351	ESTs	5.4
432837	AA310693	Hs.279512	HSPC072 protein	5.4
447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.4
456027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34) fus	5.4
425217	AU076696	Hs.155174	CDC5 (cell division cycle 5, S. pombe, homolo	5.4
422938	NM_001809	Hs.1594	centromere protein A (17kD)	5.4
450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.elegan	5.4
438279	AA805166	Hs.165165	ESTs, Moderately similar to ALU8_HUMAN ALU SU	5.4
413384	NM_000401	Hs.75334	exostoses (multiple) 2	5.3
420328	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein) hom	5.3
436586	AI308862	Hs.167028	ESTs	5.3
435793	AB037734	Hs.4993	ESTs	5.3
422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	5.3
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.2
453293	AA382267	Hs.10653	ESTs	5.2
429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence	5.2
434891	AA814309	Hs.123583	ESTs	5.2
415263	AA948033	Hs.130853	ESTs	5.2
409506	NM_006153	Hs.54589	NCK adaptor protein 1	5.2
412848	AA121514	Hs.70832	ESTs	5.2
421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 pro	5.2
431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP30	5.2
412719	AW016610	Hs.129911	ESTs	5.2
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	5.1
424078	AB006625	Hs.139033	paternally expressed gene 3	5.1
433558	AA833757	Hs.201769	ESTs	5.1
434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone LNG070	5.1
453911	AW503857	Hs.4007	Sarcolemmal-associated protein	5.1
415539	AI733881	Hs.72472	BMPR-Ib; bone morphogenetic protein receptor	5.1
442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	5.1
432358	AI093491	Hs.72830	ESTs	5.0
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	5.0
419699	AA248998	Hs.31246	ESTs	5.0
420313	AB023230	Hs.96427	KIAA1013 protein	5.0
422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed cell deat	5.0
425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	5.0
434160	BE551196	Hs.114275	ESTs	5.0
435094	AI560129	Hs.277523	EST	5.0
436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Ho	5.0
432415	T16971	Hs.289014	ESTs	4.9
406117			0	4.9
438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.9
447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from cl	4.9
448621	AI097144	Hs.5250	ESTs, Weakly similar to BACR37P7.g [D.melanog	4.9
453001	AW131636	Hs.191260	ESTs	4.9
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	4.9
418811	AK001407	Hs.88663	hypothetical protein FLJ10545	4.9
436754	AI061288	Hs.133437	ESTs, Moderately similar to gonadotropin indu	4.8
437212	AI765021	Hs.210775	ESTs	4.8
447312	AI434345	Hs.36908	activating transcription factor 1	4.8
409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.8
434690	AI867679	Hs.148410	ESTs	4.8
444172	BE147740	Hs.104558	ESTs	4.8
424539	L02911	Hs.150402	activin A receptor, type I	4.8
418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.8
406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from cl	4.8
420179	N74530	Hs.21168	ESTs	4.7
450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.7
419247	S65791	Hs.89764	fragile X mental retardation 1	4.7
420850	BE139590	Hs.122406	ESTs	4.7
425420	BE536911	Hs.234545	ESTs	4.7
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	4.7
419131	AA406293	Hs.301622	ESTs	4.7
422278	AF072873	Hs.114218	ESTs	4.7
451684	AF216751	Hs.26813	CDA14	4.6
400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR/MRP)	4.6
408425	AW058674	Hs.44787	Homo sapiens mRNA; cDNA DKFZp434O0227 (from c	4.6
417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	4.6
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	4.6
442917	AA314907	Hs.85950	ESTs	4.6
443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.6
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.6

457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone COL088	4.6
459551	AI472808		gb:tj70e07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom	4.6
421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.6
429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	4.6
449722	BE280074	Hs.23960	cyclin B1	4.6
431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransfe	4.5
425178	H16097	Hs.161027	ESTs	4.5
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	4.5
436556	AI364997	Hs.7572	ESTs	4.5
400534			0	4.5
417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from c	4.5
423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selenium d	4.5
448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	4.5
441006	AW605267	Hs.7627	CGI-60 protein	4.5
414569	AF109298	Hs.118258	Prostate cancer associated protein 1	4.5
447924	AI817226	Hs.170337	ESTs	4.5
425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (JEM-1)	4.5
411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.4
432842	AW674093	Hs.279525	hypothetical protein PRO2605	4.4
413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	4.4
414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of amyloid	4.4
412733	AA984472	Hs.74554	KIAA0080 protein	4.4
419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitocho	4.4
433377	AI752713	Hs.43845	ESTs	4.4
449535	W15267	Hs.23672	low density lipoprotein receptor-related prot	4.4
453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	4.4
443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT2RP40	4.4
423025	AA831267	Hs.12244	Homo sapiens cDNA: FLJ23581 fis, clone LNG136	4.4
408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; fetal br	4.3
416241	N52639	Hs.32683	ESTs	4.3
432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYME	4.3
435532	AW291488	Hs.117305	ESTs	4.3
451813	NM_016117	Hs.27182	phospholipase A2-activating protein	4.3
454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo sapi	4.3
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	4.3
406069			0	4.3
419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone LNG055	4.3
418413	R95735	Hs.117753	ESTs, Weakly similar to antigen of the monocl	4.3
452028	AK001859	Hs.27595	hypothetical protein FLJ10997	4.3
418693	AI750878	Hs.87409	thrombospondin 1	4.3
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.2
409763	AL043212		gb:DKFZp434H0623_r1 434 (synonym: htes3) Homo	4.2
455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2, partial	4.2
408908	BE296227	Hs.48915	serine/threonine kinase 15	4.2
413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone HEP057	4.2
423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	4.2
425024	R39235	Hs.12407	ESTs	4.2
447153	AA805202	Hs.173912	eukaryotic translation initiation factor 4A,	4.2
447406	BE618060	Hs.282882	ESTs	4.2
449347	AV649748	Hs.295901	ESTs	4.2
414279	AW021691	Hs.3804	DKFZP564C1940 protein	4.2
428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP066	4.2
407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	4.2
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	4.2
436406	AW105723	Hs.125346	ESTs	4.2
438209	AL120659	Hs.6111	KIAA0307 gene product	4.2
443653	AA137043	Hs.9663	programmed cell death 6-interacting protein	4.1
454556	AW807073		gb:MR4-ST0062-031199-018-d06 ST0062 Homo sapi	4.1
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	4.1
412593	Y07558	Hs.74088	early growth response 3	4.1
416566	NM_003914	Hs.79378	cyclin A1	4.1
426342	AF093419	Hs.169378	multiple PDZ domain protein	4.1
428417	AK001699	Hs.184227	F-box only protein 21	4.1
429317	AA831552	Hs.268016	solute carrier family 5 (inositol transporter	4.1
446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT2RM40	4.1
422988	AW673847	Hs.97321	ESTs	4.0
434657	AA641876	Hs.191840	ESTs	4.0
412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1, 64k	4.0
443271	BE568568	Hs.195704	ESTs	4.0
421437	AW821252	Hs.104336	ESTs	4.0
401644			0	4.0
405095			0	4.0
418417	R77182		gb:yi65e02.r1 Soares placenta Nb2HP Homo sapi	4.0
420807	AA280627	Hs.57846	ESTs	4.0
429529	AA454190	Hs.193811	ESTs, Moderately similar to reduced expressio	4.0
457726	AI217477	Hs.194591	ESTs	4.0
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	4.0
453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PLACE10	4.0
442768	AL048534	Hs.48458	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	4.0
413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT2RP30	4.0
424081	NM_006413	Hs.139120	ribonuclease P (30kD)	4.0
425692	D90041	Hs.155956	NAT1; arylamine N-acetyltransferase	4.0
407792	AI077715	Hs.39384	putative secreted ligand homologous to fjx1	4.0
408353	BE439838	Hs.44298	hypothetical protein	4.0

421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transcripti	3.9
420324	AF163474	Hs.96744	DKFZP586D0823 protein, Prostate androgen-regu	3.9
417531	NM_003157	Hs.1087	serine/threonine kinase 2	3.9
458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.9
400195			0	3.9
401480			0	3.9
410360	AW663690		gb:hj21g03.x1 NCI_CGAP_U8 Homo sapiens cDNA	3.9
410908	AA121686	Hs.10592	ESTs	3.9
420159	AI572490	Hs.99785	ESTs	3.9
422805	AA436989	Hs.121017	H2A histone family, member A	3.9
424639	AI917494	Hs.131329	ESTs	3.9
428555	NM_002214	Hs.184908	Integrin, beta 8	3.9
431699	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 fis, clone NT2RP20	3.9
433703	AA210863	Hs.3532	nemo-like kinase	3.9
437144	AL049466	Hs.7859	ESTs	3.9
452728	AI915676	Hs.239708	ESTs	3.9
430447	W17064	Hs.241451	SWI/SNF related, matrix associated, actin dep	3.9
440594	AW445167	Hs.126036	ESTs	3.9
408938	AA059013	Hs.22607	ESTs	3.9
427051	BE178110	Hs.173374	ESTs	3.9
447568	AF155655	Hs.18885	CGI-116 protein	3.9
457211	AW972565	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP l	3.9
443475	AI066470	Hs.134482	ESTs	3.9
433447	U29195	Hs.3281	neuronal pentraxin II	3.9
428093	AW594506	Hs.104830	ESTs	3.8
437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprotein [	3.8
408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	3.8
429250	H56585	Hs.198308	tryptophan rich basic protein	3.8
441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT	3.8
437700	AA766060	Hs.122848	ESTs	3.8
439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	3.8
429474	AA453441	Hs.31511	ESTs	3.8
431965	BE175190		gb:QV2-HT0577-010500-165-g04 HT0577 Homo sapi	3.8
454018	AW016892	Hs.241652	ESTs	3.8
426320	W47595	Hs.169300	transforming growth factor, beta 2	3.8
439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone HSI156	3.8
417517	AF001176	Hs.82238	POP4 (processing of precursor , S. cerevisiae	3.8
446402	AI681145	Hs.160724	ESTs	3.8
450236	AW162998	Hs.24684	KIAA1376 protein	3.8
410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxi	3.8
400268			0	3.8
418217	AI910647	Hs.13442	ESTs	3.8
421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	3.8
417300	AI765227	Hs.55610	solute carrier family 30 (zinc transporter),.	3.8
414136	AA812434	Hs.178227	ESTs	3.8
453945	NM_005171	Hs.36908	activating transcription factor 1	3.7
400240			0	3.7
407877	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone HSI073	3.7
450581	AF081513	Hs.25195	endometrial bleeding associated factor (left-	3.7
418223	NM_014733	Hs.83790	KIAA0305 gene product	3.7
411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.7
432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta-5-de	3.7
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.7
402820			0	3.7
408090	BE173621	Hs.292478	ESTs	3.7
416421	AA134006	Hs.79306	eukaryotic translation initiation factor 4E	3.7
418282	AA215535	Hs.98133	ESTs	3.7
418454	AA315308		gb:EST187095 Colon carcinoma (HCC) cell line	3.7
418668	AW407987	Hs.87150	Human clone A9A2BR11 (CAC)n/(GTG)n repeat-con	3.7
422290	AA495854	Hs.48827	hypothetical protein FLJ12085	3.7
432824	AK001783	Hs.279012	hypothetical protein FLJ10921	3.7
439907	AA853978	Hs.124577	ESTs	3.7
447479	AB037834	Hs.18685	Homo sapiens mRNA for KIAA1413 protein, parti	3.7
451073	AI758905	Hs.206063	ESTs	3.7
450377	AB033091	Hs.24936	ESTs	3.7
414343	AL036166	Hs.75914	coated vesicle membrane protein	3.7
448807	AI571940	Hs.7549	ESTs	3.7
442821	BE391929	Hs.8752	Putative type II membrane protein	3.7
426300	U15979	Hs.169228	delta-like homolog (Drosophila)	3.7
418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxylase	3.7
411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.7
443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PLACE10	3.7
411402	BE297855	Hs.69855	NRAS-related gene	3.7
450447	AF212223	Hs.25010	hypothetical protein P15-2	3.6
414706	AW340125	Hs.76989	KIAA0097 gene product	3.6
434228	Z42047	Hs.283978	ESTs; KIAA0738 gene product	3.6
434164	AW207019	Hs.148135	ESTs	3.6
409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase kinas	3.6
402222			0	3.6
404915			0	3.6
404996			0	3.6
411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo sapi	3.6

419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP40	3.6
426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone CAE038	3.6
427038	NM_014633	Hs.173288	KIAA0155 gene product	3.6
439255	BE164500		gb:RC4-HT0469-230300-014-e10 HT0469 Homo sapi	3.6
458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.6
415115	AA214228	Hs.127751	hypothetical protein	3.6
453468	W00712	Hs.32990	DKFZP566F084 protein	3.6
441205	AW137827	Hs.176904	ESTs	3.6
452693	T79153	Hs.48589	zinc finger protein 228	3.6
417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2)	3.6
448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	3.6
451522	BE565817	Hs.26498	hypothetical protein FLJ21657	3.6
440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	3.5
419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)-like	3.5
452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from c	3.5
400666			0	3.5
422646	H87863	Hs.151380	ESTs	3.5
407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	3.5
408730	AV660717	Hs.47144	DKFZP586N0819 protein	3.5
401517			0	3.5
413775	AW409934	Hs.75528	nucleolar GTPase	3.5
417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4	3.5
427943	AW959075		gb:EST371145 MAGE resequences, MAGE Homo sapi	3.5
439107	AL046134	Hs.27895	ESTs	3.5
447268	AI370413	Hs.36563	Homo sapiens cDNA: FLJ22418 fis, clone HRC085	3.5
412604	AW978324	Hs.47144	DKFZP586N0819 protein	3.5
427134	AA398409	Hs.173561	EST	3.5
430273	AI311127	Hs.125522	ESTs	3.5
436671	AW137159	Hs.146151	ESTs	3.5
433037	NM_014158	Hs.279938	HSPC067 protein	3.5
453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	3.5
400531	AF151064	Hs.36069	hypothetical protein	3.5
433345	AI681545	Hs.152982	EST cluster (not in UniGene)	3.4
406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	3.4
407596	R86913		gb:yq30f05.r1 Soares fetal liver spleen 1NFLS	3.4
453779	N35187	Hs.43388	ESTs	3.4
444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	3.4
447688	N87079	Hs.19236	NADH dehydrogenase (ubiquinone) 1 beta subcom	3.4
424856	AA347746	Hs.9521	ESTs, Weakly similar to KIAA1015 protein [H.s	3.4
407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.4
404108			0	3.4
403729			0	3.4
404232			0	3.4
423687	AA329633	Hs.133011	ESTs, Highly similar to Z117_HUMAN ZINC FINGE	3.4
428372	AK000684	Hs.183887	hypothetical protein FLJ22104	3.4
439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDNA clo	3.4
441447	AA934077	Hs.126980	ESTs	3.4
448358	R44433	Hs.106614	Human DNA sequence from clone RP4-534K7 on ch	3.4
450926	AI744361	Hs.205591	ESTs, Weakly similar to zinc finger protein P	3.4
458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated in mu	3.4
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-C	3.4
452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone HSI056	3.4
441111	AI806867	Hs.126594	ESTs	3.4
447519	U46258	Hs.23448	ESTs	3.4
446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetraspan	3.4
449581	AI989517	Hs.181605	ESTs	3.4
456132	BE219771	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT2RP40	3.4
448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT2RP30	3.4
422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltran	3.4
441433	AA933809	Hs.42746	ESTs	3.4
417837	AL079905	Hs.1103	transforming growth factor, beta 1	3.4
450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe homo	3.4
407796	AA195509	Hs.272239	lymphocyte activation-associated protein	3.3
419200	AW966405	Hs.288856	prefoldin 5	3.3
423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from c	3.3
445679	AI343868	Hs.58800	Homo sapiens cDNA FLJ12488 fis, clone NT2RM20	3.3
435014	BE560898	Hs.10026	ribosomal protein L17 isolog	3.3
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	3.3
439170	AA332365	Hs.165539	ESTs	3.3
429830	AI537278	Hs.225841	DKFZP434D193 protein	3.3
428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein [H.s	3.3
445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.3
408805	H69912	Hs.48269	vaccinia related kinase 1	3.3
441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	3.3
408532	AI453137	Hs.63176	ESTs	3.3
409517	X90780	Hs.54668	troponin I, cardiac	3.3
414304	AI621276	Hs.165998	DKFZP564M2423 protein	3.3
436427	AI344378	Hs.143399	ESTs	3.3
436662	AI582393	Hs.126695	ESTs	3.3
440304	BE159984	Hs.125395	ESTs	3.3
447385	F12863		gb:HSC3FE081 normalized infant brain cDNA Hom	3.3
451177	AI969716	Hs.13034	ESTs	3.3
428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 [H.	3.3
451743	AW074266	Hs.23071	ESTs	3.3

421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long f	3.3
446351	AW444551	Hs.258532	ESTs	3.3
435102	AW899053	Hs.76917	F-box only protein 8	3.3
418216	AA662240	Hs.283099	AF15q14 protein	3.3
401508			0	3.3
437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HSI009	3.3
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	3.3
443171	BE281128	Hs.9030	TONDU	3.3
458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [	3.3
412078	X69699	Hs.73149	paired box gene 8	3.3
414080	AA135257	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	3.3
401197			0	3.3
422134	AW179019	Hs.112110	ESTs	3.3
409044	AI129586	Hs.33033	ESTs	3.3
416198	H27332	Hs.99598	ESTs	3.2
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	3.2
436525	AA721428	Hs.26145	Homo sapiens cDNA FLJ14127 fis, clone MAMMA10	3.2
409142	AL136877	Hs.50758	chromosome-associated polypeptide C	3.2
428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
428728	NM_016625	Hs.191381	ESTs; Weakly similar to hypothetical protein	3.2
421261	AA600853	Hs.98133	ESTs	3.2
446219	AI287344	Hs.149827	ESTs	3.2
457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC086 [H	3.2
409172	Z99399	Hs.118145	ESTs	3.2
419388	T67012	Hs.75323	prohibitin	3.2
434187	AA627098	Hs.99103	ESTs, Weakly similar to I38428 T-complex prot	3.2
445060	AA830811	Hs.88808	ESTs	3.2
448254	AI829900	Hs.22929	ESTs	3.2
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	3.2
411393	AW797437	Hs.69771	B-factor, properdin	3.2
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.2
408418	AW963897	Hs.44743	KIAA1435 protein	3.2
442025	AW887434	Hs.11810	ESTs, Weakly similar to CD4.2 [C.elegans]	3.2
417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	3.2
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransf	3.2
444755	AA431791	Hs.183001	ESTs	3.2
402829			0	3.2
451593	AF151879	Hs.26706	CGI-121 protein	3.2
419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.2
434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-REPAIR	3.2
445929	AI089660	Hs.7838	makorin, ring finger protein, 1	3.2
409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	3.2
418836	AI655499	Hs.161712	ESTs	3.2
441020	W79283	Hs.35962	ESTs	3.1
422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38kD)	3.1
413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochondrial	3.1
452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.1
410486	AW235094	Hs.193424	ESTs, Weakly similar to KIAA1064 protein [H.s	3.1
434540	NM_016045	Hs.5184	TH1 drosophila homolog	3.1
409178	BE393948	Hs.50915	kallikrein 5	3.1
439480	AL038511	Hs.125316	ESTs	3.1
417848	AA205581	Hs.39457	ESTs	3.1
446293	AI420213	Hs.149722	ESTs	3.1
408108	AI580492	Hs.42743	hypothetical protein	3.1
415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	3.1
410519	AW612264	Hs.131705	ESTs	3.1
421987	AI133161	Hs.286131	CGI-101 protein	3.1
440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
453931	AL121278	Hs.25144	ESTs	3.1
454423	AW603985	Hs.179662	nucleosome assembly protein 1-like 1	3.1
459089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (from c	3.1
418735	N48769	Hs.44609	ESTs	3.1
414245	BE148072	Hs.75850	WAS protein family, member 1	3.1
410909	AW898161	Hs.53112	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.1
434926	BE543269	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	3.1
409239	AA740875	Hs.44307	ESTs	3.1
429017	AA463605	Hs.238995	ESTs	3.1
447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	3.1
426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic prot	3.1
448133	AA723157	Hs.73769	folate receptor 1 (adult)	3.1
418792	AB037805	Hs.88442	KIAA1384 protein	3.1
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. cere	3.1
402077			0	3.1
440671	AW297920	Hs.130054	ESTs	3.1
419890	X17360	Hs.278255	homeo box D4	3.1
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	3.1
409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. cerevi	3.1
431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B; yeast)	3.1
443584	AI807036	Hs.101619	ESTs	3.1
445525	BE149866	Hs.14831	ESTs	3.1
410441	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens cDNA c	3.1
422634	NM_016010	Hs.118821	CGI-62 protein	3.0
420022	AA256253	Hs.120817	ESTs	3.0
453912	AL121031	Hs.32556	KIAA0379 protein	3.0

456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	3.0
414941	C14865	Hs.182159	ESTs	3.0
407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on chrom	3.0
414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis, clone NT2RP30	3.0
444420	AI148157	Hs.146766	ESTs	3.0
431742	NM_016652	Hs.268281	CGI-201 protein	3.0
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	3.0
418348	AI537167	Hs.96322	Homo sapiens cDNA: FLJ23560 fis, clone LNG098	3.0
444261	AA298958	Hs.10724	MDS023 protein	3,0
457465	AW301344	Hs.195969	ESTs	3.0
443933	AI091631	Hs.135501	Homo sapiens two pore potassium channel KT3.3	3.0
442150	AI368158	Hs.128864	ESTs	3.0
414883	AA926960	Hs.77550	CDC28 protein kinase 1	3.0
442879	AF032922	Hs.8813	syntaxin binding protein 3	3.0
437949	U78519	Hs.41654	ESTs	3.0
403515			0	3.0
403864			0	3.0
407785	AW207285	Hs.98279	ESTs	3.0
426199	AA371865	Hs.97090	ESTs	3.0
426324	AW291787	Hs.200933	ESTs	3.0
427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Zellweg	3.0
427837	U87309	Hs.180941	vacuolar protein sorting 41 (yeast homolog)	3.0
439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	3.0
442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [R.norvegicus]	3.0
446978	NM_001938	Hs.16697	down-regulator of transcription 1, TBP-bindin	3.0
452431	U88879	Hs.29499	toll-like receptor 3	3.0
452841	T17431	Hs.65412	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	3.0
432114	AL036021	Hs.225597	ESTs	3.0
445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	3.0
442607	AA507576	Hs.288361	KIAA0741 gene product	3.0
453920	AI133148	Hs.36602	I factor (complement)	3.0
430000	AW205931	Hs.99598	ESTs	3.0
429164	AI688663	Hs.116586	ESTs	3.0
453331	AI240665	Hs.8895	ESTs	3.0
448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar to syn	3.0
425776	U25128	Hs.159499	parathyroid hormone receptor 2	3.0
401714			0	3.0
400903			0	3.0
428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.0
443761	AI525743	Hs.160603	ESTs	3.0
451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on chrom	3.0
442580	AI733682	Hs.130239	ESTs	3.0

TABLE 10B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
407596	1003489_1	R86913 R86901 H25352 R01370 H43764 AW044451 W21298
409763	115392_1	AL043212 AA077575 AA077655 R19502 BE545457 AI638421 R14093
410360	1197225_-2	AW663690
410441	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
411560	1249443_1	AW851186 AW996967 BE143456
414315	143512_1	Z24878 AA494098 F13654 AA494040 AA143127
418417	1750818_1	R77182 R77197 R80484
418454	175699_1	AA315308 AA223392 BE538098 BE087173
419346	184129_1	AI830417 AA236612
424770	243504_1	AA425562 AI880208 AA346646 N22655 AW811775 AW811786
427943	284802_1	AW959075 W06838 AA417863
431965	33959_2	BE175190 BE003348
436812	427323_1	AW298067 AA731645 AA810101 AW194180 AI690673 AW978773
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282916 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 .
439255	470321_1	BE164500 AA832198 BE164502
447385	719912_1	F12863 AI377223 T75099
454193	1050256_1	BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091 AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220 AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129 AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108 AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156 AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
454556	1223878_1	AW807073 AW807055 AW807067 AW807276 AW807030 AW807363 AW845892 AW807091 AW807275 AW807284 AW807287 AW845891 AW807195 AW807271
454933	1245515_1	BE141714 AW845993 AW845989

TABLE 10C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400534	6981826	Minus	278637-279292
400666	8118496	Plus	17982-18115,20297-20456
400903	2911732	Plus	59112-59228
401197	9719705	Plus	176341-176452
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401508	7534110	Minus	110779-110983
401517	7677912	Plus	29278-29770
401644	8576138	Plus	82655-83959
401714	6715702	Plus	96484-96681
402077	8117414	Plus	65014-65195
402222	9958106	Plus	3261-3834,3939-4269
402408	9796239	Minus	110326-110491
402820	6456853	Minus	82274-82443
402829	8918414	Plus	101532-101852,102006-102263
403381	9438267	Minus	26009-26178
403515	7656757	Minus	173358-179553
403729	7543752	Minus	37662-37909.,
403864	7709019	Minus	51753-51890,79290-79445
404108	8247074	Minus	63603-64942
404232	8218045	Minus	71800-71956
404552	7243881	Plus	19854-20010
404567	7249169	Minus	101320-101501
404599	8705107	Plus	110443-110733
404915	7341766	Minus	100915-101087
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405095	8072599	Plus	138877-139066
406069	9117732	Plus	68880-69374
406117	9142932	Plus	54304-54584

Table 11A lists about 222 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted.

TABLE 11A: ABOUT 222 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
PFAM domains: predicted protein structural domains
ratio: ratio tumor vs normal tissue

Pkey	Ex. Accn	UG ID	Title	PFAM domains	ratio
400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic pro	pkinase,Activin_recp	30.0
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	25.2
427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid m	C1q,Collagen	22.7
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular m	tsp_1	19.0
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	17.4
443646	AI085198	Hs.298699	ESTs	TSPN,vwc,tsp_1,EGF	15.1
436209	AW850417	Hs.254020	ESTs, Moderately similar to unname	TM	14.1
418601	AA279490	Hs.86368	calmegin	SS,calreticulin	13.8
428532	AF157326	Hs.184786	TBP-interacting protein	TM	13.6
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) rec	TM,neur_chan	11.8
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamin	TM,Glycos_transf_2,Ri	11.0
404567	NM_015902	Hs.278428	progestin induced protein (DD5)	TM,HECT,zf-UBR1	10.8
445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,MAM,EGF	8.9
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	TM,MSP_domain	8.8
407001	U12471	Hs.247954	Human thrombospondin-1 gene, par	TSPN,vwc,tsp_1,EGF	8.5
453370	AI470523	Hs.182356	ESTs, Moderately similar to translat	ABC_tran,ABC_membr	8.4
400298	AA032279	Hs.61635	STEAP1	TM	8.1
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	SS,Cys_knot	7.9
429609	AF002246	Hs.210863	cell adhesion molecule with homolo	TM,fn3,ig	7.8
412170	D16532	Hs.73729	very low density lipoprotein recepto	TM,ldl_recept_a,ldl_rec	7.4
428954	AF100781	Hs.194678	WNT1 inducible signaling pathway	SS,IGFBP,Cys_knot,tsp	7.4
418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitia	SS,hemopexin,Peptidas	7.2
424001	W67883	Hs.137476	KIAA1051 protein	Pep_M12B_propep,Rep	7.2
456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetica	TM	7.1
446142	AI754693	Hs.145968	ESTs	Cadherin_C_term,cadhe	7.0
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP	Kunitz_BPTI,G-gamma	6.8
438167	R28363	Hs.24286	ESTs	7tm_1	6.6
452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and	Pep_M12B_propep,Rep	6.4
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose in	SS	5.8
425371	D49441	Hs.155981	mesothelin	SS	5.7
407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha p	TM,E1-E2_ATPase,Hy	5.6
424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum c	SS,trypsin	5.5
420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH,I_LWEQ	5.4

413384	NM_000401	Hs.75334	exostoses (multiple) 2	TM	5.3
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	Collagen,TSPN	5.2
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral	TGF-beta,TGFb_propep	5.1
415539	AI733881	Hs.72472	BMPR-Ib; bone morphogenetic pro	pkinase,Activin_recp	5.1
438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	4.9
424539	L02911	Hs.150402	activin A receptor, type I	Activin_recp,pkinase	4.8
450375	AA009647	Hs.8850	a disintegrin and metalloproteinase d	disintegrin,Reprolysin,P	4.7
451684	AF216751	Hs.26813	CDA14	TM	4.6
400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran,ABC_m	4.6
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase d	TM	4.5
400534	AP000541		predicted exons	TM,KRAB,zf-C2H2	4.5
425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1	TM,Folate_carrier	4.5
413472	BE242870	Hs.75379	solute carrier family 1 (glial high aff	TM,SDF	4.4
449535	W15267	Hs.23672	low density lipoprotein receptor-rela	SS,ldl_recept_b,ldl_rece	4.4
452028	AK001859	Hs.27595	hypothetical protein FLJ10997	Zn_carbOpept,Propep_M	4.3
418693	AI750878	Hs.87409	thrombospondin 1	EGF,TSPN,tsp_1,tsp_3,	4.3
410361	BE391804	Hs.62661	guanylate binding protein 1, interfer	TM,GBP	4.2
407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	Frizzled,Fz,7tm_2	4.2
421502	AF111856	Hs.105039	solute carrier family 34 (sodium pho	TM,Na_Pi_cotrans	4.2
412494	AL133900	Hs.792	ADP-ribosylation factor domain pro	arf,zf-B_box,zf-C3HC4	4.0
405095	NM_014479	Hs.145296	disintegrin protease	Reprolysin,disintegrin	4.0
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic pro	SS,wap	4.0
407792	AI077715	Hs.39384	putative secreted ligand homologous	SS	4.0
408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-s	TM	3.8
450581	AF081513	Hs.25195	endometrial bleeding associated fact	SS,TGF-beta,TGFb_pro	3.7
432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3,	TM,Sterol_desat	3.7
450447	AF212223	Hs.25010	hypothetical protein P15-2	TM,ANF_receptor,guan	3.6
414706	AW340125	Hs.76989	KIAA0097 gene product	TM	3.6
417389	BE260964	Hs.82045	Midkine (neurite growth-promoting	TM,PTN_MK	3.6
400666	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	3.5
406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	SS,trypsin	3.4
407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	TM,FHA,BRCT	3.4
452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis,	EGF,fn3,pkinase	3.4
446913	AA430650	Hs.16529	transmembrane 4 superfamily memb	TM,transmembrane4	3.4
422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fuc	SS	3.4
423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZ	cadherin,Cadherin_C_te	3.3
435102	AW899053	Hs.76917	F-box only protein 8	TM,Sec7	3.3
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SS,TM,trypsin	3.3
401197			predicted exons	arf,Ets	3.3
436525	AA721428	Hs.26145	Homo sapiens cDNA FLJ14127 fis,	TM	3.2
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	TM	3.2
411393	AW797437	Hs.69771	B-factor, properdin	SS,sushi,trypsin,vwa,fib	3.2
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-s	SS	3.2
418836	AI655499	Hs.161712	ESTs	pkinase,Activin_recp	3.2
409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	3.1
421987	AI133161	Hs.286131	CGI-101 protein	TM	3.1
447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	SS	3.1
426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteo	SS,TGFb_propeptide,T	3.1
448133	AA723157	Hs.73769	folate receptor 1 (adult)	TM	3.1
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS,Peptidase_M10,hem	3.1
456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosp	TM,Cytidylyltrans	3.0
414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis,	SPRY,7tm_1	3.0
407785	AW207285	Hs.98279	ESTs	Sema,ig	3.0
427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35	TM,zf-C3HC4	3.0
452431	U88879	Hs.29499	toll-like receptor 3	TM,TIR,LRRCT	3.0
453920	AI133148	Hs.36602	I factor (complement)	ldl_recept_a,trypsin,SRC	3.0
453331	AI240665	Hs.8895	ESTs	disintegrin,Reprolysin,P	3.0
425776	U25128	Hs.159499	parathyroid hormone receptor 2	TM,7tm_2	3.0
428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog	TM,pkinase	3.0
407910	AA650274	Hs.41296	fibronectin leucine rich transmembra	TM,LRRCT,LRRNT,LR	2.9
408380	AF123050	Hs.44532	diubiquitin	TM,ubiquitin,7tm_3,AN	2.9
407783	AW996872	Hs.172028	a disintegrin and metalloproteinase d	disintegrin,Reprolysin	2.9
420757	X78592	Hs.99915	androgen receptor (dihydrotestostero	TM,Androgen_recep,ho	2.9
424406	D54120	Hs.146409	wingless-type MMTV integration sit	cadherin,Cadherin_C_te	2.9
428549	AA430064	Hs.220929	ESTs, Moderately similar to ARF-fa	arf	2.9
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	TM,pkinase,ig	2.9
452281	T93500	Hs.28792	ESTs	TGFb_propeptide,TGF-	2.9
420440	NM_002407	Hs.97644	mammaglobin 2	SS,Uteroglobin	2.9
418848	AI820961	Hs.193465	ESTs	pkinase,Activin_recp	2.9
421991	NM_014918	Hs.110488	KIAA0990 protein	SS	2.9
433190	M26901	Hs.3210	renin	SS,asp	2.9
424538	NM_005095	Hs.150390	zinc finger protein 262	TM	2.8
433002	AF048730	Hs.279906	cyclin T1	SS	2.8
444342	NM_014398	Hs.10887	similar to lysosome-associated mem	TM,Lamp	2.8
430598	AK001764	Hs.247112	hypothetical protein FLJ10902	TM	2.8
428450	NM_014791	Hs.184339	KIAA0175 gene product	TM,pkinase,KA1	2.8
450171	AL133661	Hs.24583	hypothetical protein DKFZp434C03	TM	2.8
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate tran	TM,GATase_2,SIS	2.8
430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus	TM	2.8
417866	AW067903	Hs.82772	collagen, type XI, alpha 1	Collagen,COLFI,TSPN	2.8
424894	H83520	Hs.153678	reproduction 8	SS,UBX	2.8
430651	AA961694	Hs.105187	kinesin protein 9 gene	SS	2.7
414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-	TM	2.7
448595	AB014544	Hs.21572	KIAA0644 gene product	TM,LRRCT,LRR	2.7

452835	AK001269	Hs.30738	ESTs	TM	2.7
403019	AA834626	Hs.66718	RAD54 (S.cerevisiae)-like	SS,Anti_proliferat	2.7
420281	AI623693	Hs.191533	ESTs	Cation_efflux	2.7
434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalact	SS	2.6
432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protea	trefoil,trypsin	2.6
430450	R23553	Hs.241489	hypothetical protein	SS	2.6
448402	BE244226	Hs.21094	RAB18, member RAS oncogene fam	ras,arf	2.6
421802	BE261458	Hs.108408	CGI-78 protein	TM	2.6
452355	N54926	Hs.29202	G protein-coupled receptor 34	TM,7tm_1	2.6
417742	R64719		gb:EST22d11 WATM1 Homo sapie	ank,death,RHD,TIG	2.6
451346	NM_006338	Hs.26312	glioma amplified on chromosome 1	TM,ig,LRR,LRRNT,LR	2.6
433147	AF091434	Hs.43080	platelet derived growth factor C	TM,PDGF,CUB	2.6
420079	NM_014051	Hs.94896	PTD011 protein	SS,TM,	2.6
419918	X80700	Hs.93728	pre-B-cell leukemia transcription fac	homeobox,ig,Acyltransf	2.5
432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	SS	2.5
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte gro	pkinase,Sema,Plexin_re	2.5
417412	X16896	Hs.82112	interleukin 1 receptor, type I	SS,TIR,ig	2.5
422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	TM	2.5
433929	AI375499	Hs.27379	ESTs	EGF,ldl_recept_a,ldl_re	2.5
443562	AF118838	Hs.9599	solute carrier family 25, member 13	TM,mito_carr	2.5
414386	X00442	Hs.75990	haptoglobin	sushi,trypsin	2.5
417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltr	AIRS,formyl_transf,GA	2.5
449207	AL044222	Hs.23255	nucleoporin 155kD	TM	2.5
416107	AA173846	Hs.79015	antigen identified by monoclonal ant	TM,ig	2.4
421750	AK000768	Hs.107872	hypothetical protein FLJ20761	TM,PH	2.4
414812	X72755	Hs.77367	monokine induced by gamma interfe	SS,IL8	2.4
406137	R42764	Hs.3248	mutS (E. coli) homolog 6	TM,MutS_C,MutS_N,P	2.4
450710	AW953381	Hs.18627	ESTs, Weakly similar to G01447 GP	TM	2.4
430291	AV660345	Hs.238126	CGI-49 protein	TM	2.4
425184	BE278288	Hs.155048	Lutheran blood group (Auberger b a	ig	2.4
451418	BE387790	Hs.26369	ESTs	TM	2.4
412277	BE277592	Hs.73799	guanine nucleotide binding protein (	TM,G-alpha	2.4
413719	BE439580	Hs.75498	small inducible cytokine subfamily A	SS,IL8	2.4
451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	TM,RCT	2.3
416224	NM_002902	Hs.79088	reticulocalbin 2, EF-hand calcium bi	SS,efhand	2.3
452268	NM_003512	Hs.28777	H2A histone family, member L	histone,Calc_CGRP_IA4	2.3
451668	Z43948	Hs.26789	ASPIC (acidic secreted protein in ca	SS,TM,	2.3
400880	M84349	Hs.119663	CD59 antigen	SS,UPAR_LY6	2.3
421340	F07783	Hs.1369	decay accelerating factor for comple	SS,sushi	2.3
443986	AI381750	Hs.283437	HTGN29 protein	TM	2.3
443037	AW500305	Hs.8906	syntaxin 7	TM,Syntaxin	2.3
440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neur	HNH,cadherin,Cadherin	2.3
404877	AI394145	Hs.18048	melanoma antigen MAGE-10	TM,MAGE	2.3
440704	M69241	Hs.162	insulin-like growth factor binding pr	SS,thyroglobulin_1,IGF	2.3
437952	D63209	Hs.5944	solute carrier family 11 (proton-coup	TM	2.3
418624	AI734080	Hs.104211	ESTs	Sema,ig	2.2
410434	AF051152	Hs.63668	toll-like receptor 2	SS,TIR,LRRCT,LRR	2.2
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatina	SS,fn2,hemopexin,Pepti	2.2
431457	NM_012211	Hs.256297	integrin, alpha 11	TM,FG-GAP,vwa	2.2
407907	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5	SS,Lysyl_hydro	2.2
400898	AF220030	Hs.125300	Homo sapiens tripartite motif protein	SPRY,7tm_1	2.2
400303	AA242758	Hs.79136	Human breast cancer, estrogen regul	SS,TM,	2.2
411789	AF245505	Hs.72157	Homo sapiens mRNA; cDNA DKFZ	ig,LRRCT	2.2
414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	TM,PA,Ribosomal_S2	2.2
401131	NM_001651	Hs.298023	Homo sapiens aquaporin 5 (AQP5),	TM,MIP	2.2
400277	Y00281	Hs.2280	Human mRNA for ribophorin I	TM	2.1
409317	U20165	Hs.53250	bone morphogenetic protein recepto	TM,pkinase	2.1
409956	AW103364	Hs.727	H.sapiens activin beta-A subunit (ex	TGF-beta,TGFb_propep	2.1
451253	H48299	Hs.26126	claudin 10	TM,PMP22_Claudin	2.1
429638	AI916662	Hs.211577	Kinectin 1 (kinesin receptor)	TM	2.1
409267	NM_012453	Hs.52515	transducin (beta)-like 2	TM,WD40	2.1
418414	J04977	Hs.84981	X-ray repair complementing defectiv	SS	2.1
449057	AB037784	Hs.22941	ESTs	TM	2.1
417666	AI345001	Hs.82380	menage a trois 1 (CAK assembly fac	zf-C3HC4	2.1
428485	NM_002950	Hs.2280	ribophorin I	TM	2.1
445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	TM,zf-C2H2	2.1
430057	AW450303	Hs.2534	bone morphogenetic protein recepto	TM,Activin_recp,pkina	2.1
425189	H16622		gb:ym26c07.r1 Soares infant brain 1	RasGEF,PH,fibrinogen_	2.1
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycopro	SS,Glyco_hydro_18	2.1
421343	BE246444	Hs.283685	hypothetical protein FLJ20396	TM	2.1
425627	AF019612	Hs.297007	ESTs	TM,Peptidase_M50	2.1
426261	AW242243	Hs.168670	peroxisomal farnesylated protein	E1-E2_ATPase,Cation_	2.1
431638	NM_000916	Hs.2820	oxytocin receptor	TM,7tm_1	2.1
456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-rela	TM	2.1
421685	AF189723	Hs.106778	calcium transport ATPase ATP2C1	TM,E1-E2_ATPase,Hy	2.1
424099	AF071202	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran,ABC_m	2.1
424800	AL035588	Hs.153203	MyoD family inhibitor	TM	2.1
410007	AW950887	Hs.57813	zinc ribbon domain containing, 1	TFIIS	2.1
436135	D85390	Hs.5057	carboxypeptidase D	SS,Zn_carbOpept	2.1
420633	NM_014581	Hs.99526	odorant-binding protein 2B	TM,lipocalin	2.1
420162	BE378432	Hs.95577	cyclin-dependent kinase 4	pkinase,ank,ArfGap,PH	2.1
426156	BE244537	Hs.167382	natriuretic peptide receptor A/guany	TM,ANF_receptor,guan	2.0
442711	AF151073	Hs.8645	hypothetical protein	TM	2.0
411872	AW327356	Hs.90918	chromosome 11 open reading frame	TM	2.0

427801	AW979155	Hs.234433	hypothetical protein PRO1068	TM,Aa_trans	2.0
430268	AK000737	Hs.237480	hypothetical protein FLJ20730	TM	2.0
431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplas	TM,ER_lumen_recept,l	2.0
431846	BE019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	2.0
404210	U02478	Hs.100469	Human AF-6 mRNA	TM,RA,DIL,PDZ,FHA	2.0
435640	AF220053	Hs.54960	uncharacterized hematopoietic stem/	TM,SET,zf-CXXC,PHD	2.0
447906	AL050062	Hs.19999	DKFZP566K023 protein	SS	2.0
412666	AL080116	Hs.74420	origin recognition complex, subunit	TM	2.0
417181	L10123	Hs.1071	surfactant protein A binding protein	TM	2.0
423945	AA410943	Hs.72472	BMPR-Ib; bone morphogenetic pro	TM,pkinase,Activin_rec	2.0
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS,trypsin	2.0
448350	L14561	Hs.78546	Homo sapiens clone 24411 mRNA s	TM,E1-E2_ATPase,Hy	2.0
401093	AI955244	Hs.121520	HYPOTHETICAL 16.4 kDa PROTE	TM,LRRCT	2.0
415664	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) bo	DEAD,helicase_C,SPRY	2.0
448165	NM_005591	Hs.202379	meiotic recombination (S. cerevisiae	DNA_repair,Glyco_tran	2.0
416391	AI878927	Hs.79284	mesoderm specific transcript (mouse	TM,abhydrolase	2.0
422926	NM_016102	Hs.121748	ring finger protein 16	SPRY,zf-C3HC4,zf-B_	2.0
446849	AU076617	Hs.16251	cleavage and polyadenylation specif	TM	2.0
427617	D42063	Hs.179825	RAN binding protein 2-like 1	TM,Ran_BP1,zf-RanBP	2.0
411678	AI907114	Hs.71465	squalene epoxidase	TM,Monooxygenase	2.0
432554	AI479813	Hs.278411	NCK-associated protein 1	TM	2.0

TABLE 11B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
417742	1696282_1	R64719 Z44680 R12451
425189	247825_1	H16622 R17322 AA351959

TABLE 11C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400534	6981826	Minus	278637-279292
401197	9719705	Plus	176341-176452

Table 12A lists about 57 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g., pkinase, peptidase, isomerase, transporters). Predicted protein domains are noted.

TABLE 12A: ABOUT 57 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
PFAM domains: predicted structural domains
ratio: ratio tumor vs. normal

Pkey	Ex. Accn	UG ID	Title	PFAM domains	ratio
400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic pro	pkinase,Activin_recp	30.0
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS, ,Peptidase_M10	25.2
426427	M86699	Hs.169840	TTK protein kinase	pkinase	18.7
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-rela	pkinase	16.2
433159	AB035898	Hs.150587	kinesin-like protein 2	kinesin	11.5
453370	AI470523	Hs.182356	ESTs, Moderately similar to translat	ABC_tran	8.4
418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitia	SS, ,Peptidase_M10	7.2
425465	L18964	Hs.1904	protein kinase C; iota	Ski_Sno,pkinase_C	6.1
409506	NM_006153	Hs.54589	NCK adaptor protein 1	SH2,SH3	5.2
415539	AI733881	Hs.72472	BMPR-Ib; bone morphogenetic pro	pkinase,Activin_recp	5.1
424539	L02911	Hs.150402	activin A receptor, type I	Activin_recp,pkinase	4.8
400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran	4.6
431699	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 fis,	RhoGAP,FF,ras	3.9
439560	BE565647	Hs.74899	hypothetical protein FLJ12820	C2,PI-PLC-Y,PI-PLC-X	3.8
450447	AF212223	Hs.25010	hypothetical protein P15-2	ANF_receptor ,pkinase	3.6
400666	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS, ,Peptidase_M10	3.5
452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis,	EGF,fn3,pkinase	3.4
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SS,TM,trypsin	3.3
411393	AW797437	Hs.69771	B-factor, properdin	SS,sushi,trypsin,vwa,fn3,	3.2
444755	AA431791	Hs.183001	ESTs	AAA	3.2
418836	AI655499	Hs.161712	ESTs	pkinase,Activin_recp	3.2
409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	3.1
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS,Peptidase_M10, ,ig	3.1
453920	AI133148	Hs.36602	I factor (complement)	ldl_recept_a,trypsin,SRCR	3.0
404653	AA923729	Hs.26322	0	pkinase	2.9
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	TM,pkinase,ig	2.9
418848	AI820961	Hs.193465	ESTs	pkinase,Activin_recp	2.9
428450	NM_014791	Hs.184339	KIAA0175 gene product	TM,pkinase,KA1	2.8

401323	AL158037		predicted exon	lactamase_B	2.7
444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E	SH3,pkinase ,ABC_tran	2.7
432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protea	trefoil,trypsin	2.6
448402	BE244226	Hs.21094	RAB18, member RAS oncogene fam	ras,arf	2.6
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte gro	pkinase,Sema	2.5
453448	AL036710	Hs.209527	ESTs	CNH,pkinase	2.5
414386	X00442	Hs.75990	haptoglobin	sushi,trypsin	2.5
421270	H56037	Hs.108146	ESTs	RhoGAP	2.4
414695	BE439915	Hs.76913	proteasome (prosome, macropain) su	proteasome	2.4
431341	AA307211	Hs.251531	proteasome (prosome, macropain) su	proteasome	2.4
424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (4	AAA,Viral_helicase1	2.2
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatina	SS,fn2, ,Peptidase_M10	2.2
416517	AA775987	Hs.79357	proteasome (prosome, macropain) 26	AAA	2.2
417601	NM_014735	Hs.82292	KIAA0215 gene product	PHD	2.1
400509	M97639	Hs.155585	receptor tyrosine kinase-like orphan	pro_isomerase	2.1
430057	AW450303	Hs.2534	bone morphogenetic protein recepto	Activin_recp,pkinase	2.1
421841	AA908197	Hs.108850	KIAA0936 protein	TPR,pkinase	2.1
453078	AF053551	Hs.31584	metaxin 2	pro_isomerase	2.1
424099	AF071202	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran	2.1
411190	AA306342	Hs.69171	protein kinase C-like 2	pkinase,pkinase_C,HR1	2.1
407740	AA295547	Hs.62666	ESTs	p450	2.1
420162	BE378432	Hs.95577	cyclin-dependent kinase 4	pkinase,ank,ArfGap ,ras	2.1
420490	H69894	Hs.193041	ESTs	PI3Ka,PI3_PI4_kinase	2.1
426156	BE244537	Hs.167382	natriuretic peptide receptor A/guany	TM,ANF_receptor ,pkinase	2.0
423945	AA410943	Hs.72472	BMPR-Ib; bone morphogenetic pro	TM,pkinase,Activin_recp	2.0
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS,trypsin	2.0
447298	BE617527	Hs.180450	ribosomal protein S24	PI3Ka, PI4_kinase	2.0
427617	D42063	Hs.179825	RAN binding protein 2-like 1	TPR,pro_isomerase	2.0
453546	AF042385	Hs.33251	peptidylprolyl isomerase E (cycloph	pro_isomerase,rrm	2.0

TABLE 12C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
401323	9212516	Plus	213509-214450

Table 13A lists about 1086 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 10A, except that the ratio was greater than or equal to 10, and the denominator was the median value for various non-malignant ovary specimens.

TABLE 13A: About 1086 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY
Pkey: Primekey
Ex. Accn: Exemplary Accession
UG ID: UniGene ID
Title: UniGene title
ratio: ration tumor vs. normal ovary

Pkey	Ex. Accn	UG ID	Title	ratio
439706	AW872527	Hs.59761	ESTs	109.2
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	107.8
422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	104.4
447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	88.3
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	82.8
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (anti	81.9
413859	AW992356	Hs.8364	ESTs	73.9
446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	72.7
426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcription f	68.1
411469	T09997	Hs.70327	cysteine-rich protein 2	66.6
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	65.7
416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, proton c	64.9
450273	AW296454	Hs.24743	hypothetical protein FLJ20171	62.5
446441	AK001782	Hs.15093	hypothetical protein	60.7
428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	59.7
441406	Z45957	Hs.7837	Homo sapiens cDNA FLJ10457 fis, clone NT2RP10	57.8
441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT	56.7
448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076	55.7
414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264	55.2
418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxylase	54.8
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin, uteri	53.4
412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	51.4
430634	AI860651	Hs.26685	ESTs	50.7
439318	AW837046	Hs.6527	G protein-coupled receptor 56	50.7
417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	50.6
407786	AA687538	Hs.38972	tetraspan 1	50.4
426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (endobr	49.7
417308	H60720	Hs.81892	KIAA0101 gene product	48.9
436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP+), mitochond	48.4
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	47.1
428289	M26301	Hs.2253	complement component 2	46.3
405484			0	46.1

425371	D49441	Hs.155981	mesothelin	45.7
403912			0	45.0
443021	AA368546	Hs.8904	Ig superfamily protein	44.6
427697	T18997	Hs.180372	BCL2-like 1	44.3
428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	44.0
404678			0	43.9
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	43.8
451035	AU076785	Hs.430	plastin 1 (I Isoform)	43.8
440848	BE314650	Hs.7476	ATPase, H+ transporting, lysosomal (vacuolar	42.8
436278	BE396290	Hs.5097	synaptogyrin 2	42.4
413936	AF113676	Hs.75621	serine (or cysteine) proteinase inhibitor, cl	42.1
420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	42.1
428411	AW291464	Hs.10338	ESTs	41.8
422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin	41.5
412477	AA150864	Hs.790	microsomal glutathione S-transferase 1	40.7
417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium prot	40.1
424673	AA345051	Hs.294092	ESTs	39.8
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	39.7
443162	T49951	Hs.9029	ESTs; Highly similar to KERATIN; TYPE I CYTO	39.5
413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cys-Cys	39.3
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92k	38.9
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprotein-39	38.5
429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	38.1
418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid	37.9
415511	AI732617	Hs.182362	ESTs	37.7
409453	AI885516	Hs.95612	ESTs	37.7
445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	37.3
442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone HSI116	37.3
408243	Y00787	Hs.624	interleukin 8	37.3
419092	J05581	Hs.89603	mucin 1, transmembrane	36.7
444172	BE147740	Hs.104558	ESTs	36.0
412115	AK001763	Hs.73239	hypothetical protein FLJ10901	35.8
420440	NM_002407	Hs.97644	mammaglobin 2	35.7
414386	X00442	Hs.75990	haptoglobin	35.3
423225	AA852604	Hs.125359	Thy-1 cell surface antigen	35.1
440596	H13032	Hs.103378	ESTs, Weakly similar to DRR1 [H.sapiens]	35.0
413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	34.9
418506	AA084248	Hs.85339	G protein-coupled receptor 39	34.8
445919	T53519	Hs.290357	ESTs	34.7
416854	H40164	Hs.80296	Purkinje cell protein 4	34.4
414186	U33446	Hs.75799	protease, serine, 8 (prostasin)	34.2
434371	AA631362		gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens cDNA	33.9
421937	AI878857	Hs.109706	HN1 protein	33.9
449722	BE280074	Hs.23960	cyclin B1	33.8
400965			0	33.7
452203	X57522	Hs.158164	ATP-binding cassette, sub-family B (MDR/TAP),	33.5
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	33.5
425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin a	33.4
408901	AK001330	Hs.48855	hypothetical protein FLJ10468	33.3
438461	AW075485	Hs.286049	phosphoserine aminotransferase	33.3
422963	M79141	Hs.13234	ESTs	33.3
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	33.2
431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	32.8
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	32.5
431211	M86849	Hs.5566	Homo sapiens connexin 26 (GJB2) mRNA, complet	32.5
436552	NM_014038	Hs.5216	HSPC028 protein	32.5
442533	AA161224	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subu	32.5
406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	32.4
450353	AI244661	Hs.103296	ESTs	32.4
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	32.4
433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (y	32.3
441020	W79283	Hs.35962	ESTs	32.2
432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protease (ECHOS1) (T	32.0
424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	31.9
453309	AI791809	Hs.32949	defensin, beta 1	31.8
408380	AF123050	Hs.44532	diubiquitin	31.7
419329	AY007220	Hs.288998	S100-type calcium binding protein A14	31.6
409231	AA446644	Hs.692	GA733-2; epithelial glycoprotein (EGP) (KSA)	31.6
423961	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specific fac	31.2
413840	AI301558	Hs.290801	ESTs	30.8
440943	AW082298	Hs.146161	ESTs, Weakly similar to KIAA0859 protein [H.s	30.8
419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone COL013	30.4
410132	NM_003480	Hs.58882	Microfibril-associated glycoprotein-2	30.2
418203	X54942	Hs.83758	CDC28 protein kinase 2	30.1
412719	AW016610	Hs.129911	ESTs	30.0
407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC10	30.0
431563	AI027643	Hs.120912	ESTs	29.9
431743	AW972642	Hs.293055	ESTs	29.8
443295	AI049783	Hs.241284	ESTs	29.7
413745	AW247252	Hs.75514	nucleoside phosphorylase	29.7
441028	AI333660	Hs.17558	ESTs	29.6
442315	AA173992	Hs.7956	ESTs	29.6
452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	29.5

432280	BE440142	Hs.2943	signal recognition particle 19kD	29.4
420158	AI791905	Hs.95549	hypothetical protein	29.3
445033	AV652402	Hs.155145	ESTs	29.2
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	29.1
432706	NM_013230	Hs.286124	CD24	29.0
422163	AF027208	Hs.297332	prominin (mouse)-like 1	28.7
447035	NM_004753	Hs.17144	short-chain dehydrogenase/reductase 1	28.6
443958	BE241880	Hs.10029	cathepsin C	28.2
422956	BE545072	Hs.122579	ESTs	28.1
450377	AB033091	Hs.24936	ESTs	28.0
447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	28.0
444725	AW952022	Hs.234174	Homo sapiens cDNA FLJ13819 fis, clone THYRO10	27.8
430250	NM_016929	Hs.283021	chloride intracellular channel 5	27.7
416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	27.6
418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	27.5
417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cys-X-C	27.4
417866	AW067903	Hs.82772	collagen, type XI, alpha 1	27.3
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	27.2
442993	BE018682	Hs.44343	ESTs	27.2
407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	27.0
419356	AI656166	Hs.7331	ESTs	27.0
433662	W07162	Hs.150826	CATX-8 protein	26.7
422576	BE548555	Hs.118554	CGI-83 protein	26.4
423271	W47225	Hs.126256	interleukin 1, beta	26.3
443715	AI583187	Hs.9700	cyclin E1	26.1
420186	NM_015925	Hs.95697	liver-specific bHLH-Zip transcription factor	26.0
419551	AW582256	Hs.91011	anterior gradient 2 (Xenepus laevis) homolog	25.9
443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate dioxyge	25.8
416889	AW250318	Hs.80395	mal, T-cell differentiation protein	25.3
408474	AA188823	Hs.83196	Homo sapiens cDNA: FLJ23597 fis, clone LNG152	25.3
411825	AK000334	Hs.72289	hypothetical protein FLJ20327	25.3
400881			0	25.2
440594	AW445167	Hs.126036	ESTs	25.1
414586	AA306160	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin)	25.1
411925	AW014588	Hs.72925	chromosome 11 open reading frame 13	25.1
417869	BE076254	Hs.82793	proteasome (prosome, macropain) subunit, beta	25.0
433447	U29195	Hs.3281	neuronal pentraxin II	25.0
450858	C18458	Hs.25597	elongation of very long chain fatty acids (FE	24.8
410619	BE512730	Hs.65114	keratin 18	24.8
434094	AA305599	Hs.238205	hypothetical protein PRO2013	24.6
421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	24.6
446859	AI494299	Hs.16297	COX17 (yeast) homolog, cytochrome c oxidase a	24.5
421451	AA291377	Hs.50831	ESTs	24.3
433929	AI375499	Hs.27379	ESTs	24.3
438930	AW843633	Hs.81256	S100 calcium-binding protein A4 (calcium prot	24.2
444212	AW503976	Hs.10649	basement membrane-induced gene	24.2
441633	AW958544	Hs.112242	ESTs	24.2
441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	24.2
417715	AW969587	Hs.86366	ESTs	24.1
409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog 1	24.1
416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5 reduc	24.1
430125	U46418	Hs.233950	serine protease inhibitor, Kunitz type 1	23.9
434078	AW880709	Hs.283683	EST	23.8
408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molecule (	23.8
439413	AI598252	Hs.37810	ESTs	23.7
449034	AI624049	Hs.277523	gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	23.7
420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR150	23.6
431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	23.6
417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated prot	23.5
451267	AI033894	Hs.117865	solute carrier family 17 (anion/sugar transpo	23.4
450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	23.4
419693	AA133749	Hs.92323	FXYD domain-containing ion transport regulato	23.4
431103	M57399	Hs.44	pleiotrophin (heparin binding growth factor 8	23.4
451110	AI955040	Hs.301584	ESTs	23.3
426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	23.2
448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to sign	23.1
424670	W61215	Hs.116651	epithelial V-like antigen 1	23.1
417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC052	23.1
449027	AJ271216	Hs.22880	dipeptidylpeptidase III	23.1
424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiquitous)	23.1
433159	AB035898	Hs.150587	kinesin-like protein 2	23.0
411393	AW797437	Hs.69771	B-factor, properdin	23.0
434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalactosamine-alp	22.8
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal	22.7
445721	H92136	Hs.13144	HSPC160 protein	22.6
448258	BE386983	Hs.85015	ESTs, Weakly similar to A4P_HUMAN INTESTINAL	22.6
456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	22.6
452698	NM_001295	Hs.301921	ESTs	22.5
418693	AI750878	Hs.87409	thrombospondin 1	22.4
414880	AW247305	Hs.119140	eukaryotic translation initiation factor 5A	22.4
401519			0	22.3
402496			0	22.3
420324	AF163474	Hs.98744	DKFZP586D0823 protein, Prostate androgen-regu	22.3
403022			0	22.2

434042	AI589941	Hs.8254	hypothetical protein PRO0899	22.1
419080	AW150835	Hs.18878	hypothetical protein FLJ21620	22.1
406545	AB018249	Hs.10458	small inducible cytokine subfamily A (Cys-Cys	22.1
447362	AW176120	Hs.9061	ESTs	22.0
429547	AW009166	Hs.99376	ESTs	22.0
427954	J03060	Hs.247551	metaxin 1	22.0
423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from c	22.0
428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (	21.9
444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polypeptide	21.7
414421	AI521130	Hs.55567	ESTs, Weakly similar to LAK-4p [H.sapiens]	21.5
412589	R28660	Hs.24305	ESTs	21.5
446525	AW967069	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone HEP162	21.5
416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like docking	21.5
436972	AA284679	Hs.25640	claudin 3	21.5
428698	AA852773	Hs.297939	ESTs; Weakly similar to neogenin [H.sapiens]	21.5
421340	F07783	Hs.1369	decay accelerating factor for complement (CD5	21.4
413966	AA133935	Hs.173704	ESTs	21.4
448243	AW369771	Hs.77496	ESTs	21.3
421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	21.3
403399			0	21.3
435793	AB037734	Hs.4993	ESTs	21.3
432629	AW860548	Hs.280658	ESTs	21.2
449057	AB037784	Hs.22941	ESTs	21.2
437575	AW954355	Hs.36529	ESTs	21.2
401131			0	21.0
407207	T03651	Hs.179661	tubulin, beta polypeptide	20.8
444783	AK001468	Hs.62180	ESTs	20.8
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	20.8
447343	AA256641	Hs.236894	ESTs; Highly similar to LOW-DENSITY LIPOPROTE	20.7
409041	AB033025	Hs.50081	KIAA1199 protein	20.6
421305	BE397354	Hs.289721	diptheria toxin resistance protein required f	20.6
411704	AI499220	Hs.71573	hypothetical protein FLJ10074	20.5
417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related oncog	20.5
432827	Z68128	Hs.3109	Rho GTPase activating protein 4	20.4
410174	AA306007	Hs.59461	DKFZP434C245 protein	20.4
425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen incl	20.4
452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	20.3
447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte chemota	20.2
447335	BE617695	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	20.2
424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	20.1
410275	U85658	Hs.61796	transcription factor AP-2 gamma (activating e	20.1
429083	Y09397	Hs.227817	BCL2-related protein A1	20.0
410173	AA706017	Hs.119944	ESTs	19.8
433047	M86135	Hs.279946	methionine-tRNA synthetase	19.8
419088	AI538323	Hs.77496	ESTs	19.7
403381			0	19.6
409162	H25530	Hs.50868	solute carrier family 22 (organic cation tran	19.5
426150	NM_003658	Hs.167218	BarH-like homeobox 2	19.4
449292	AI990292	Hs.225457	ESTs	19.4
425207	AB014551	Hs.155120	rho/rac guanine nucleotide exchange factor (G	19.4
419950	AK001645	Hs.93871	hypothetical protein FLJ10783	19.3
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	19.3
445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	19.2
446608	N75217	Hs.257846	ESTs	19.1
425222	M85430	Hs.155191	villin 2 (ezrin)	19.1
428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	19.1
420005	AW271106	Hs.133294	ESTs	19.1
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	19.0
407142	AA412535	Hs.55235	sphingomyelin phosphodiesterase 2, neutral me	19.0
430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood Leuke	18.9
446293	AI420213	Hs.149722	ESTs	18.9
444825	AW167613	Hs.248	mitogen-activated protein kinase kinase kinas	18.9
407634	AW016569	Hs.301280	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosami	18.9
445200	AA084460	Hs.12409	somatostatin	18.9
418917	X02994	Hs.1217	adenosine deaminase	18.8
435777	AW419202	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	18.8
431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene	18.7
426427	M86699	Hs.169840	TTK protein kinase	18.7
436281	AW411194	Hs.120051	ESTs	18.6
425907	AA365752	Hs.155965	ESTs	18.6
459720			ESTs	18.6
421242	AW161386	Hs.13561	ESTs, Weakly similar to dJ37E16.5 [H.sapiens]	18.5
457715	AA642402	Hs.59142	ESTs	18.5
451668	Z43948	Hs.26789	ASPIC (acidic secreted protein in cartilage)A	18.4
437142	AI791617	Hs.145068	ESTs	18.4
418588	BE387040	Hs.182476	ESTs, Weakly similar to similar to alpha/beta	18.3
433068	NM_006456	Hs.288215	sialyltransferase	18.3
419854	AW664873	Hs.87836	Homo sapiens PAC clone RP5-1087M19 from 7q11.	18.3
444726	NM_006147	Hs.11801	interferon regulatory factor 6	18.3
423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA-2C-2	18.2
451428	AW083384	Hs.11067	ESTs, Weakly similar to K02E10.2 [C.elegans]	18.2
424865	AF011333	Hs.153563	lymphocyte antigen 75	18.2
418742	AW451197	Hs.113418	ESTs	18.1
446627	AI973016	Hs.15725	ESTs; hypothetical protein SB8I48	18.1

424885	AI333771	Hs.82204	ESTs	18.1
402926			0	18.0
405452			0	18.0
428641	AA431367	Hs.234546	GMPR2 for guanosine monophosphate reductase i	18.0
454390	AB020713	Hs.56966	KIAA0906 protein	18.0
441784	AI522132	Hs.28700	ESTs	18.0
418758	AW959311	Hs.87019	ESTs	17.9
408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; fetal br	17.9
426201	AW182614	Hs.128499	ESTs	17.8
410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta polype	17.8
456423	AW748920		gb:CM2-BT0306-171199-034-g02 BT0306 Homo sapi	17.8
422867	L32137	Hs.1584	cartilage oligomeric matrix protein	17.8
448110	AA626937	Hs.181551	ESTs	17.7
421750	AK000768	Hs.107872	hypothetical protein FLJ20761	17.7
405224			0	17.7
447630	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	17.7
407663	NM_016429	Hs.37482	COPZ2 for nonclathrin coat protein zeta-COP	17.7
427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	17.6
414812	X72755	Hs.77367	monokine induced by gamma interferon	17.6
427691	AW194426	Hs.20726	ESTs	17.6
420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	17.5
439841	AF038961	Hs.6710	mannose-P-dolichol utilization defect 1	17.5
425810	AI923627	Hs.31903	ESTs	17.5
425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	17.5
456098	AW747800	Hs.55016	hypothetical protein FLJ21935	17.4
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	17.4
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	17.4
442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	17.4
411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 19, cosmid F	17.3
405295			0	17.3
408340	AB037762	Hs.44268	myelin gene expression factor 2	17.3
456068	AI677897	Hs.76640	RGC32 protein	17.3
448571	AA486794	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [H.sap	17.2
441829	AL117482	Hs.7978	DKFZP434C131 protein	17.2
418004	U37519	Hs.87539	aldehyde dehydrogenase 8	17.2
412078	X69699	Hs.73149	paired box gene 8	17.2
414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD), mem	17.1
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	17.0
426805	AB032945	Hs.172506	myosin VB	17.0
410247	AF181721	Hs.61345	RU2S	17.0
434516	AA807814	Hs.70582	ESTs, Moderately similar to AF144056 1 apopto	16.9
428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-	16.9
417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide B	16.9
454163	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo sapi	16.9
415402	AA164687	Hs.297889	ESTs	16.9
420309	AW043637	Hs.21766	ESTs	16.9
419201	M22324	Hs.1239	alanyl (membrane) aminopeptidase (aminopeptid	16.9
444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	16.9
457705	AW974668		gb:EST386757 MAGE resequences, MAGM Homo sapi	16.8
412723	AA648459	Hs.179912	ESTs	16.8
435774	R88066	Hs.4992	tumor suppressing subtransferable candidate 1	16.8
408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich protein	16.8
447783	AF054178	Hs.19561	NADH dehydrogenase (ubiquinone) 1 alpha subco	16.8
418085	R40328	Hs.258822	ESTs	16.7
452472	AW957300	Hs.294142	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	16.7
409112	BE243971	Hs.50649	quinone oxidoreductase homolog	16.7
410250	AI082777	Hs.61384	KIAA1445 protein	16.7
446219	AI287344	Hs.149827	ESTs	16.6
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial)	16.6
425812	AA364128	Hs.245633	ESTs	16.6
411742	AW247593	Hs.71819	eukaryotic translation initiation factor 4E b	16.6
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	16.6
440667	BE076969	Hs.7337	hypothetical protein FLJ10936	16.6
430375	AW371048	Hs.93758	H4 histone family, member H	16.6
419607	R52557	Hs.91579	Homo sapiens clone 23783 mRNA sequence	16.6
410328	BE080190	Hs.62275	CGI-141 protein	16.5
405426			0	16.5
432636	AA340864	Hs.278562	claudin 7	16.5
434725	AK000796	Hs.4104	hypothetical protein	16.5
414683	S78296	Hs.76888	internexin neuronal intermediate filament pro	16.5
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	16.5
449944	AF290512	Hs.58215	Homo sapiens rhotekin mRNA, partial cds	16.4
400666			0	16.4
421536	BE250690	Hs.105509	CTL2 gene	16.4
436032	AA150797	Hs.109276	latexin protein	16.4
418196	AI745649	Hs.26549	ESTs, Weakly similar to T00066 hypothetical p	16.4
452323	W44356	Hs.292812	ESTs, Weakly similar to C43H8.1 [C.elegans]	16.4
407699	AA825974	Hs.32646	Homo sapiens cDNA: FLJ21901 fis, clone HEP034	16.4
414617	AI339520	Hs.20524	ESTs, Moderately similar to hexokinase I [H.s	16.3
408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, member	16.3
452650	AW270150	Hs.254516	ESTs	16.3
432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	16.3
402408			0	16.3

408805	H69912	Hs.48269	vaccinia related kinase 1	16.3
447155	AA100605	Hs.121557	ESTs, Weakly similar to AF251041 1 SGC32445 p	16.3
405699			0	16.2
406893	M22406		gb:Human intestinal mucin mRNA, partial cds,	16.2
418629	BE247550	Hs.86859	growth factor receptor-bound protein 7 (GRB7)	16.2
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	16.2
424243	AI949359	Hs.301837	ESTs, Highly similar to cis Golgi-localized c	16.2
418462	BE001596	Hs.85266	integrin, beta 4	16.1
457205	AI905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	16.1
428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epidermal t	16.1
449845	AW971183	Hs.60054	ESTs	16.1
406429			0	16.1
407375	AA091354		gb:l0815.seq.F Human fetal heart, Lambda ZAP	16.1
448377	AI494514	Hs.171380	ESTs	16.1
431156	NM_002220	Hs.2722	inositol 1,4,5-trisphosphate 3-kinase A	16.0
450043	AA885699	Hs.24332	CGI-26 protein	16.0
403121			0	16.0
400214			0	15.9
453252	R02436	Hs.215725	ESTs	15.9
451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate, RC3)	15.9
416855	AA188763	Hs.36793	Homo sapiens cDNA: FLJ23188 fis, clone LNG120	15.9
424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interacting pro	15.9
423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein, parti	15.9
428187	AI687303	Hs.285529	ESTs	15.9
438817	AI023799	Hs.163242	ESTs	15.9
425692	D90041	Hs.155956	NAT1; arylamine N-acetyltransferase	15.9
421674	T10707	Hs.296355	neuronal PAS domain protein 2	15.9
439999	AA115811	Hs.6838	ras homolog gene family, member E	15.9
411351	W02919	Hs.283476	peroxisomal acyl-CoA thioesterase	15.9
413027	NM_002885	Hs.75151	RAP1, GTPase activating protein 1	15.9
453884	AA355925	Hs.36232	KIAA0186 gene product	15.8
407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase C-bet	15.8
422748	AA316266	Hs.129349	ESTs	15.8
414591	AI888490	Hs.55902	ESTs	15.8
421877	AW250380	Hs.109059	mitochondrial ribosomal protein L12	15.8
404780			0	15.8
401192			0	15.8
447519	U46258	Hs.23448	ESTs	15.8
434262	AF121858	Hs.12169	sorting nexin 8	15.7
451253	H48299	Hs.26126	claudin 10	15.7
435499	R89344	Hs.14148	ESTs	15.7
422424	AI186431	Hs.116577	prostate differentiation factor; placental bo	15.7
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	15.7
424562	AI420859	Hs.150557	basic transcription element binding protein 1	15.7
443247	BE614387	Hs.47378	ESTs	15.7
430696	AA531276	Hs.59509	ESTs	15.6
437044	AL035864	Hs.69517	ESTs, highly similar to differentially expres	15.6
428237	AF175206	Hs.183125	killer cell lectin-like receptor F1	15.6
440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	15.6
414922	D00723	Hs.77631	glycine cleavage system protein H (aminomethy	15.6
422030	X51416	Hs.110849	estrogen-related receptor alpha	15.6
408716	AI567839	Hs.151714	ESTs	15.5
410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-biphosp	15.5
410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR A	15.5
447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	15.5
409015	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S protein	15.5
447549	AI871120	Hs.231265	ESTs	15.5
449704	AK000733	Hs.23900	GTPase activating protein	15.4
427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, recept	15.4
421630	NM_001956	Hs.1407	endothelin 2	15.4
433018	AI669760	Hs.188881	ESTs	15.4
422938	NM_001809	Hs.1594	centromere protein A (17kD)	15.3
407014	U38268		gb:Human cytochrome b pseudogene, partial cds	15.2
429311	AF080157	Hs.198998	conserved helix-loop-helix ubiquitous kinase	15.2
431842	NM_005764	Hs.271473	epithelial protein up-regulated in carcinoma,	15.2
406907	Z25427		gb:H.sapiens protein-serine/threonine kinase	15.2
458495	AI202029	Hs.148593	ESTs	15.2
420551	AL137692	Hs.98790	Homo sapiens mRNA; cDNA DKFZp434P182 (from cl	15.1
448443	AW167128	Hs.231934	ESTs	15.1
443646	AI085198	Hs.298699	ESTs	15.1
431538	AL137547	Hs.259619	Homo sapiens mRNA; cDNA DKFZp434B1120 (from c	15.1
436687	AA868643	Hs.120461	ESTs	15.1
420917	AW135716	Hs.117330	ESTs	15.0
428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibitor, cl	15.0
403482			0	15.0
421499	AI271438	Hs.105022	Homo sapiens PAC clone RP4-701O16 from 7q33-q	15.0
401047			0	14.9
417749	U09196	Hs.82520	polymerase (DNA-directed), delta 4	14.9
416693	AI373204	Hs.79531	Homo sapiens TTF-I interacting peptide 20 mRN	14.9
428474	AB023182	Hs.184523	KIAA0965 protein	14.9
428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (campome	14.9
430271	T06199	Hs.237506	heat shock cognate 40	14.9
414328	Z21666	Hs.75900	aconitase 2, mitochondrial	14.9
415314	N88802	Hs.5422	glycoprotein M6B	14.8

453735	AI066629	Hs.125073	ESTs	14.8
424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	14.8
423575	C18863	Hs.163443	ESTs	14.8
438081	H49546	Hs.298964	ESTs	14.8
403485			0	14.8
452114	N22687	Hs.8236	ESTs	14.8
426559	AB001914	Hs.170414	paired basic amino acid cleaving system 4	14.8
412869	AA290712	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	14.8
452101	T60298		gb:yb87f12.r1 Stratagene liver (937224) Homo	14.7
420505	AW967984	Hs.291612	ESTs	14.7
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	14.7
433336	AF017986	Hs.31386	ESTs; Highly similar to FRIZZLED PROTEIN PRE	14.7
428977	AK001404	Hs.194698	cyclin B2	14.7
429785	H82114	Hs.301769	ESTs	14.7
402424			0	14.7
424971	AA479005	Hs.154036	tumor suppressing subtransferable candidate 3	14.7
433037	NM_014158	Hs.279938	HSPC067 protein	14.6
421670	BE207318	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy	14.6
438598	AI805943	Hs.5723	Homo sapiens cDNA: FLJ23439 fis, clone HSI001	14.6
453370	AI470523	Hs.182356	ESTs, Moderately similar to translation initi	14.6
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	14.6
402287			0	14.6
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	14.6
442047	AA974598	Hs.150324	ESTs	14.5
428582	BE336699	Hs.185055	BENE protein	14.5
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	14.5
406851	AA609784	Hs.180255	major histocompatibility complex, class II, D	14.5
457316	AI123657	Hs.127264	ESTs	14.5
420453	AL157500	Hs.97840	Homo sapiens mRNA; cDNA DKFZp434G015 (from cl	14.5
436406	AW105723	Hs.125346	ESTs	14.5
420736	AI263022	Hs.82204	ESTs	14.5
419743	AW408762	Hs.127478	ESTs	14.5
429113	D28235	Hs.196384	Prostaglandin-endoperoxide synthase 2 (COX-2)	14.5
450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-rich tan	14.5
424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untr	14.5
427414	F11750	Hs.6647	Homo sapiens cDNA FLJ13088 fis, clone NT2RP30	14.4
419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activat	14.4
418738	AW388633	Hs.6682	solute carrier family 7, member 11	14.3
429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	14.3
424669	AA417181	Hs.120858	Homo sapiens cDNA FLJ13945 fis, clone Y79AA10	14.3
408989	AW361666	Hs.49500	KIAA0746 protein	14.3
406788	AI911841	Hs.5184	TH1 drosophila homolog	14.3
417861	AA334551	Hs.82767	sperm specific antigen 2	14.3
402104			0	14.3
416368	R88849		gb:ym96a06.r1 Soares adult brain N2b4HB55Y Ho	14.2
405802			0	14.2
448357	N20169	Hs.108923	ESTs	14.2
444261	AA298958	Hs.10724	MDS023 protein	14.2
407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	14.2
425163	D10040	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain 2	14.1
402520			0	14.1
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	14.1
430044	AA464510	Hs.152812	EST cluster (not in UniGene)	14.1
429663	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolase (cP	14.1
427036	AA397625	Hs.163913	ESTs	14.1
444381	BE387335	Hs.283713	ESTs	14.1
432090	AW972855	Hs.292853	ESTs	14.0
406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (from cl	14.0
404961	AW972195	Hs.284236	aldo-keto reductase family 7, member A3 (afla	14.0
452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	14.0
452355	N54926	Hs.29202	G protein-coupled receptor 34	14.0
429942	AI338993	Hs.134535	ESTs	14.0
403165			0	13.9
442150	AI368158	Hs.128864	ESTs	13.9
439709	AW401433	Hs.6649	hypothetical protein FLJ20128	13.9
456799	AC004923	Hs.135187	Homo sapiens clone CDABP0025 mRNA sequence	13.9
427356	AW023482	Hs.97849	ESTs	13.9
448982	AI638164	Hs.225520	ESTs	13.9
432025	BE407132	Hs.111286	hypothetical protein FLJ22512	13.8
427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	13.8
402965			0	13.8
418601	AA279490	Hs.86368	calmegin	13.8
436954	AA740151	Hs.130425	ESTs	13.8
405024			0	13.8
453976	BE463830	Hs.163714	ESTs	13.8
431921	N46466	Hs.58879	ESTs	13.8
401735			0	13.8
445496	AB007860	Hs.12802	development and differentiation enhancing fac	13.8
425007	AA456483	Hs.172081	phosphodiesterase 4D, cAMP-specific (dunce (D	13.7
409463	AI458165	Hs.17296	ESTs	13.7
430193	AI826653	Hs.102928	Homo sapiens cDNA FLJ13479 fis, clone PLACE10	13.7
458869	AI637934	Hs.224978	ESTs	13.7
426769	AA075596	Hs.172153	glutathione peroxidase 3 (plasma)	13.7
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7

439901	N73885	Hs.124169	ESTs	13.7
431374	BE258532	Hs.251871	CTP synthase	13.7
432861	AA339526	Hs.279593	HSPC171 protein	13.7
441172	AI279652	Hs.132879	ESTs	13.7
410001	AB041036	Hs.57771	kallikrein 11; serine protease (TLSP)	13.7
430315	NM_004293	Hs.239147	guanine deaminase	13.6
422769	AA938905	Hs.289112	CGI-43 protein	13.6
402389			0	13.6
448977	X91809	Hs.22698	regulator of G-protein signalling 19	13.6
459648			gb:IL3-CT0220-150200-070-B02 CT0220 Homo sapi	13.6
452972	M31732	Hs.31210	B-cell CLL/lymphoma 3	13.6
431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	13.6
448585	AB020676	Hs.21543	KIAA0869 protein	13.6
428385	AF112213	Hs.184062	putative Rab5-interacting protein	13.6
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	13.6
447238	AW451676	Hs.158564	ESTs	13.6
437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HSI009	13.6
425749	AW328587	Hs.159448	surfeit 2	13.5
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	13.5
413753	U17760	Hs.301103	Laminin, beta 3 (nicein (125kD), kalinin (140	13.5
419034	NM_002110	Hs.89555	hemopoietic cell kinase	13.5
448361	H82028	Hs.238707	Homo sapiens cDNA: FLJ22457 fis, clone HRC099	13.5
412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein 1	13.5
419081	AI798863	Hs.87191	ESTs	13.5
407732	AW138839	Hs.24210	ESTs	13.5
423329	AF054910	Hs.127111	tektin 2 (testicular)	13.5
422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68k	13.4
439636	AF086467		gb:Homo sapiens full length insert cDNA clone	13.4
417605	AF006609	Hs.82294	regulator of G-protein signalling 3	13.4
445861	BE293423	Hs.11809	single Ig IL-1R-related molecule	13.4
447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	13.4
451807	W52854	Hs.27099	DKFZP564J0863 protein	13.4
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long f	13.4
422443	NM_014707	Hs.116753	histone deacetylase 7B	13.4
412504	Z44496	Hs.26039	Homo sapiens cDNA FLJ13937 fis, clone Y79AA10	13.4
453344	BE349075	Hs.44571	ESTs	13.4
402885			0	13.4
438712	AW978161	Hs.169877	ESTs	13.4
421774	AL050374	Hs.108169	DKFZP586C1619 protein	13.3
425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific protein 1	13.3
401897			0	13.3
425601	AW629485	Hs.293352	ESTs	13.3
450779	AW204145	Hs.156044	ESTs	13.3
444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	13.3
442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 protein x	13.3
434263	N34895	Hs.44648	ESTs	13.3
426059	BE292842	Hs.166120	interferon regulatory factor 7	13.3
407467	D55638		gb:Human B-cell PABL (pseudoautosomal boundar	13.3
412560	R24601	Hs.108300	CCR4-NOT transcription complex, subunit 3	13.2
442986	AI025990	Hs.285520	ESTs	13.2
420317	AB006628	Hs.96485	KIAA0290 protein	13.2
443211	AI128388	Hs.143655	ESTs	13.2
434361	AF129755	Hs.117772	ESTs	13.2
423493	AI815965	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homologou	13.2
414183	AW957446	Hs.301711	ESTs	13.2
447778	BE620592	Hs.71190	ESTs	13.2
435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box prot	13.1
439490	AW249197	Hs.100043	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	13.1
409606	AW444594	Hs.2387	transglutaminase 4 (prostate)	13.1
421308	AA687322	Hs.192843	ESTs	13.1
414950	C15407		gb:C15407 Clontech human aorta polyA+ mRNA (6	13.1
416783	AA206186	Hs.79889	monocyte to macrophage differentiation-associ	13.1
415927	AL120168	Hs.78919	Kell blood group precursor (McLeod phenotype)	13.1
422605	H16646	Hs.118666	Human clone 23759 mRNA, partial cds	13.0
430427	AA296701	Hs.241413	opticin	13.0
424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	13.0
421693	X71490	Hs.106876	ATPase, H+ transporting, lysosomal (vacuolar	13.0
407727	AW411148	Hs.38044	DKFZP564M082 protein	13.0
427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	13.0
406709	AI355761	Hs.242463	keratin 8	13.0
405353			0	13.0
453060	AW294092	Hs.21594	ESTs	13.0
459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	13.0
447843	AW337186	Hs.224891	ESTs	13.0
446576	AI659477	Hs.51820	ESTs, Moderately similar to ALU7_HUMAN ALU SU	13.0
449700	L02867	Hs.78358	ESTs	13.0
436476	AA326108	Hs.53631	ESTs	13.0
432532	AW058459	Hs.162246	ESTs	13.0
408405	AK001332	Hs.44672	hypothetical protein FLJ10470	13.0
432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40 co-ch	12.9
414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart, mitoc	12.9
447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase A1a	12.9
427923	AW274357	Hs.268384	Fzr1 protein	12.9
437395	AL365408	Hs.10632	hypothetical protein DKFZp762M136	12.9

441627	AA947552	Hs.58086	ESTs	12.9
419084	AA496539	Hs.179902	transporter-like protein	12.9
423067	AA321355	Hs.285401	ESTs	12.9
423070	R55677	Hs.155569	ESTs	12.8
441344	BE250144	Hs.41514	ESTs	12.8
423527	AI206965	Hs.105861	Homo sapiens cDNA FLJ13824 fis, clone THYRO10	12.8
417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	12.8
453552	AL041941	Hs.154729	3-phosphoinositide dependent protein kinase-1	12.8
453657	W23237	Hs.296162	ESTs	12.8
434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA	12.7
456051	T85626	Hs.76239	hypothetical protein FLJ20608	12.7
451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
418216	AA662240	Hs.283099	AF15q14 protein	12.7
423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-recog	12.7
424275	AW673173	Hs.144505	DKFZP566F0546 protein	12.7
440062	AI350518	Hs.129692	ESTs	12.7
444371	BE540274	Hs.239	Forkhead box M1	12.7
412520	AA442324	Hs.795	H2A histone family, member O	12.7
413349	BE086692		gb:QV1-BT0678-130400-156-g07 BT0678 Homo sapi	12.7
414500	W24087	Hs.76285	DKFZP564B167 protein	12.6
429261	AW176254	Hs.143475	ESTs	12.6
402238			0	12.6
400280			0	12.6
421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 pro	12.6
442029	AW956698	Hs.14456	neural precursor cell expressed, developmenta	12.6
435502	L13266	Hs.105	glutamate receptor, ionotropic, N-methyl D-as	12.6
409964	AW368226	Hs.67928	ESTs	12.6
418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	12.5
452117	AI421760	Hs.77870	Homo sapiens cDNA FLJ12750 fis, clone NT2RP20	12.5
448074	BE621355	Hs.27160	ESTs	12.5
442655	AW027457	Hs.30323	ESTs	12.5
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	12.5
400240			0	12.5
413048	M93221	Hs.75182	mannose receptor, C type 1	12.5
426215	AW963419	Hs.155223	ESTs	12.5
430024	AI808780	Hs.227730	integrin, alpha 6	12.5
445655	AA873830	Hs.167746	B cell linker protein	12.5
419941	X98654	Hs.93837	phosphatidylinositol transfer protein, membra	12.5
425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (soluble)	12.5
427767	AI879283	Hs.180714	cytochrome c oxidase subunit VIa polypeptide	12.4
450243	AW119084	Hs.201037	ESTs	12.4
408930	AA146721	Hs.49005	hypothetical protein	12.4
418783	T41368		gb:ph1d1_19/1TV Outward Alu-primed hncDNA lib	12.4
452096	BE394901	Hs.226785	ESTs	12.4
424513	BE385864	Hs.149894	mitochondrial translational initiation factor	12.4
422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	12.4
409031	AA376836	Hs.76728	ESTs	12.4
435515	N40080	Hs.6879	DC13 protein	12.4
429583	NM_006412	Hs.209119	1-acylglycerol-3-phosphate O-acyltransferase	12.3
449643	R05989	Hs.19603	ESTs	12.3
440313	AL050060	Hs.7158	DKFZP566H073 protein	12.3
425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	12.3
447357	AI375922	Hs.159367	ESTs	12.3
405089			0	12.3
414972	BE263782	Hs.77695	KIAA0008 gene product	12.3
435039	AW043921	Hs.130526	ESTs	12.3
447033	AI357412	Hs.157601	EST - not in UniGene	12.3
427521	AW973352	Hs.299056	ESTs	12.3
409377	AA300274	Hs.115659	Homo sapiens cDNA: FLJ23461 fis, clone HSI077	12.3
400116			0	12.3
445806	AL137516	Hs.13323	hypothetical protein FLJ22059	12.2
457817	AA247751	Hs.79572	cathepsin D (lysosomal aspartyl protease)	12.2
442410	AW996503	Hs.197680	ESTs	12.2
445404	AI261687	Hs.145541	ESTs, Weakly similar to JC4974 sodium iodide	12.2
403372	AW249152	Hs.44017	SIR2 (silent mating type information regulati	12.2
427082	AB037858	Hs.173484	hypothetical protein FLJ10337	12.2
433764	AW753676	Hs.39982	ESTs	12.2
400268			0	12.2
433190	M26901	Hs.3210	renin	12.2
444863	AW384082	Hs.301323	ESTs	12.2
434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, subfam	12.2
451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein (leu	12.2
430262	AA218780	Hs.237323	N-acetylglucosamine-phosphate mutase	12.2
421071	AI311238	Hs.104476	ESTs	12.2
426773	NM_015556	Hs.172180	KIAA0440 protein	12.1
409178	BE393948	Hs.50915	kallikrein 5	12.1
400250			0	12.1
428450	NM_014791	Hs.184339	KIAA0175 gene product	12.1
414531	T69387	Hs.76364	allograft inflammatory factor 1	12.1
448210	AW247775	Hs.7393	hypothetical protein from EUROIMAGE 1987170	12.1
440081	AA853389	Hs.135643	ESTs	12.1
413179	N99692	Hs.75227	NADH dehydrogenase (ubiquinone) 1 alpha subco	12.1
447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	12.1
400517	AF242388	Hs.149585	lengsin	12.1

401610			0	12.0
454381	AI935093	Hs.193428	ESTs	12.0
443997	AW081465	Hs.299644	ESTs	12.0
402944			0	12.0
430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizzarin	12.0
415099	AI492170	Hs.77917	ubiquitin carboxyl-terminal esterase L3 (ubiq	12.0
445422	AV653731	Hs.282829	ESTs	12.0
416667	AK000526	Hs.79457	hypothetical protein FLJ20519	12.0
442611	BE077155	Hs.177537	ESTs	12.0
443271	BE568568	Hs.195704	ESTs	12.0
415120	N64464	Hs.34950	ESTs	12.0
439574	AI469788	Hs.165190	ESTs	12.0
405804			0	12.0
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	12.0
414135	NM_004419	Hs.2128	dual specificity phosphatase 5	12.0
447075	AV662037	Hs.124740	ESTs	12.0
416841	N33878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	12.0
402943			0	11.9
416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypeptide A	11.9
439744	AL389994	Hs.301272	ESTs, Weakly similar to homologue of Drosphil	11.9
405762			0	11.9
406983	NM_000492	Hs.663	cystic fibrosis transmembrane conductance reg	11.9
455102	BE005496		gb:CM1-BN0117-110400-183-b09 BN0117 Homo sapi	11.9
402840			0	11.9
449183	AW445022	Hs.196985	Homo sapiens cDNA: FLJ21135 fis, clone CAS072	11.9
439273	AW139099	Hs.269701	ESTs	11.9
450484	BE220675		gb:hl98f11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	11.9
445431	AF137386	Hs.12701	plasmolipin	11.9
401888			0	11.9
426037	AW160780	Hs.166071	cyclin-dependent kinase 5	11.9
416742	R38644	Hs.248420	ESTs	11.9
418324	AW246273	Hs.84131	threonyl-tRNA synthetase	11.8
412870	N22788	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	11.8
432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	11.8
421478	AI683243	Hs.97258	ESTs	11.8
426635	BE395109	Hs.129327	ESTs	11.8
420523	AA262999	Hs.42788	ESTs	11.8
426227	U67058	Hs.168102	Human proteinase activated receptor-2 mRNA; 3	11.8
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	11.8
441816	AI401807	Hs.149997	ESTs	11.8
424596	AB020639	Hs.151017	estrogen-related receptor gamma	11.8
400640			0	11.8
448133	AA723157	Hs.73769	folate receptor 1 (adult)	11.8
401532			0	11.8
400161			0	11.8
442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (from c	11.7
451002	AA013299	Hs.8018	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	11.7
401879			0	11.7
415989	AI267700	Hs.111128	ESTs	11.7
416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	11.7
410616	AW873401	Hs.273599	ESTs	11.7
449239	T24653	Hs.23360	likely ortholog of yeast ARV1	11.7
447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (from cl	11.7
436877	AA931484	Hs.121255	ESTs, Weakly similar to cDNA EST EMBL:D67419	11.7
434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	11.7
448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	11.7
400279			0	11.6
440497	AA887266	Hs.144979	ESTs	11.6
451260	AW750773		gb:CM0-CN0044-260100-164-h03 CN0044 Homo sapi	11.6
429175	AI953040	Hs.127714	ESTs, Moderately similar to SOX30 protein [H.	11.6
408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule)	11.6
428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP066	11.6
420153	N22120	Hs.75277	hypothetical protein FLJ13910	11.6
428760	AI351459	Hs.192398	ESTs	11.6
421401	AW410478	Hs.104019	transforming, acidic coiled-coil containing p	11.6
404502			0	11.6
430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical protein	11.6
405192			0	11.6
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	11.6
401714			0	11.5
439335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen alpha	11.5
406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (isoform	11.5
401010			0	11.5
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	11.5
409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodiester	11.5
459684			gb:ao86a08.x1 Schiller meningioma Homo sapien	11.5
451051	BE254309	Hs.125262	DKFZP586G1624 protein	11.5
415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chronic	11.5
412153	R87934		gb:yo47b10.r1 Soares adult brain N2b4HB55Y Ho	11.5
427256	AL042436	Hs.97723	ESTs	11.5
406708	AI282759	Hs.242463	keratin 8	11.4
457644	AA770080	Hs.144962	ESTs, Moderately similar to I59365 ubiquitin	11.4
422848	Z25884	Hs.121483	chloride channel 1, skeletal muscle (Thomsen	11.4
424134	AF070637	Hs.140950	hypothetical protein	11.4

451931	AK000208	Hs.27267	Homo sapiens cDNA FLJ20201 fis, clone COLF121	11.4
400438	AF185611	Hs.115352	growth hormone 1	11.4
412994	D32257	Hs.75113	general transcription factor IIIA	11.4
408124	U89337	Hs.42853	cAMP responsive element binding protein-like	11.4
452249	BE394412	Hs.61252	ESTs	11.4
424627	AA344555		gb:EST50715 Gall bladder I Homo sapiens cDNA	11.4
405626			0	11.4
436690	AA373970	Hs.183096	ESTs	11.4
415862	R51034	Hs.144513	ESTs	11.4
406755	N80129	Hs.94360	metallothionein 1L	11.4
433657	AI244368	Hs.8124	PH domain containing protein in retina 1	11.4
429612	AF062649	Hs.252587	pituitary tumor-transforming 1	11.4
423334	AK000906	Hs.127273	hypothetical protein FLJ10044	11.4
433053	BE301909	Hs.279952	glutathione S-transferase subunit 13 homolog	11.4
428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen exch	11.3
442353	BE379594	Hs.49136	ESTs	11.3
447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
402077			0	11.3
409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypeptide 1	11.3
405145			0	11.3
428248	AI126772	Hs.40479	ESTs	11.3
425508	AA991551	Hs.97013	ESTs	11.3
428340	AF261088	Hs.154721	aconitase 1, soluble	11.3
431452	AI073641	Hs.152372	ESTs	11.3
446651	AA393907	Hs.97179	ESTs	11.3
443755	C18397	Hs.9730	tachykinin 3 (neuromedin K, neurokinin beta)	11.3
436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p	11.3
401020			0	11.3
456724	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	11.2
407227	H94949	Hs.171955	trophinin associated protein (tastin)	11.2
402066			0	11.2
442721	AI015892	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (from cl	11.2
401025			0	11.2
452423	AA991724	Hs.180535	Homo sapiens cDNA: FLJ22711 fis, clone HSI133	11.2
431685	AW296135	Hs.267659	vav 3 oncogene	11.2
425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-relate	11.2
409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130; oncos	11.2
456995	T89832	Hs.170278	ESTs	11.2
419223	X60111	Hs.1244	CD9 antigen (p24)	11.2
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	11.2
407604	AW191962	Hs.288061	actin, beta	11.2
437929	T09353	Hs.106642	ESTs, Weakly similar to hypothetical protein	11.1
415789	H01581		gb:yj33f08.r1 Soares placenta Nb2HP Homo sapi	11.1
424447	AL137376	Hs.147368	Homo sapiens mRNA; cDNA DKFZp434J0226 (from c	11.1
436034	AF282693	Hs.150185	inflammation-related G protein-coupled recept	11.1
404931			0	11.1
445979	AI695047	Hs.202395	ESTs	11.1
446733	AA863360	Hs.26040	ESTs; Highly similar to CYTOCHROME P45 IVA2	11.1
433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
445258	AI635931	Hs.147613	ESTs	11.1
417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	11.1
421041	N36914	Hs.14691	ESTs	11.1
425537	AB007913	Hs.158291	KIAA0444 protein	11.1
435763	AI243929	Hs.190419	ESTs	11.1
444790	AB030506	Hs.11955	B9 protein	11.1
453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.1
433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxyge	11.1
405358			0	11.1
435814	AW615179	Hs.152870	ESTs	11.0
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	11.0
446772	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clone HEMBA10	11.0
456694	AW016382	Hs.105642	Homo sapiens cDNA: FLJ23271 fis, clone HEP001	11.0
441128	AA570256	Hs.54628	ESTs	11.0
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	11.0
412576	AA447718	Hs.107057	ESTs	11.0
411122	F00809	Hs.143696	coactivator-associated arginine methyltransfe	11.0
427225	AA432391	Hs.258903	Homo sapiens mRNA for KIAA1640 protein, parti	11.0
426260	NM_002541	Hs.168669	oxoglutarate dehydrogenase (lipoamide)	11.0
444652	BE513613	Hs.11538	actin related protein 2/3 complex, subunit 1A	11.0
431947	AL359613	Hs.49933	hypothetical protein DKFZp762D1011	11.0
414432	BE378174	Hs.26506	Homo sapiens clone CDABP0005 mRNA sequence	11.0
458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [	10.9
409142	AL136877	Hs.50758	chromosome-associated polypeptide C	10.9
447627	AF090922	Hs.285902	CGI-113 protein	10.9
447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of 55 kD	10.9
454227	AW963897	Hs.44743	KIAA1435 protein	10.9
402927			0	10.9
422380	AA309881	Hs.136246	ESTs	10.9
455986	BE177736		gb:RC1-HT0598-140300-021-g06 HT0598 Homo sapi	10.9
410962	BE273749	Hs.752	FK506-binding protein 1A (12kD)	10.9
450361	BE327108	Hs.202512	ESTs	10.9
457484	H57645		gb:yr21e01.r1 Soares fetal liver spleen 1NFLS	10.9
407903	AI287341	Hs.154029	bHLH factor Hes4	10.9

403398			0	10.9
401405			0	10.9
405570			0	10.9
421240	R72730	Hs.29283	ESTs, Weakly similar to PLK_HUMAN PROTEOGLYCA	10.9
403649			0	10.9
447824	BE620800		gb:601483379T1 NIH_MGC_69 Homo sapiens cDNA c	10.9
450935	BE514743	Hs.25664	tumor suppressor deleted in oral cancer-relat	10.9
439853	AL119566	Hs.6721	lysophospholipase-like	10.9
451852	R51928		gb:yj71c05.r1 Soares breast 2NbHBst Homo sapi	10.9
431218	NM_002145	Hs.2733	homeo box B2	10.9
457794	AA689292	Hs.246850	ESTs	10.9
444374	AA009841	Hs.11039	Homo sapiens cDNA FLJ12798 fis, clone NT2RP20	10.9
456566	AW235317	Hs.259214	ESTs	10.8
405552			0	10.8
439436	BE140845	Hs.57868	ESTs	10.8
435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprotein	10.8
411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	10.8
415807	H03139	Hs.24683	ESTs	10.8
409430	R21945	Hs.166975	splicing factor, arginine/serine-rich 5	10.8
417033	H83784	Hs.40532	ESTs, Weakly similar to PEBP MOUSE PHOSPHATID	10.8
418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	10.8
404567			0	10.8
418384	AW149266	Hs.25130	ESTs	10.8
421971	U63127	Hs.110121	SEC7 homolog	10.8
428769	AW207175	Hs.106771	ESTs	10.8
459104	R19238	Hs.282057	ESTs	10.8
410896	AW809637		gb:MR4-ST0124-261099-015-b07 ST0124 Homo sapi	10.8
416969	AI815443	Hs.283404	organic cation transporter	10.8
408796	AA688292	Hs.118553	ESTs	10.8
426298	AW965058	Hs.111583	ESTs	10.8
421595	AB014520	Hs.105958	Homo sapiens cDNA: FLJ22735 fis, clone HUV001	10.8
408007	AW135965	Hs.246783	ESTs	10.8
400167			0	10.7
445243	AI217439	Hs.109854	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	10.7
421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	10.7
412241	AW948343		gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapi	10.7
425827	W28316		gb:45b6 Human retina cDNA randomly primed sub	10.7
420255	NM_007289	Hs.1298	membrane metallo-endopeptidase (neutral endop	10.7
430891	U22492	Hs.248118	G protein-coupled receptor 8	10.7
402883			0	10.7
423811	AW299598	Hs.50895	homeo box C4	10.7
447078	AW885727	Hs.301570	ESTs	10.7
414343	AL036166	Hs.75914	coated vesicle membrane protein	10.7
446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetraspan	10.7
452279	AA286844	Hs.61260	hypothetical protein FLJ13164	10.7
401220			0	10.7
459259	AJ003294		gb:AJ003294 Selected chromosome 21 cDNA libra	10.7
414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	10.7
448449	BE314567	Hs.211440	ESTs	10.7
429670	L01087	Hs.211593	protein kinase C, theta	10.7
446759	R61463	Hs.16165	expressed in activated T/LAK lymphocytes	10.7
400776			0	10.7
428093	AW594506	Hs.104830	ESTs	10.7
412801	AA121055		gb:zm22b01.r1 Stratagene pancreas (937208) Ho	10.6
440545	AW183201	Hs.190559	ESTs	10.6
434540	NM_016045	Hs.5184	TH1 drosophila homolog	10.6
414273	BE269057		gb:601184231F1 NIH_MGC_8 Homo sapiens cDNA cl	10.6
401817			0	10.6
410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-receptor ty	10.6
430590	AW383947	Hs.246381	CD68 antigen	10.6
426680	AA320160	Hs.171811	adenylate kinase 2	10.6
445413	AA151342	Hs.12677	CGI-147 protein	10.6
402947			0	10.6
457426	AW971119		gb:EST383206 MAGE resequences, MAGL Homo sapi	10.6
424148	BE242274	Hs.1741	integrin, beta 7	10.6
404944			0	10.6
405421			0	10.6
416772	AI733872	Hs.79769	protocadherin 1 (cadherin-like 1)	10.6
414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	10.6
457588	AI571225	Hs.284171	KIAA1535 protein	10.6
406038	Y14443	Hs.88219	zinc finger protein 200	10.6
404790			0	10.6
418922	AW956580	Hs.42699	Thrombospondin-1 (Hs.87409)	10.6
425940	AB023184	Hs.163990	KIAA0967 protein	10.6
448749	AW859679	Hs.21902	Homo sapiens clone 25237 mRNA sequence	10.6
418870	AF147204	Hs.89414	CXCR4; chemokine CXC receptor 4 (fusin)	10.5
417933	X02308	Hs.82962	thymidylate synthetase	10.5
450538	AW297396	Hs.227052	ESTs	10.5
427928	AA417662	Hs.119217	ESTs	10.5
432721	AL121478	Hs.3132	steroidogenic acute regulatory protein	10.5
429267	AA299290	Hs.246857	ESTs, Highly similar to S71100 protein kinase	10.5
439190	AW978693	Hs.293811	ESTs	10.5
408975	AW958693	Hs.49391	hypothetical protein LOC54149	10.5
415130	W85893	Hs.249867	ESTs	10.5

425738	H29630	Hs.159408	Homo sapiens clone 24420 mRNA sequence	10.5
440232	AI766925	Hs.112554	ESTs	10.5
425065	AA371906	Hs.294151	ESTs, Moderately similar to KIAA0544 protein	10.5
420829	AW665612	Hs.221969	ESTs	10.5
430466	AF052573	Hs.241517	polymerase (DNA directed), theta	10.5
407771	AL138272	Hs.62713	ESTs	10.5
444611	AK002180	Hs.11449	DKFZP564O123 protein	10.5
444665	BE613126	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	10.5
448030	N30714	Hs.20161	HDCME31P protein	10.5
438982	AW979101	Hs.291980	ESTs	10.5
446224	AW450551	Hs.13308	ESTs	10.5
405108			0	10.5
438233	W52448	Hs.56147	ESTs	10.5
401799			0	10.5
454038	X06374	Hs.37040	platelet-derived growth factor alpha polypept	10.5
414222	AL135173	Hs.878	sorbitol dehydrogenase	10.5
421828	AW891965	Hs.289109	dimethylarginine dimethylaminohydrolase 1	10.5
422626	AA344932	Hs.118786	metallothionein 2A	10.5
449261	AI637592	Hs.224958	ESTs	10.4
416218	R21499	Hs.23213	ESTs	10.4
457848	W26524	Hs.125682	ESTs; Weakly similar to D2092.2 [C.elegans]	10.4
442577	AA292998	Hs.163900	ESTs	10.4
406505	AF016272	Hs.115418	cadherin 16, KSP-cadherin	10.4
412258	AA376768	Hs.288977	Homo sapiens cDNA: FLJ22622 fis, clone HSI056	10.4
429224	AI905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	10.4
447774	BE018118	Hs.19554	chromosome 1 open reading frame 2	10.4
403914			0	10.4
406329			0	10.4
402423			0	10.4
431986	AA536130	Hs.149018	ESTs	10.4
423145	BE264548	Hs.222190	ESTs, Weakly similar to secretory carrier mem	10.4
414402	BE294186		gb:601172959F1 NIH_MGC_17 Homo sapiens cDNA c	10.4
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	10.4
426095	AI278023	Hs.89986	ESTs	10.4
434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone HRC109	10.4
442415	AI005101	Hs.129550	ESTs	10.3
421506	BE302796	Hs.105097	thymidine kinase 1, soluble	10.3
435084	D17516	Hs.301607	adenylate cyclase activating polypeptide 1 (p	10.3
431724	AA514535	Hs.283704	ESTs	10.3
456798	AJ006422	Hs.135183	centaurin-alpha	10.3
417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	10.3
422596	AF063611	Hs.118633	2'-5'oligoadenylate synthetase-like	10.3
435226	AI248938	Hs.270106	ESTs	10.3
433192	AB040880	Hs.225594	ESTs, Moderately similar to KIAA1447 protein	10.3
419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	10.3
416228	AW505190	Hs.79089	sema domain, immunoglobulin domain (Ig), tran	10.3
453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PLACE10	10.3
447906	AL050062	Hs.19999	DKFZP566K023 protein	10.3
401782	NM_012434	Hs.117865	solute carrier family 17 (anion/sugar transpo	10.3
453927	AA082465	Hs.301751	ESTs, Weakly similar to /prediction	10.3
450737	AW007152	Hs.203330	ESTs	10.3
421633	AF121860	Hs.106260	sorting nexin 10	10.3
409881	AF139799	Hs.202830	ESTs	10.3
432883	U48936	Hs.3112	sodium channel, nonvoltage-gated 1, gamma	10.3
440099	AL080058	Hs.6909	DKFZP564G202 protein	10.3
419024	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi polype	10.3
401835			0	10.3
408896	AI610447	Hs.48778	niban protein	10.3
443120	AW402677	Hs.290801	ESTs	10.3
400208			0	10.2
416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	10.2
400166			0	10.2
434642	W25739	Hs.135287	ESTs	10.2
424837	BE276113	Hs.153436	N-acetyltransferase, homolog of S. cerevisiae	10.2
435075	R51094	Hs.12400	ESTs	10.2
425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pleckst	10.2
435080	AI831760	Hs.155111	ESTs	10.2
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin-like	10.2
410020	T86315	Hs.728	ribonuclease, RNase A family, 2 (liver, eosin	10.2
411410	R20693	Hs.69954	laminin, gamma 3	10.2
450294	H42587	Hs.238730	ESTs	10.2
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PLACE10	10.2
414271	AK000275	Hs.75871	protein kinase C binding protein 1	10.2
400812			0	10.2
425843	BE313280	Hs.159627	death associated protein 3	10.2
449392	Z41698	Hs.26039	Homo sapiens cDNA FLJ13937 fis, clone Y79AA10	10.2
409089	NM_014781	Hs.50421	KIAA0203 gene product	10.2
401383			0	10.2
456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Drosoph	10.2
442912	AI088060	Hs.131450	ESTs	10.2
400954	D25969	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone LNG082	10.2
401029	BE382701	Hs.25960	v-myc avian myelocytomatosis viral related on	10.2
416602	NM_006159	Hs.79389	nel (chicken)-like 2	10.2
421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H.sapi	10.2

405094			0	10.2
450832	AW970602	Hs.105421	ESTs	10.2
440076	R32052	Hs.178617	ESTs, Weakly similar to AF151840 1 CGI-82 pro	10.2
447563	BE536115	Hs.160983	ESTs	10.2
421238	AB033101	Hs.102796	KIAA1275 protein	10.2
400882			0	10.2
415738	BE539367	Hs.295953	ESTs, Weakly similar to AF220049 1 uncharacte	10.1
445464	AW172389	Hs.249999	ESTs	10.1
459042	AW272058	Hs.210338	ESTs	10.1
414469	R51952	Hs.32587	steriod receptor RNA activator 1 (complexes w	10.1
434732	AI078443		gb:oz05g05.x1 Soares_fetal_liver_spleen_1NFLS	10.1
441030	AW204139	Hs.174424	ESTs, Weakly similar to p140mDia [M.musculus]	10.1
446855	BE616767	Hs.16269	B-cell CLL/lymphoma 7B	10.1
456785	AF151074	Hs.132744	hypothetical protein	10.1
404182			0	10.1
410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	10.1
430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, beta po	10.1
442152	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PLACE10	10.1
436354	AI879252	Hs.5151	Homo sapiens mRNA; cDNA DKFZp564C2163 (from c	10.1
426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	10.1
450599	AA460865	Hs.48516	ESTs	10.1
454393	BE153288		gb:PM0-HT0335-180400-008-c08 HT0335 Homo sapi	10.1
403383			0	10.1
415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	10.1
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.1
412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymphocyte	10.1
413808	J00287	Hs.182183	caldesmon 1	10.0
458572	AI223423	Hs.292794	ESTs	10.0
403295			0	10.0
403910			0	10.0
453400	AI991901	Hs.82590	ESTs, Moderately similar to ALU7_HUMAN ALU SU	10.0
406502			0	10.0
404743			0	10.0
412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo sapiens cDNA cl	10.0
402679			0	10.0
455864	BE148970		gb:CM0-HT0245-031199-085-h05 HT0245 Homo sapi	10.0
425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	10.0
419280	W07506	Hs.283725	Homo sapiens cDNA FLJ12627 fis, clone NT2RM40	10.0
443503	AV645438	Hs.282927	ESTs	10.0
423165	AI937547	Hs.124915	Human DNA sequence from clone 380A1 on chromo	10.0
450206	AI796450	Hs.201600	ESTs	10.0
459052	AA298812	Hs.98539	ESTs	10.0
456248	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5	10.0
428438	NM_001955	Hs.2271	Endothelin 1	10.0
456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	10.0
426127	L36983	Hs.167013	dynamin 2	10.0

TABLE 13B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410896	1226053_1	AW809637 AW809697 AW810554 AW809707 AW809885 AW810000 AW810088 AW809742 AW809816 AW809749 AW809639 AW809722 AW809836 AW809774 AW810023 AW810013 AW809813 AW809660 AW809728 AW809768 AW809951 AW809657 AW809954
412153	1279701_1	R87934 AW898205 AW896020 AW896035
412241	1284681_1	AW948343 AW948341 AW902855 AW984737
412517	130281_1	BE271584 AA112511
412801	132825_1	AA121055 AA330917
413349	1363558_1	BE086692 BE087077 BE087072
414273	1431911_1	BE269057 BE513434 BE396654
414402	1443240_1	BE294186 BE298975
414950	1509777_1	C15407 D81769 D61133
415789	1555357_1	H01581 H12850 R65905 H13053
416368	1591066_1	R88849 R84573 H50890
418464	1759038_-2	R87580
418783	1789791_1	T41368 T41369 T41294
424627	241724_1	AA344555 AA344312 AW963070
425827	256834_1	W28316 W26507 AA364334
434371	384839_1	AA631362 AA631438
434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570
434732	392447_1	AI078443 AA648102 AI765577 AW974381
439092	468554_1	AA830149 AW978407 M85983 AW503637
439636	47467_1	AF086467 W81444 W81445
447824	73861_-1	BE620800
450484	83645_1	BE220675 AA345621 AA009992
451260	863912_1	AW750773 AI768154
451852	888359_1	R51928 AI820698 R48360 AI820694
452101	898742_1	T60298 AI858257 T69667 T67634 T61224 T71537 T68933

454163	1048369_1	AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
454393	115888_1	BE153288 BE153151 BE152925 AA078302
455102	1253524_1	BE005496 BE005494 AW856324 AW900199
455864	1377038_1	BE148970 BE148975 BE148957 BE148937
455986	1397521_1	BE177736 BE177735 BE177734
456423	187241_1	AW748920 AA487506 AA248914 AA780494
457426	336189_1	AW971119 AA574265 AA513268
457484	342113_1	H57645 T19302 AA527038 Z24851 H93171
457705	389383_1	AW974668 AA661959 AA649572 AA640401 AA640402
459259	966269_1	AJ003294 AJ003315 AJ003293

TABLE 13C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400640	8117686	Plus	144324-144429
400666	8118496	Plus	17982-18115,20297-20456
400776	8131651	Plus	103576-103720
400812	8568711	Plus	71708-72153
400881	2842777	Minus	91446-91603,92123-92265
400882	2842777	Minus	110431-110708
400965	7770576	Minus	173043-173564
401010	8117391	Minus	83967-84180
401020	8117458	Minus	59085-60227
401025	8117518	Minus	179287-179483,181044-181166,181844-182039
401047	6705887	Minus	4804-5035,5133-5314
401131	8699812	Minus	94802-94987,95804-95887,96323-96487,97596-97826
401192	9719502	Minus	69559-70101
401220	9929324	Minus	48079-48279
401383	6721135	Minus	155543-157381
401405	7768126	Minus	69276-69452,69548-69958
401519	6649315	Plus	157315-157950
401532	7798785	Plus	124414-124950,125050-125418
401610	7705041	Minus	18921-19505
401714	6715702	Plus	96484-96681
401735	3252819	Plus	217235-217356,217621-217873
401799	7331447	Plus	147802-148251
401817	7417850	Minus	45888-46535
401835	7139700	Plus	142257-142742
401879	8099914	Minus	101064-102827
401888	8516069	Minus	189498-190514
401897	8569218	Plus	604-767
402066	6649269	Plus	135543-136031
402077	8117414	Plus	65014-65195
402104	8119072	Plus	122409-122600
402238	7690126	Plus	24726-24880,26791-27021
402287	4559317	Plus	40811-42447
402389	9885999	Minus	771-972,1571-1683
402408	9796239	Minus	110326-110491
402423	9796344	Minus	62487-62664
402424	9796344	Minus	64925-65073
402496	9797769	Minus	8615-9103
402520	7596899	Minus	171761-171996
402679	8113438	Plus	132079-132216
402840	9369121	Minus	57118-57306
402883	9926562	Plus	38666-38803,38885-39019,39097-39231,39308-39445
402885	9926751	Plus	71919-72049
402926	8217647	Minus	41261-41443
402927	8217647	Minus	47247-47396
402943	6456831	Plus	38467-39068
402944	9368423	Plus	110411-110716,111173-111640
402947	9368458	Minus	101629-101991
402965	9581599	Minus	46865-46941,47032-47148
403022	3132351	Plus	92097-92864
403121	9180223	Plus	4059-4258
403165	9838098	Minus	90595-91848
403295	8096528	Plus	22386-22708
403381	9438267	Minus	26009-26178
403383	9438267	Minus	119837-121197
403398	6862689	Minus	13685-14699
403399	6684178	Plus	61841-62145,62367-62756
403482	9966050	Plus	196964-197135
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
403649	8705159	Minus	27141-27247
403910	7710710	Minus	5761-6188
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
403914	7417588	Minus	7431-8472
404182	4775644	Plus	18163-18444
404502	7229863	Minus	56277-56819
404567	7249169	Minus	101320-101501

404678	9797204	Plus	115196-115448
404743	8894169	Minus	120556-120999
404780	9887810	Minus	175708-175871
404790	7230958	Plus	38611-38761
404931	7342203	Plus	44226-44382
404944	6899705	Plus	4256-4581
405024	7107727	Plus	88500-88697
405089	8072523	Plus	103182-103973
405094	8072579	Plus	135587-135758
405108	7107890	Minus	135020-135472
405145	9438278	Plus	37883-38052,38138-38332
405192	7230070	Plus	115629-116071
405224	6731245	Minus	14413-15979
405295	3818412	Plus	56933-57099
405353	2811095	Plus	118525-118892
405358	2341017	Minus	18016-18315
405421	7243869	Minus	97411-97687
405426	7243900	Minus	37640-37817
405452	7656638	Minus	93876-94275
405484	5922025	Plus	199214-199579,199672-199920,200262-200495
405552	1552506	Plus	45199-45647
405570	2808656	Plus	98208-98331
405626	4508116	Minus	89275-89384,92450-92629,97091-97279,98546-98666
405699	4165331	Plus	100727-100859
405762	5931935	Plus	160502-161110
405802	5924004	Minus	27743-28264
405804	7274891	Minus	122557-123551
406329	6982072	Minus	607903-608271
406429	9256476	Minus	83206-83365,94051-94193
406502	7711350	Minus	63430-63602

Table 14A lists about 695 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 14A: ABOUT 695 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
ratio: ratio of tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	70.4
438817	AI023799	Hs.163242	ESTs	62.8
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	57.8
421478	AI683243	Hs.97258	ESTs	45.7
415989	AI267700	Hs.111128	ESTs	42.7
418179	X51630	Hs.1145	Wilms tumor 1	36.0
449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone	34.0
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	30.5
428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-box c	30.1
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix protei	29.4
427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal chon	27.0
435094	AI560129	Hs.277523	EST	26.2
430691	C14187	Hs.103538	ESTs	26.2
430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clone EU	26.1
415511	AI732617	Hs.182362	ESTs	24.8
448243	AW369771	Hs.77496	ESTs	24.7
428187	AI687303	Hs.285529	ESTs	23.9
408081	AW451597	Hs.167409	ESTs	21.9
418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitial collagenase	20.6
400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic protein receptor; typ	20.6
422956	BE545072	Hs.122579	ESTs	20.0
413335	AI613318	Hs.48442	ESTs	19.9
423739	AA398155	Hs.97600	ESTs	18.9
410929	H47233	Hs.30643	ESTs	18.5
424086	AI351010	Hs.102267	lysyl oxidase	17.7
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase 2	17.4
427356	AW023482	Hs.97849	ESTs	17.4
407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB Homo sapien	17.1
407638	AJ404672	Hs.288693	EST	17.1
427469	AA403084	Hs.269347	ESTs	17.0
438993	AA828995		Integrin; beta 8	16.7
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.5
439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clone EU	16.5
421155	H87879	Hs.102267	lysyl oxidase	16.1
426635	BE395109	Hs.129327	ESTs	15.9
431989	AW972870	Hs.291069	ESTs	15.9
422805	AA436989	Hs.121017	H2A histone family; member A	15.9
444783	AK001468	Hs.62180	ESTs	15.8

424581	M62062	Hs.150917	catenin (cadherin-associated protein), alpha 2	15.7
453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMIL	15.7
459325	AW088369	Hs.282184	ESTs	15.6
428976	AL037824	Hs.194695	ras homolog gene family, member I	15.1
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-li	15.0
408660	AA525775	Hs.292523	ESTs	15.0
410247	AF181721	Hs.61345	RU2S	15.0
418738	AW388633	Hs.6682	solute carrier family 7, member 11	15.0
459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapiens cDNA, mR	14.8
413623	AA825721	Hs.246973	ESTs	14.8
439706	AW872527	Hs.59761	ESTs	14.7
409041	AB033025	Hs.50081	KIAA1199 protein	14.6
451110	AI955040	Hs.301584	ESTs	14.5
436775	AA731111	Hs.291891	ESTs	14.3
443211	AI128388	Hs.143655	ESTs	14.3
445258	AI635931	Hs.147613	ESTs	14.2
447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	14.2
428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	14.1
453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.9
447033	AI357412	Hs.157601	EST - not in UniGene	13.7
423811	AW299598	Hs.50895	homeo box C4	13.7
452461	N78223	Hs.108106	transcription factor	13.7
451106	BE382701	Hs.25960	N-myc	13.6
416208	AW291168	Hs.41295	ESTs	13.5
452249	BE394412	Hs.61252	ESTs	13.4
452055	AI377431	Hs.293772	ESTs	13.2
439243	AA593254	Hs.191349	ESTs	13.1
420149	AA255920	Hs.88095	ESTs	12.9
429125	AA446854	Hs.271004	ESTs	12.9
413597	AW302885	Hs.117183	ESTs	12.8
416566	NM_003914	Hs.79378	cyclin A1	12.8
442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clon	12.7
407710	AW022727	Hs.23616	ESTs	12.6
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.6
428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (7B2 p	12.4
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	12.3
447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serine/threonin	12.2
458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34) fusion g	12.2
408460	AA054726	Hs.285574	ESTs	12.2
424735	U31875	Hs.152677	short-chain alcohol dehydrogenase family member	12.0
415263	AA948033	Hs.130853	ESTs	11.9
400298	AA032279	Hs.61635	STEAP1	11.8
452096	BE394901	Hs.226785	ESTs	11.7
421451	AA291377	Hs.50831	ESTs	11.6
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-related pro	11.6
443715	AI583187	Hs.9700	cyclin E1	11.5
402606	#(NOCAT)			11.5
436954	AA740151	Hs.130425	ESTs	11.5
413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity gluta	11.5
410102	AW248508	Hs.279727	ESTs;	11.4
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, partial cd	11.4
452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from clon	11.4
442353	BE379594	Hs.49136	ESTs	11.3
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.2
453160	AI263307	Hs.146228	ESTs	11.2
426427	M86699	Hs.169840	TTK protein kinase	11.1
449433	AI672096	Hs.9012	ESTs	11.1
412723	AA648459	Hs.179912	ESTs	11.1
400250			0	11.1
419752	AA249573	Hs.152618	ESTs	11.1
438167	R28363	Hs.24286	ESTs	11.1
434539	AW748078	Hs.214410	ESTs	10.9
429918	AW873986	Hs.119383	ESTs	10.8
450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (mel	10.8
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	10.8
420900	AL045633	Hs.44269	ESTs	10.8
428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE2000132	10.8
446142	AI754693	Hs.145968	ESTs	10.7
421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid 17-alpha-	10.6
433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNTHETASE	10.6
418506	AA084248	Hs.85339	G protein-coupled receptor 39	10.5
433447	U29195	Hs.3281	neuronal pentraxin II	10.4
424188	AW954552	Hs.142634	zinc finger protein	10.4
414245	BE148072	Hs.75850	WAS protein family, member 1	10.3
426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	10.3
418601	AA279490	Hs.86368	calmegin	10.3
444170	AW613879	Hs.102408	ESTs	10.3
453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypeptide	10.3
407378	AA299264		gb:EST11752 Uterus Homo sapiens cDNA 5' end simila	10.2
440901	AA909358	Hs.128612	ESTs	10.2
407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	10.2
415227	AW821113	Hs.72402	ESTs	10.2
409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone OVARC1002165	10.1
450480	X82125	Hs.25040	zinc finger protein 239	10.1

419088	AI538323	Hs.77496	ESTs	10.0
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast hom	9.9
428253	AL133640	Hs.183357	Homo sapiens mRNA; cDNA DKFZp586C1021 (from clone	9.8
426471	M22440	Hs.170009	transforming growth factor, alpha	9.8
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransferase	9.7
452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolo	9.7
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	9.7
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	9.6
423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (from clon	9.6
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	9.6
407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation regu	9.6
438209	AL120659	Hs.6111	KIAA0307 gene product	9.5
429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding p	9.5
424945	AI221919	Hs.173438	hypothetical protein FLJ10582	9.5
414972	BE263782	Hs.77695	KIAA0008 gene product	9.4
439262	AA832333	Hs.124399	ESTs	9.4
403381	#(NOCAT)		0	9.3
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.3
435509	AI458679	Hs.181915	ESTs	9.3
445413	AA151342	Hs.12677	CGI-147 protein	9.2
414083	AL121282	Hs.257786	ESTs	9.2
421373	AA808229	Hs.167771	ESTs	9.2
430510	AW162916	Hs.241576	hypothetical protein PRO2577	9.1
446999	AA151520	Hs.279525	hypothetical protein PRO2605	9.1
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Homo sa	9.1
414569	AF109298	Hs.118258	Prostate cancer associated protein 1	9.1
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	9.0
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	9.0
408908	BE296227	Hs.48915	serine/threonine kinase 15	9.0
431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP3000685	9.0
433764	AW753676	Hs.39982	ESTs	9.0
434636	AA083764	Hs.241334	ESTs	8.9
451807	W52854	Hs.27099	DKFZP564J0863 protein	8.8
437872	AK002015	Hs.5887	RNA binding motif protein 7	8.8
443054	AI745185	Hs.8939	yes-associated protein 65 kDa	8.8
420092	AA814043	Hs.88045	ESTs	8.8
420159	AI572490	Hs.99785	ESTs	8.8
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	8.8
451254	AI571016	Hs.172967	ESTs	8.8
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-a	8.7
450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.elegans]	8.7
400301	X03635	Hs.1657	Estrogen receptor 1	8.7
408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransferase	8.7
434891	AA814309	Hs.123583	ESTs	8.7
436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Homo s	8.7
438885	AI886558	Hs.184987	ESTs	8.7
449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN ALU SUBFAM	8.7
447342	AI199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNI	8.6
434424	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone LNG05548	8.6
438078	AI016377	Hs.131693	ESTs	8.6
437212	AI765021	Hs.210775	ESTs	8.5
417728	AW138437	Hs.24790	KIAA1573 protein	8.5
438081	H49546	Hs.298964	ESTs	8.5
411571	AA122393	Hs.70811	hypothetical protein FLJ20516	8.4
435663	AI023707	Hs.134273	ESTs	8.4
424717	H03754	Hs.152213	wingless-type MMTV integration site family, member	8.4
425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase COOH	8.4
450505	NM_004572	Hs.25051	plakophilin 2	8.4
436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	8.3
436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HEMBA1001323	8.3
425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor type 14	8.3
438180	AA808189	Hs.272151	ESTs	8.2
447268	AI370413	Hs.36563	Homo sapiens cDNA: FLJ22418 fis, clone HRC08590	8.2
433159	AB035898	Hs.150587	kinesin-like protein 2	8.1
400195			0	8.1
424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untransla	8.1
438202	AW169287	Hs.22588	ESTs	8.1
438915	AA280174	Hs.23282	ESTs	8.1
448776	BE302464	Hs.30057	transporter similar to yeast MRS2	8.1
453884	AA355925	Hs.36232	KIAA0186 gene product	8.0
420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone receptor; t	8.0
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clone EU	8.0
453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	8.0
424001	W67883	Hs.137476	KIAA1051 protein	8.0
434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo sapiens c	8.0
417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransferase, phosp	7.9
438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo sapiens c	7.9
415245	N59650	Hs.27252	ESTs	7.9
422352	AA766296	Hs.99200	ESTs	7.9
425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	7.8
442655	AW027457	Hs.30323	ESTs	7.8
445657	AW612141	Hs.279575	ESTs	7.8
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.8
426320	W47595	Hs.169300	transforming growth factor, beta 2	7.8

414142	AW368397	Hs.150042	ESTs	7.7
412170	D16532	Hs.73729	very low density lipoprotein receptor	7.6
410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	7.6
436476	AA326108	Hs.53631	ESTs	7.6
414132	AI801235	Hs.48480	ESTs	7.6
437789	AI581344	Hs.127812	ESTs, Weakly similar to AF141326 1 RNA helicase HD	7.6
450192	AA263143	Hs.24596	RAD51-interacting protein	7.6
449328	AI962493	Hs.197647	ESTs	7.5
440238	AW451970	Hs.155644	paired box gene 2	7.5
403657	#(NOCAT)		0	7.5
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	7.5
418735	N48769	Hs.44609	ESTs	7.5
413627	BE182082	Hs.246973	ESTs	7.4
446293	AI420213	Hs.149722	ESTs	7.4
441627	AA947552	Hs.58086	ESTs	7.4
425465	L18964	Hs.1904	protein kinase C, iota	7.3
409242	AL080170	Hs.51692	DKFZP434C091 protein	7.3
450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	7.3
440250	AA876179	Hs.134650	ESTs	7.3
451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	7.3
458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Cells (LCB:a	7.3
436032	AA150797	Hs.109276	latexin protein	7.2
407771	AL138272	Hs.62713	ESTs	7.2
435039	AW043921	Hs.130526	ESTs	7.2
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glycoprote	7.2
407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fis, clone NT2RP3004451	7.2
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma cells	7.2
404253	#(NOCAT)		0	7.1
424120	T80579	Hs.290270	ESTs	7.1
429126	AW172356	Hs.99083	ESTs	7.1
413573	AI733859	Hs.149089	ESTs	7.1
421464	AA291553	Hs.190086	ESTs	7.0
430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 20kD	7.0
437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprotein [M.mus	7.0
420362	U79734	Hs.97206	huntingtin interacting protein 1	7.0
444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiety X)-typ	7.0
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	6.9
410568	AW162948	Hs.64542	pre-mRNA cleavage factor Im (68kD)	6.9
429418	AI381028	Hs.99283	ESTs	6.9
409178	BE393948	Hs.50915	kallikrein 5	6.9
446608	N75217	Hs.257846	ESTs	6.9
425905	AB032959	Hs.161700	KIAA1133 protein	6.9
428532	AF157326	Hs.184786	TBP-interacting protein	6.9
433426	H69125	Hs.133525	ESTs	6.9
431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo sapiens	6.8
437960	AI669586	Hs.222194	ESTs	6.8
423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif, Y is	6.8
424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	6.8
448674	W31178	Hs.154140	ESTs	6.8
438122	AI620270	Hs.129837	ESTs	6.8
440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.sapien	6.7
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanoma, p1	6.7
407162	N63855	Hs.142634	zinc finger protein	6.7
410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxia 3,	6.7
424639	AI917494	Hs.131329	ESTs	6.7
432415	T16971	Hs.289014	ESTs	6.7
421470	R27496	Hs.1378	annexin A3	6.7
445459	AI478629	Hs.158465	ESTs	6.7
418203	X54942	Hs.83758	CDC28 protein kinase 2	6.6
432809	AA565509	Hs.131703	ESTs	6.6
409234	AI879419	Hs.27206	ESTs	6.6
438394	BE379623	Hs.27693	CGI-124 protein	6.6
452097	AB002364	Hs.27916	ADAM-TS3 ; a disintegrin-like and metalloproteas	6.6
453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	6.6
414136	AA812434	Hs.178227	ESTs	6.6
423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.6
454018	AW016892	Hs.241652	ESTs	6.6
452281	T93500	Hs.28792	ESTs	6.5
424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	6.5
452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transporter), me	6.5
434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subunit [H.sap	6.5
425776	U25128	Hs.159499	parathyroid hormone receptor 2	6.4
418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	6.4
409517	X90780	Hs.54668	troponin I, cardiac	6.4
432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein product [H	6.4
448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDN	6.4
413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone HEP05790	6.4
419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (from clone	6.4
424153	AA451737	Hs.141496	MAGE-like 2	6.4
434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone LNG07061	6.4
435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone THYRO1000187	6.4
441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H.sapi	6.4
443539	AI076182	Hs.134074	ESTs	6.4

443830	AI142095	Hs.143273	ESTs	6.4
452606	N45202	Hs.90012	Homo sapiens cDNA: FLJ23441 fis, clone HSI00612	6.4
418384	AW149266	Hs.25130	ESTs	6.3
425371	D49441	Hs.155981	mesothelin	6.3
429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), prostate	6.3
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced gene	6.3
437117	AL049256	Hs.122593	ESTs	6.3
449579	AW207260	Hs.134014	prostate cancer associated protein 6	6.3
453370	AI470523	Hs.182356	ESTs, Moderately similar to translation initiation	6.3
426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1	6.3
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	6.3
408155	AB014528	Hs.43133	KIAA0628 gene product	6.2
452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (from clone	6.2
439138	AI742605	Hs.193696	ESTs	6.2
457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.2
436281	AW411194	Hs.120051	ESTs	6.1
407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	6.1
406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferase	6.1
430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PLACE1008369	6.1
428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (from clone	6.1
415139	AW975942	Hs.48524	ESTs	6.1
417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family A, member	6.1
433527	AW235613	Hs.133020	ESTs	6.1
449448	D60730	Hs.57471	ESTs	6.1
457733	AW974812	Hs.291971	ESTs	6.1
457979	AA776655	Hs.270942	ESTs	6.1
422867	L32137	Hs.1584	cartilage oligomeric matrix protein	6.0
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1	6.0
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate), membe	6.0
412733	AA984472	Hs.74554	KIAA0080 protein	6.0
422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	6.0
449347	AV649748	Hs.295901	ESTs	6.0
440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO1000085	6.0
437478	AL390172	Hs.118811	ESTs	6.0
411598	BE336654	Hs.70937	H3 histone family, member K	6.0
418134	AA397769	Hs.86617	ESTs	6.0
418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	6.0
452039	AI922988	Hs.172510	ESTs	6.0
410555	U92649	Hs.64311	a disintegrin and metalloproteinase domain 17 (tum	5.9
412719	AW016610	Hs.129911	ESTs	5.9
410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PLACE1009150	5.9
437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN LAMININ ALPH	5.9
453431	AF094754	Hs.32973	glycine receptor, beta	5.9
408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2	5.9
417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	5.9
420440	NM_002407	Hs.97644	mammaglobin 2	5.9
430291	AV660345	Hs.238126	CGI-49 protein	5.9
405547	#(NOCAT)		0	5.9
427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypeptide	5.9
435793	AB037734	Hs.4993	ESTs	5.8
427975	AI536065	Hs.122460	ESTs	5.8
428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 [H.sapie	5.8
452693	T79153	Hs.48589	zinc finger protein 228	5.8
440138	AB033023	Hs.6982	hypothetical protein FLJ10201	5.8
421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 protein	5.8
445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	5.8
448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT2RP3003264	5.8
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.7
419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP2004081	5.7
420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapiens	5.7
431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone ADKA01954	5.7
446868	AV660737	Hs.135100	ESTs	5.7
452971	AI873878	Hs.91789	ESTs	5.7
428927	AA441837	Hs.90250	ESTs	5.7
425282	AW163518	Hs.155485	huntingtin interacting protein 2	5.7
419247	S65791	Hs.89764	fragile X mental retardation 1	5.7
445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	5.7
422938	NM_001809	Hs.1594	centromere protein A (17kD)	5.6
447078	AW885727	Hs.301570	ESTs	5.6
421247	BE391727	Hs.102910	general transcription factor IIH, polypeptide 4 (5	5.6
407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophila homolog	5.6
436556	AI364997	Hs.7572	ESTs	5.6
417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncogene	5.6
429826	N93266	Hs.40747	ESTs	5.6
432030	AI908400	Hs.143789	ESTs	5.6
443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.5
453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	5.5
411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.5
419558	AW953679	Hs.278394	ESTs	5.5
427386	AW836261	Hs.177486	amyloid beta (A4) precursor protein (protease nexi	5.5
427961	AW293165	Hs.143134	ESTs	5.5
404561	#(NOCAT)		0	5.5
429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1, yea	5.5
407216	N91773	Hs.102267	lysyl oxidase	5.5

410658	AW105231	Hs.192035	ESTs	5.5
413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	5.5
414315	Z24878		gb:HSB65D052 STRATAGENE Human skeletal muscle cD	5.5
427878	C05766	Hs.181022	CGI-07 protein	5.5
431041	AA490967	Hs.105276	ESTs	5.5
441645	AI222279	Hs.201555	ESTs	5.5
428071	AF212848	Hs.182339	transcription factor ESE-3B	5.4
436406	AW105723	Hs.125346	ESTs	5.4
429181	AW979104	Hs.294009	ESTs	5.4
410909	AW898161	Hs.53112	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	5.4
424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP2000814	5.4
451996	AW514021	Hs.245510	ESTs	5.4
449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanogaster]	5.4
441433	AA933809	Hs.42746	ESTs	5.4
445495	BE622641	Hs.38489	ESTs	5.4
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM4002571	5.4
442611	BE077155	Hs.177537	ESTs	5.4
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein 6	5.4
453161	AA628608	Hs.61656	ESTs	5.4
419948	AB041035	Hs.93847	NADPH oxidase 4	5.3
427718	AI798680	Hs.25933	ESTs	5.3
453867	AI929383	Hs.108196	HSPC037 protein	5.3
422634	NM_016010	Hs.118821	CGI-62 protein	5.3
444478	W07318	Hs.240	M-phase phosphoprotein 1	5.3
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapiens cDNA c	5.3
443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.3
451177	AI969716	Hs.13034	ESTs	5.3
408298	AI745325	Hs.271923	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB2	5.3
435867	AA954229	Hs.114052	ESTs	5.3
423698	AA329796	Hs.1098	DKFZp434J1813 protein	5.3
448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone	5.3
427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE06654	5.3
430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.3
433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFA	5.3
449532	W74653	Hs.271593	ESTs	5.3
452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone HSI05658	5.3
437641	AA811452	Hs.291911	ESTs	5.2
418379	AA218940	Hs.137516	fidgetin-like 1	5.2
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.2
433589	AA886530	Hs.188912	ESTs	5.2
409143	AW025980	Hs.138965	ESTs	5.2
410303	AA324597	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321	5.2
413384	NM_000401	Hs.75334	exostoses (multiple) 2	5.2
424698	AA164366	Hs.151973	hypothetical protein FLJ10378	5.2
431229	AA496479		gb:zv37h05.r1 Soares ovary tumor NbHOT Homo sapien	5.2
433377	AI752713	Hs.43845	ESTs	5.2
445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.2
406367	#(NOCAT)		0	5.2
442500	AI819068	Hs.209122	ESTs	5.2
450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	5.2
419140	AI982647	Hs.215725	ESTs	5.2
411078	AI222020	Hs.182364	ESTs, Weakly similar to 25 kDa trypsin inhibitor [	5.2
423020	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
427061	AB032971	Hs.173392	KIAA1145 protein	5.2
439042	AW979172		gb:EST391282 MAGE resequences, MAGP Homo sapiens c	5.2
452930	AW195285	Hs.194097	ESTs	5.2
417791	AW965339	Hs.111471	ESTs	5.1
433277	W27268	Hs.151010	ESTs	5.1
447835	AW591623	Hs.164129	ESTs	5.1
434401	AI864131	Hs.71119	Putative prostate cancer tumor suppressor	5.1
437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (from clone D	5.1
418849	AW474547	Hs.53565	ESTs, Weakly similar to B0491.1 [C.elegans]	5.1
428093	AW594506	Hs.104830	ESTs	5.1
408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; fetal brain (	5.1
453096	AW294631	Hs.11325	ESTs	5.1
418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.1
436787	AA908554	Hs.192756	ESTs	5.1
446577	AB040933	Hs.15420	KIAA1500 protein	5.1
437267	AW511443	Hs.258110	ESTs	5.0
419423	D26488	Hs.90315	KIAA0007 protein	5.0
404939			0	5.0
439052	AF085917	Hs.37921	ESTs	5.0
447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.0
453878	AW964440	Hs.19025	ESTs	5.0
410824	AW994813	Hs.33264	ESTs	5.0
427701	AA411101	Hs.221750	ESTs	5.0
424602	AK002055	Hs.301129	Homo sapiens clone 23859 mRNA sequence	5.0
430044	AA464510	Hs.152812	EST cluster (not in UniGene)	5.0
417423	AA197341	Hs.111164	ESTs	5.0
421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.0
433384	AI021992	Hs.124244	ESTs	5.0
434160	BE551196	Hs.114275	ESTs	5.0
443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMAN GLUCOSAM	5.0
416198	H27332	Hs.99598	ESTs	4.9

424539	L02911	Hs.150402	activin A receptor, type I	4.9
436645	AW023424	Hs.156520	ESTs	4.9
417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevisiae]	4.9
447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.9
416565	AW000960	Hs.44970	ESTs	4.9
425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.9
435420	AI928513	Hs.59203	ESTs	4.9
435532	AW291488	Hs.117305	ESTs	4.9
443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.9
446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone HEP03830	4.9
452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapiens]	4.9
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type; fou	4.9
408938	AA059013	Hs.22607	ESTs	4.9
432842	AW674093	Hs.279525	hypothetical protein PRO2605	4.9
436754	AI061288	Hs.133437	ESTs, Moderately similar to gonadotropin inducible	4.9
442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosolic, U215	4.9
409049	AI423132	Hs.146343	ESTs	4.9
422475	AL359938	Hs.117313	Meis (mouse) homolog 3	4.9
447112	H17800	Hs.7154	ESTs	4.9
458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [H.sap	4.8
431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase,	4.8
410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR AT	4.8
429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	4.8
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP), mem	4.8
422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed cell death 9;	4.8
425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.8
428555	NM_002214	Hs.184908	integrin, beta 8	4.8
452909	NM_015368	Hs.30985	pannexin 1	4.8
449535	W15267	Hs.23672	low density lipoprotein receptor-related protein 6	4.8
452232	AW020603	Hs.271698	ESTs	4.8
409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.8
415115	AA214228	Hs.127751	hypothetical protein	4.7
423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from clon	4.7
441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200	4.7
423575	C18863	Hs.163443	ESTs	4.7
415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN SP1	4.7
418804	AA809632		gb:nz17h04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clo	4.7
428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha polypeptide	4.7
432865	AI753709	Hs.152484	ESTs	4.7
433330	AW207084	Hs.132816	ESTs	4.7
453047	AW023798	Hs.286025	ESTs	4.7
421308	AA687322	Hs.192843	ESTs	4.7
456273	AF154846	Hs.1148	zinc finger protein	4.7
443933	AI091631	Hs.135501	Homo sapiens two pore potassium channel KT3.3	4.7
434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-REPAIR PRO	4.7
440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	4.7
426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.7
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	4.7
446102	AW168067	Hs.252956	ESTs	4.7
420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA helicase	4.7
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	4.7
429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence	4.7
433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HEMBA1004610	4.7
434988	AI418055	Hs.161160	ESTs	4.6
452571	W31518	Hs.34665	ESTs	4.6
434361	AF129755	Hs.117772	ESTs	4.6
406400	#(NOCAT)		0	4.6
410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.6
419945	AW290975	Hs.118923	ESTs	4.6
428301	AW628666	Hs.98440	ESTs	4.6
430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo sapiens c	4.6
431349	AA503653	Hs.156942	ESTs, Moderately similar to ALU2_HUMAN ALU SUBFA	4.6
446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone NT2RP2003137	4.6
447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from clone	4.6
448027	AI458437	Hs.177224	ESTs	4.6
449611	AI970394	Hs.197075	ESTs	4.6
459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT2RP4000035	4.6
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.6
409387	AW384900	Hs.123526	ESTs	4.6
424078	AB006625	Hs.139033	paternally expressed gene 3	4.6
435244	N77221	Hs.187824	ESTs	4.6
404996	#(NOCAT)		0	4.6
407905	AW103655	Hs.252905	ESTs	4.6
411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo sapiens c	4.6
424341	AA385074		gb:EST98673 Thyroid Homo sapiens cDNA 5' end simil	4.6
441675	AI914329	Hs.5461	ESTs	4.6
452172	H00797	Hs.133207	Homo sapiens mRNA for KIAA1230 protein, partial cd	4.6
420276	AA290938	Hs.190561	ESTs, Highly similar to mosaic protein LR11 [H.sap	4.5
402820	#(NOCAT)		0	4.5
419699	AA248998	Hs.31246	ESTs	4.5
422529	AW015128	Hs.256703	ESTs	4.5
438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.5
441826	AW503603	Hs.129915	phosphotriesterase related	4.5
453931	AL121278	Hs.25144	ESTs	4.5

435538	AB011540	Hs.4930	low density lipoprotein receptor-related protein 4	4.5
457465	AW301344	Hs.195969	ESTs	4.5
418848	AI820961	Hs.193465	ESTs	4.5
408321	AW405882	Hs.44205	cortistatin	4.5
447499	AW262580	Hs.147674	KIAA1621 protein	4.5
424513	BE385864	Hs.149894	mitochondrial translational initiation factor 2	4.5
432731	R31178	Hs.287820	fibronectin 1	4.5
448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1 (homolog	4.5
430371	D87466	Hs.240112	KIAA0276 protein	4.5
448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG07690	4.5
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA100042	4.4
448141	AI471598	Hs.197531	ESTs	4.4
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304	4.4
417718	T86540	Hs.193981	ESTs	4.4
436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.4
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. cerevisia	4.4
409092	AI735283	Hs.172608	ESTs	4.4
416241	N52639	Hs.32683	ESTs	4.4
432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYMER	4.4
440234	AW117264	Hs.126252	ESTs	4.4
448743	AB032962	Hs.21896	KIAA1136 protein	4.4
451389	N73222	Hs.21738	KIAA1008 protein	4.4
453331	AI240665	Hs.8895	ESTs	4.4
454036	AA374756	Hs.93560	ESTs, Weakly similar to unnamed protein product (H	4.4
448133	AA723157	Hs.73769	folate receptor 1 (adult)	4.4
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9 (melt	4.4
453279	AW893940	Hs.59698	ESTs	4.4
409459	D86407	Hs.54481	low density lipoprotein receptor-related protein 8	4.4
431708	AI698136	Hs.108873	ESTs	4.4
433906	AI167816	Hs.43355	ESTs	4.4
437958	BE139550	Hs.121668	ESTs	4.4
441423	AI793299	Hs.126877	ESTs	4.4
429876	AB028977	Hs.225974	KIAA1054 protein	4.3
446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasmolipin (H.	4.3
412078	X69699	Hs.73149	paired box gene 8	4.3
422093	AF151852	Hs.111449	CGI-94 protein	4.3
423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selenium	4.3
448390	AL035414	Hs.21068	hypothetical protein	4.3
453628	AW243307	Hs.170187	ESTs	4.3
449722	BE280074	Hs.23960	cyclin B1	4.3
436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein product (H	4.3
431592	R69016	Hs.293871	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.3
432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone COL07137	4.3
419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.3
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.3
401644	#(NOCAT)		0	4.3
410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine heptad	4.3
413775	AW409934	Hs.75528	nucleolar GTPase	4.3
424296	AI631874	Hs.169391	ESTs	4.3
431118	BE264901	Hs.250502	carbonic anhydrase VIII	4.3
432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protease (ECHOS1) (TADG-1	4.3
451073	AI758905	Hs.206063	ESTs	4.3
451592	AI805416	Hs.213897	ESTs	4.3
452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapiens cDNA, m	4.3
441020	W79283	Hs.35962	ESTs	4.2
439024	R96696	Hs.35598	ESTs	4.2
453619	H87648	Hs.33922	H.sapiens novel gene from PAC 117P20, chromosome 1	4.2
453459	BE047032	Hs.257789	ESTs	4.2
408427	AW194270	Hs.177236	ESTs	4.2
419311	AA689591		gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clo	4.2
426460	D79721	Hs.183702	Homo sapiens cDNA FLJ11752 fis, clone HEMBA1005582	4.2
444540	AI693927	Hs.265165	ESTs	4.2
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	4.2
453913	AW004683	Hs.233502	ESTs	4.2
417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC05262	4.2
428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP06638	4.2
428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sapiens cDNA	4.2
441006	AW605267	Hs.7627	CGI-60 protein	4.2
436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein produc	4.2
446936	H10207	Hs.47314	ESTs	4.2
406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from clone	4.2
428819	AL135623	Hs.193914	KIAA0575 gene product	4.2
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor recep	4.2
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	4.2
417048	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	4.2
431750	AA514986	Hs.283705	ESTs	4.2
439314	AA382413	Hs.178144	ESTs	4.2
448582	AI538880	Hs.94812	ESTs	4.2
449554	AA682382	Hs.59982	ESTs	4.2
455700	BE068115		gb:CM1-BT0368-061299-060-g07 BT0368 Homo sapiens c	4.2
409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG Homo sapie	4.1
433929	AI375499	Hs.27379	ESTs	4.1
415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.1
444381	BE387335	Hs.283713	ESTs	4.1

451024	AA442176		gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_9w Homo sa	4.1
415539	AI733881	Hs.72472	BMPR-Ib; bone morphogenetic protein receptor; typ	4.1
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long form	4.1
420736	AI263022	Hs.82204	ESTs	4.1
453293	AA382267	Hs.10653	ESTs	4.1
409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	4.1
418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo sapiens	4.1
429628	H09604	Hs.13268	ESTs	4.1
439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone HSI15685	4.1
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCYPHOSIN	4.1
443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal short-c	4.1
448816	AB033052	Hs.22151	KIAA1226 protein	4.1
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.1
443171	BE281128	Hs.9030	TONDU	4.1
425322	U63630	Hs.155637	protein kinase; DNA-activated; catalytic polypepti	4.1
442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	4.1
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)	4.1
417300	AI765227	Hs.55610	solute carrier family 30 (zinc transporter), membe	4.1
417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2)	4.1
448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	4.1
419131	AA406293	Hs.301622	ESTs	4.1
406348	#(NOCAT)		0	4.1
419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP4000515	4.1
419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitochondria	4.1
420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from clone	4.1
421039	NM_003478	Hs.101299	cullin 5	4.1
426890	AA393167	Hs.41294	ESTs	4.1
428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease, autosomal	4.1
452834	AI638627	Hs.105685	ESTs	4.1
428771	AB028992	Hs.193143	KIAA1069 protein	4.0
437949	U78519	Hs.41654	ESTs	4.0
450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448	4.0
424081	NM_006413	Hs.139120	ribonuclease P (30kD)	4.0
418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	4.0
447204	AI366881	Hs.157897	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU CL	4.0
407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane protein 3	4.0
412314	AA825247	Hs.250899	heat shock factor binding protein 1	4.0
436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulating cytokin	4.0
450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.0
426991	AK001536	Hs.285803	Homo sapiens cDNA FLJ12852 fis, clone NT2RP2003445	4.0
409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	4.0
410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapiens c	4.0
413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.0
413425	F20956		gb:HSPD05390 HM3 Homo sapiens cDNA clone 032-X4-1	4.0
417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein [H.sapien	4.0
424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated factor,	4.0
425024	R39235	Hs.12407	ESTs	4.0
445941	AI267371	Hs.172636	ESTs	4.0
448595	AB014544	Hs.21572	KIAA0644 gene product	4.0
453448	AL036710	Hs.209527	ESTs	4.0
458944	N93227	Hs.98403	ESTs	4.0
400284			Estrogen receptor 1	4.0
441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	4.0
408796	AA688292	Hs.118553	ESTs	4.0
408296	AL117452	Hs.44155	DKFZP586G1517 protein	4.0
438913	AI380429	Hs.172445	ESTs	4.0
402408			0	4.0
411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.0
450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MAMMA100174	4.0
439780	AL109688		gb:Homo sapiens mRNA full length insert cDNA clone	4.0
418301	AW976201	Hs.187618	ESTs	4.0
420077	AW512260	Hs.87767	ESTs	4.0
426572	AB037783	Hs.170623	hypothetical protein FLJ11183	4.0
403721			0	4.0
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene homolo	4.0
408684	R61377	Hs.12727	hypothetical protein FLJ21610	4.0
414869	AA157291	Hs.72163	ESTs	4.0
437980	R50393	Hs.278436	KIAA1474 protein	4.0
451050	AW937420	Hs.69662	ESTs	4.0

TABLE 14B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409073	109851_1	AA063458 AA063018 AI444822
410784	1221005_1	AW803201 BE079700 BE062940
411560	1249443_1	AW851186 AW996967 BE143456
413425	136885_1	F20956 AA129374 AA133740 AW819878
414315	143512_1	Z24878 AA494098 F13654 AA494040 AA143127
418378	174656_1	AW962081 AA218925 AA354237
418804	179138_1	AA809632 AI917245 AI701732 AA228406
419311	183793_1	AA689591 AW974261 AA236240 AI077451 AA631399 AW974262

420637	195241_1	AW976153 AA278945 AA747691
424341	238294_1	AA385074 AA339054 AA339115 AW956359
428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
428679	294049_1	AA431765 AA432015
429163	300543_1	AA884766 AW974271 AA592975 AA447312
430153	313709_1	AW968128 AA468102 AA468165
431229	330060_1	AA496479 T89859 AW020056 AW135251 AI221100 AA628705 AI263148 T79074
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
434415	385931_1	BE177494 AW276909 AA632849
436812	427323_1	AW298067 AA731645 AA810101 AW194180 AI690673 AW978773
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438966	467436_1	AW979074 AA834841 AA828650
438993	467651_1	AA828995 AA834879 AI926361
439042	468079_1	AW979172 AA829595 R96050
439780	47673_1	AL109688 R23665 R26578
442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
449034	794817_1	AI624049 AW117770 AI858360
451024	85565_1	AA442176 AA259181
452453	918300_1	AI902519 AI902518 AI902516
455700	1351264_1	BE068115 BE068104 BE068102 BE068096 BE068103 BE068154 BE068198
458861	798085_1	AI630223 AI630470

TABLE 14C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
401644	8576138	Plus	82655-83959
402408	9796239	Minus	110326-110491
402606	9909429	Minus	81747-82094
402820	6456853	Minus	82274-82443
403381	9438267	Minus	26009-26178
403657	8843996	Minus	156223-156370
403721	7528046	Minus	156647-157368
404253	9367202	Minus	55675-56055
404561	9795980	Minus	69039-70100
404939	6862697	Plus	175318-175476
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405547	1054740	Plus	124361-124520,124914-125050
406348	9255985	Minus	71754-71944
406367	9256126	Minus	58313-58489
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 15A lists about 499 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 14A, except that the ratio was greater than or equal to 3.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., ig, fn3, egf, 7tm domains). Predicted protein domains are noted.

TABLE 15A: ABOUT 499 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
UG ID: UniGene ID
Title: UniGene title
Prot. Dom.: Predicted protein structural domains
ratio: ration tumor vs normal tissues

Pkey	Ex. Accn	UG ID	Title	Prot. Dom.	ratio
415989	AI267700	Hs.111128	ESTs	TM	42.7
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	30.5
428153	AW513143	Hs.98367	similar to SRY-box containing gene 17	TM	30.1
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix	SS	29.4
427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphy	C1q,Collagen	27.0
430691	C14187	Hs.103538	ESTs	TM	26.2
418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitial collag	SS,,Peptidase_M10	20.6
400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic protein rec	TM	20.6
424086	AI351010	Hs.102267	lysyl oxidase	Lysyl_oxidase	17.7
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kin	pkise,pkinase	17.4
427356	AW023482	Hs.97849	ESTs	TM	17.4
407638	AJ404672	Hs.288693	EST	TM	17.1
427469	AA403084	Hs.269347	ESTs	TM	17.0
438993	AA828995		integrin; beta 8	SS,integrin_B	16.7
421155	H87879	Hs.102267	lysyl oxidase	SS	16.1
431989	AW972870	Hs.291069	ESTs	SS	15.9
428976	AL037824	Hs.194695	ras homolog gene family, member I	ras	15.1
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, hom	TM	15.0

413623	AA825721	Hs.246973	ESTs	TM	14.8
447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	SS,TM,Furin-like,pkinase	14.2
428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PRO	IL8	14.1
452461	N78223	Hs.108106	transcription factor	G9a,PHD	13.7
451106	BE382701	Hs.25960	N-myc	Myc_N_term	13.6
416208	AW291168	Hs.41295	ESTs	TM	13.5
452249	BE394412	Hs.61252	ESTs	homeobox	13.4
416566	NM_003914	Hs.79378	cyclin A1	cyclin	12.8
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	TM	12.6
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	SS,Cys_knot	12.3
458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34) f	TM	12.2
408460	AA054726	Hs.285574	ESTs	TM	12.2
415263	AA948033	Hs.130853	ESTs	histone	11.9
400298	AA032279	Hs.61635	STEAP1	TM	11.8
421451	AA291377	Hs.50831	ESTs	TM	11.6
443715	AI583187	Hs.9700	cyclin E1	cyclin	11.5
413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity gl	TM,SDF	11.5
410102	AW248508	Hs.279727	ESTs;	SS	11.4
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote	TM	11.4
442353	BE379594	Hs.49136	ESTs	TM	11.3
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3	TM,neur_chan	11.2
453160	AI263307	Hs.146228	ESTs	histone	11.2
412723	AA648459	Hs.179912	ESTs	TM	11.1
400250			0	Hist_deacetyl+F105	11.1
438167	R28363	Hs.24286	ESTs	7tm_1	11.1
434539	AW748078	Hs.214410	ESTs	TM	10.9
450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	TM	10.8
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2	SS,hemopexin	10.8
446142	AI754693	Hs.145968	ESTs	Cadherin_C_term	10.7
421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	TM,p450	10.6
433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNT	SS,TM	10.6
418506	AA084248	Hs.85339	G protein-coupled receptor 39	TM	10.5
433447	U29195	Hs.3281	neuronal pentraxin II	SS	10.4
414245	BE148072	Hs.75850	WAS protein family, member 1	TM	10.3
426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	SS,LRRNT	10.3
418601	AA279490	Hs.86368	calmegin	SS	10.3
415227	AW821113	Hs.72402	ESTs	TM	10.2
409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone O	TM	10.1
426471	M22440	Hs.170009	transforming growth factor, alpha	SS,EGF	9.8
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotran	SS	9.7
445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,EGF	9.7
414972	BE263782	Hs.77695	KIAA0008 gene product	TM	9.4
435509	AI458679	Hs.181915	ESTs	TM	9.3
445413	AA151342	Hs.12677	CGI-147 protein	UPF0099	9.2
446999	AA151520	Hs.279525	hypothetical protein PRO2605	TM	9.1
414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	9.1
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	hemopexin	9.0
408908	BE296227	Hs.48915	serine/threonine kinase 15	pkinase,TM	9.0
451807	W52854	Hs.27099	DKFZP564J0863 protein	TM	8.8
420159	AI572490	Hs.99785	ESTs	TM	8.8
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:poly	TM,Ricin_B_lectin	8.7
408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotran	TM	8.7
438885	AI886558	Hs.184987	ESTs	TM	8.7
447342	AI199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAM	TM	8.6
437212	AI765021	Hs.210775	ESTs	UDPGT	8.5
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	8.4
450505	NM_004572	Hs.25051	plakophilin 2	TM	8.4
436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone H	wnt	8.3
425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor	Y_phosphatase	8.3
447268	AI370413	Hs.36563	Homo sapiens cDNA: FLJ22418 fis, clone	Ribosomal_S8	8.2
400195			0	TM	8.1
424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein,	TM	8.1
438202	AW169287	Hs.22588	ESTs	TM	8.1
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	TM	8.0
453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	TM,Fz,Frizzled	8.0
424001	W67883	Hs.137476	KIAA1051 protein	TM	8.0
442655	AW027457	Hs.30323	ESTs	TM	7.8
445657	AW612141	Hs.279575	ESTs	7tm_1	7.8
426320	W47595	Hs.169300	transforming growth factor, beta 2	SS,TGF-beta	7.8
412170	D16532	Hs.73729	very low density lipoprotein receptor	TM,ldl_recept_b,EGF	7.6
436476	AA326108	Hs.53631	ESTs	TM	7.6
414132	AI801235	Hs.48480	ESTs	TM	7.6
437789	AI581344	Hs.127812	ESTs, Weakly similar to AF141326 1 RNA	TM	7.6
450192	AA263143	Hs.24596	RAD51-interacting protein	TM	7.6
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	TM	7.5
413627	BE182082	Hs.246973	ESTs	TM	7.4
446293	AI420213	Hs.149722	ESTs	LIM,homeobox	7.4
409242	AL080170	Hs.51692	DKFZP434C091 protein	TM,7tm_1	7.3
450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA	TM	7.3
451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN A	TM	7.3
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane g	TM	7.2
429126	AW172356	Hs.99083	ESTs	7tm_1	7.1
421464	AA291553	Hs.190086	ESTs	TM	7.0
420362	U79734	Hs.97206	huntingtin interacting protein 1	TM	7.0

444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiet	TM	7.0
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	Kunitz_BPTI,G-gamma	6.9
429418	AI381028	Hs.99283	ESTs	AAA	6.9
409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	6.9
425905	AB032959	Hs.161700	KIAA1133 protein	TM	6.9
428532	AF157326	Hs.184786	TBP-interacting protein	TM	6.9
433426	H69125	Hs.133525	ESTs	TM	6.9
448674	W31178	Hs.154140	ESTs	TM	6.8
432415	T16971	Hs.289014	ESTs	TM	6.7
418203	X54942	Hs.83758	CDC28 protein kinase 2	TM	6.6
438394	BE379623	Hs.27693	CGI-124 protein	pro_isomerase	6.6
452097	AB002364	Hs.27916	ADAM-TS3 ; a disintegrin-like and metal	Reprolysin	6.6
453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cd	TGFb_propeptide	6.6
423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	filament	6.6
452281	T93500	Hs.28792	ESTs	TGF-beta	6.5
424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum	SS,trypsin	6.5
452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transporter)	TM,Sulfate_transp	6.5
434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subun	pkinase,fn3	6.5
425776	U25128	Hs.159499	parathyroid hormone receptor 2	TM,7tm_2	6.4
409517	X90780	Hs.54668	troponin I, cardiac	Y_phosphatase	6.4
432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein p	TM	6.4
448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	SS	6.4
413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone	TM	6.4
424153	AA451737	Hs.141496	MAGE-like 2	TM	6.4
441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	6.4
443539	AI076182	Hs.134074	ESTs	TM	6.4
418384	AW149266	Hs.25130	ESTs	TM	6.3
425371	D49441	Hs.155981	mesothelin	SS	6.3
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced g	SS	6.3
437117	AL049256	Hs.122593	ESTs	TM	6.3
453370	AI470523	Hs.182356	ESTs, Moderately similar to translation init	ABC_tran	6.3
426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic p	SS,TGF-beta	6.3
452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E	TM	6.2
457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	TM	6.2
436281	AW411194	Hs.120051	ESTs	TM	6.1
415139	AW975942	Hs.48524	ESTs	TM	6.1
449448	D60730	Hs.57471	ESTs	TM	6.1
457979	AA776655	Hs.270942	ESTs	TM	6.1
422867	L32137	Hs.1584	cartilage oligomeric matrix protein	SS,EGF,tsp_3	6.0
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate)	TM	6.0
412733	AA984472	Hs.74554	KIAA0080 protein	C2	6.0
422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	SS	6.0
418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alp	Chromo_shadow	6.0
410555	U92649	Hs.64311	a disintegrin and metalloproteinase domain	TM,disintegrin,Reprolysin	5.9
437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	5.9
453431	AF094754	Hs.32973	glycine receptor, beta	TM,neur_chan	5.9
417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	TSPN,Collagen,COLFI	5.9
430291	AV660345	Hs.238126	CGI-49 protein	TM	5.9
405547	#(NOCAT)		0	TM,ABC_membrane	5.9
435793	AB037734	Hs.4993	ESTs	TM	5.8
440138	AB033023	Hs.6982	hypothetical protein FLJ10201	TM	5.8
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	SS,Collagen,TSPN	5.7
419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N	TM	5.7
452971	AI873878	Hs.91789	ESTs	TM	5.7
428927	AA441837	Hs.90250	ESTs	TM	5.7
419247	S65791	Hs.89764	fragile X mental retardation 1	TM	5.7
445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sap	TM	5.7
447078	AW885727	Hs.301570	ESTs	kazal	5.6
421247	BE391727	Hs.102910	general transcription factor IIH, polypeptid	TM	5.6
432030	AI908400	Hs.143789	ESTs	SS	5.6
443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	TM	5.5
411096	U80034	Hs.68583	mitochondrial intermediate peptidase	Peptidase_M3	5.5
419558	AW953679	Hs.278394	ESTs	SS	5.5
427386	AW836261	Hs.177486	amyloid beta (A4) precursor protein (protea	TM	5.5
427961	AW293165	Hs.143134	ESTs	TM	5.5
407216	N91773	Hs.102267	lysyl oxidase	TM	5.5
413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	ras,TM	5.5
414315	Z24878		gb:HSB65D052 STRATAGENE Human sk	TM	5.5
441645	AI222279	Hs.201555	ESTs	SS	5.5
449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanoga	TM	5.4
441433	AA933809	Hs.42746	ESTs	TM	5.4
445495	BE622641	Hs.38489	ESTs	I_LWEQ,ENTH	5.4
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone N	Glycos_transf_2	5.4
442611	BE077155	Hs.177537	ESTs	TM	5.4
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	Xlink,CUB	5.4
419948	AB041035	Hs.93847	NADPH oxidase 4	TM	5.3
427718	AI798680	Hs.25933	ESTs	histone	5.3
453867	AI929383	Hs.108196	HSPC037 protein	TM	5.3
408298	AI745325	Hs.271923	ESTs; Moderately similar to !!!! ALU SUB	Glycos_transf_2,DSPc	5.3
448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P	TM	5.3
433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMA	TM	5.3
449532	W74653	Hs.271593	ESTs	TM	5.3
452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone	TM,EGF,fn3	5.3
418379	AA218940	Hs.137516	fidgetin-like 1	AAA	5.2

416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	TM,trypsin	5.2
413384	NM_000401	Hs.75334	exostoses (multiple) 2	TM	5.2
445236	AK001676	Hs.12457	hypothetical protein FLJ10814	TM	5.2
406367	#(NOCAT)		0	proteasome,trypsin	5.2
442500	AI819068	Hs.209122	ESTs	SS	5.2
450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	TM	5.2
419140	AI982647	Hs.215725	ESTs	TM	5.2
417791	AW965339	Hs.111471	ESTs	Ald_Xan_dh_C	5.1
437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J1	TSPN,Folate_carrier	5.1
418849	AW474547	Hs.53565	ESTs, Weakly similar to B0491.1 [C.elegan	TM	5.1
428093	AW594506	Hs.104830	ESTs	TM	5.1
408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; feta	TM	5.1
418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.1
404939			0	TM	5.0
447020	T27308	Hs.16986	hypothetical protein FLJ11046	TM	5.0
410824	AW994813	Hs.33264	ESTs	TM	5.0
417423	AA197341	Hs.111164	ESTs	TM	5.0
421477	AI904743	Hs.104650	hypothetical protein FLJ10292	TM	5.0
443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMA	Glucosamine_iso	5.0
424539	L02911	Hs.150402	activin A receptor, type I	SS,Activin_recp,pkinase	4.9
416565	AW000960	Hs.44970	ESTs	TM	4.9
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein ty	SS	4.9
408938	AA059013	Hs.22607	ESTs	TM	4.9
436754	AI061288	Hs.133437	ESTs, Moderately similar to gonadotropin i	TM	4.9
409049	AI423132	Hs.146343	ESTs	TM	4.9
458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family pro	TM	4.8
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	TM,ABC_membrane	4.8
422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed ce	TM	4.8
428555	NM_002214	Hs.184908	integrin, beta 8	SS,integrin_B	4.8
452909	NM_015368	Hs.30985	pannexin 1	TM	4.8
449535	W15267	Hs.23672	low density lipoprotein receptor-related pro	SS,ldl_recept_a,EGF	4.8
452232	AW020603	Hs.271698	ESTs	TM	4.8
423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N	Cadherin_C_term	4.7
428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha polype	TM,neur_chan	4.7
433330	AW207084	Hs.132816	ESTs	TM	4.7
443933	AI091631	Hs.135501	Homo sapiens two pore potassium channel	TM	4.7
440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	TM	4.7
426300	U15979	Hs.169228	delta-like homolog (Drosophila)	TM,EGF	4.7
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	AAA,DEAD,helicase_C	4.7
429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequenc	TM	4.7
434988	AI418055	Hs.161160	ESTs	TM	4.6
406400	#(NOCAT)		0	trypsin,TM	4.6
428301	AW628666	Hs.98440	ESTs	TM	4.6
446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone N	TM	4.6
459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone N	TM	4.6
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	TM	4.6
435244	N77221	Hs.187824	ESTs	pkinase,fn3	4.6
404996	#(NOCAT)		0	Peptidase_C1	4.6
407905	AW103655	Hs.252905	ESTs	SS,Ephrin	4.6
441675	AI914329	Hs.5461	ESTs	TM	4.6
420276	AA290938	Hs.190561	ESTs, Highly similar to mosaic protein LR1	TM,fn3,ldl_recept_a	4.5
422529	AW015128	Hs.256703	ESTs	TM	4.5
438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	4.5
457465	AW301344	Hs.195969	ESTs	Pribosyltran	4.5
418848	AI820961	Hs.193465	ESTs	TM,pkise	4.5
447499	AW262580	Hs.147674	KIAA1621 protein	TM	4.5
432731	R31178	Hs.287820	fibronectin 1	SS	4.5
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone H	Nucleoside_tra2	4.4
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	TM	4.4
409092	AI735283	Hs.172608	ESTs	TM	4.4
451389	N73222	Hs.21738	KIAA1008 protein	TM	4.4
453331	AI240665	Hs.8895	ESTs	TM	4.4
448133	AA723157	Hs.73769	folate receptor 1 (adult)	TM	4.4
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	TM	4.4
453279	AW893940	Hs.59698	ESTs	TM	4.4
409459	D86407	Hs.54481	low density lipoprotein receptor-related pro	TM,EGF,ldl_recept_a	4.4
431708	AI698136	Hs.108873	ESTs	TM	4.4
433906	AI167816	Hs.43355	ESTs	TM	4.4
441423	AI793299	Hs.126877	ESTs	TM	4.4
446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasm	TM	4.3
412078	X69699	Hs.73149	paired box gene 8	TM	4.3
423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; H	AIRS	4.3
448390	AL035414	Hs.21068	hypothetical protein	TM	4.3
453628	AW243307	Hs.170187	ESTs	TM	4.3
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM	4.3
413775	AW409934	Hs.75528	nucleolar GTPase	MMR_HSR1	4.3
451592	AI805416	Hs.213897	ESTs	TM	4.3
419311	AA689591		gb:nv66a12.s1 NCI_CGAP_GC81 Homo s	TM	4.2
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	TM	4.2
428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo s	TM	4.2
436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prote	TM	4.2
406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P	TM	4.2
428819	AL135623	Hs.193914	KIAA0575 gene product	TM	4.2
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fac	F-actin_cap_A	4.2

431750	AA514986	Hs.283705	ESTs	TM	4.2
449554	AA682382	Hs.59982	ESTs	TM	4.2
409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HP	SEA	4.1
433929	AI375499	Hs.27379	ESTs	TM	4.1
415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN A	TM	4.1
444381	BE387335	Hs.283713	ESTs	TM	4.1
415539	AI733881	Hs.72472	BMPR-Ib; bone morphogenetic protein rec	TM	4.1
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long	TM	4.1
453293	AA382267	Hs.10653	ESTs	TM	4.1
409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	TM	4.1
429628	H09604	Hs.13268	ESTs	TM	4.1
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN	TM	4.1
443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retina	TM	4.1
425322	U63630	Hs.155637	protein kinase; DNA-activated; catalytic po	TM	4.1
417300	AI765227	Hs.55610	solute carrier family 30 (zinc transporter), m	TM	4.1
417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	SS,TM	4.1
452834	AI638627	Hs.105685	ESTs	kinesin	4.1
428771	AB028992	Hs.193143	KIAA1069 protein	PI-PLC-X,PI-PLC-Y	4.0
412314	AA825247	Hs.250899	heat shock factor binding protein 1	TM	4.0
436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulating c	TM	4.0
450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	KRAB	4.0
409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequenc	TM	4.0
413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	ribonuc_red	4.0
417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	TM	4.0
445941	AI267371	Hs.172636	ESTs	TM,lectin_c	4.0
441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	lipocalin	4.0
411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	TM	4.0
418301	AW976201	Hs.187618	ESTs	TM	4.0
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	TGF-beta,Myc_N_term	4.0
408684	R61377	Hs.12727	hypothetical protein FLJ21610	TM	4.0
414869	AA157291	Hs.72163	ESTs	TM	4.0
420281	AI623693	Hs.191533	ESTs	Cation_efflux	3.9
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	EGF,TB	3.9
411274	NM_002776	Hs.69423	kallikrein 10	trypsin,TM	3.9
437222	AL117588	Hs.299963	ESTs	TM	3.9
431958	X63629	Hs.2877	Cadherin 3, P-cadherin (placental)	TM,cadherin,	3.9
430634	AI860651	Hs.26685	ESTs	TM	3.9
415716	N59294	Hs.301141	Homo sapiens cDNA FLJ11689 fis, clone H	NAP_family	3.9
420179	N74530	Hs.21168	ESTs	TM	3.8
451250	AA491275	Hs.236940	Homo sapiens cDNA FLJ12542 fis, clone N	TM	3.8
429496	AA453800	Hs.192793	ESTs	TM	3.8
421764	AI681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN C	TM	3.8
447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Hom	TM,SDF	3.8
422939	AW394055	Hs.98427	ESTs	TM	3.8
414737	AI160386	Hs.125087	ESTs	TM	3.8
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS,trypsin	3.8
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	SS,Peptidase_M10	3.7
424433	H04607	Hs.9218	ESTs	TM	3.7
431846	BE019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	3.7
407792	AI077715	Hs.39384	putative secreted ligand homologous to fjx1	SS	3.7
417531	NM_003157	Hs.1087	serine/threonine kinase 2	pkinase,pkinase	3.7
434836	AA651629	Hs.118088	ESTs	TM	3.7
439810	AL109710	Hs.85568	EST	TM	3.7
418693	AI750878	Hs.87409	thrombospondin 1	SS,EGF,TSPN	3.7
407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	TM	3.7
436304	AA339622	Hs.108887	ESTs	TM	3.7
452259	AA317439	Hs.28707	signal sequence receptor, gamma (transloco	TM	3.7
453468	W00712	Hs.32990	DKFZP566F084 protein	TM	3.6
428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein	TM	3.6
411402	BE297855	Hs.69855	NRAS-related gene	CSD,ras,CSD	3.6
425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMA	TM	3.6
400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR	ABC_tran	3.6
407340	AA810168	Hs.232119	ESTs	TM	3.6
418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	TM	3.6
438279	AA805166	Hs.165165	ESTs, Moderately similar to ALU8_HUMA	TM	3.6
439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	AAA,AAA	3.6
441111	AI806867	Hs.126594	ESTs	TM	3.6
451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	TM	3.6
409542	AA503020	Hs.36563	ESTs	Ribosomal_S8	3.6
425441	AA449644	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone N	Aa_trans	3.6
428137	AA421792	Hs.170999	ESTs	AAA	3.6
433692	AI805860	Hs.208675	ESTs, Weakly similar to neuronal thread pr	TM	3.6
438689	AW129261	Hs.250565	ESTs	TM	3.6
443341	AW631480	Hs.8688	ESTs	TM	3.6
446261	AA313893	Hs.13399	hypothetical protein FLJ12615 similar to m	ATP-synt_D,PH	3.6
414343	AL036166	Hs.75914	coated vesicle membrane protein	TM	3.5
414812	X72755	Hs.77367	monokine induced by gamma interferon	SS,IL8	3.5
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-indu	TM	3.5
415786	AW419196	Hs.257924	ESTs	TM	3.5
427177	AB006537	Hs.173880	interleukin 1 receptor accessory protein	TM,ig	3.5
427687	AW003867	Hs.112403	ESTs	7tm_1	3.5
444619	BE538082	Hs.8172	ESTs	TM	3.5
447336	AW139383	Hs.245437	ESTs	AhpC-TSA	3.5
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	TM	3.5

418792	AB037805	Hs.88442	KIAA1384 protein	TM	3.5
408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone N	TM	3.5
416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	TM	3.5
418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (pro	EGF	3.5
448089	AI467945	Hs.173696	ESTs	SS	3.5
422278	AF072873	Hs.114218	ESTs	TM,Fz,Frizzled	3.5
442133	AW874138	Hs.129017	ESTs	TM	3.5
410908	AA121686	Hs.10592	ESTs	GTP_EFTU	3.5
452198	AI097560	Hs.61210	ESTs	TM	3.5
408730	AV660717	Hs.47144	DKFZP586N0819 protein	pkinase	3.4
436488	BE620909	Hs.261023	hypothetical protein FLJ20958	TM	3.4
409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cD	TM	3.4
445870	AW410053	Hs.13406	syntaxin 18	TM	3.4
451743	AW074266	Hs.23071	ESTs	TM	3.4
407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with G	TM	3.4
432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	SS	3.4
412848	AA121514	Hs.70832	ESTs	TM	3.4
413625	AW451103	Hs.71371	ESTs	filament	3.4
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat d	SS	3.4
422972	N59319	Hs.145404	ESTs	TM	3.4
429170	NM_001394	Hs.2359	dual specificity phosphatase 4; MAP kinas	DSPc,Rhodanese	3.4
450377	AB033091	Hs.24936	ESTs	TM	3.4
443475	AI066470	Hs.134482	ESTs	TM	3.4
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	TM,pkise,ig,SRF-TF	3.4
409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P	TM	3.4
422789	AK001113	Hs.120842	hypothetical protein FLJ10251	TM	3.4
404440	#(NOCAT)		0	TM,neur_chan	3.4
417412	X16896	Hs.82112	interleukin 1 receptor, type I	SS,TIR,ig	3.4
411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	wnt	3.4
417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4	SS	3.4
421013	M62397	Hs.1345	mutated in colorectal cancers	TM	3.4
427072	H38046		gb:yp58c10.r1 Soares fetal liver spleen 1NF	Ribosomal_L22e	3.4
433703	AA210863	Hs.3532	nemo-like kinase	pkinase	3.4
434294	AJ271379	Hs.21175	ESTs	TM	3.4
444188	AI393165	Hs.19175	ESTs	TM	3.4
446109	N67953	Hs.145920	ESTs	TM	3.4
400881			0	Asparaginase_2	3.3
450236	AW162998	Hs.24684	KIAA1376 protein	TM	3.3
418836	AI655499	Hs.161712	ESTs	TM	3.3
437951	T34530	Hs.4210	Homo sapiens cDNA FLJ13069 fis, clone N	TM	3.3
446896	T15767	Hs.22452	Homo sapiens cDNA: FLJ21084 fis, clone	TM	3.3
430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to rat	rrm	3.3
410060	NM_001448	Hs.58367	glypican-4	SS	3.3
419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapi	TM	3.3
429609	AF002246	Hs.210863	cell adhesion molecule with homology to L	TM,fn3,ig	3.3
413289	AA128061	Hs.114992	ESTs	TM	3.3
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	3.3
401435	#(NOCAT)		0	TM	3.3
420072	AW961196	Hs.207725	ESTs	TM	3.3
421426	AA291101	Hs.33020	Homo sapiens cDNA FLJ20434 fis, clone K	TM	3.3
425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, core	SS	3.3
443295	AI049783	Hs.241284	ESTs	TM	3.2
453116	AI276680	Hs.146086	ESTs	Ribosomal_L5_C	3.2
456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-related acid	TM	3.2
430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus recepto	TM	3.2
418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9,	asp,Glyco_hydro_18	3.2
433800	AI034361	Hs.135150	lung type-I cell membrane-associated glyco	TM	3.2
425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspartat	TM	3.2
428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMA	carb_anhydrase	3.2
409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase kin	TM	3.2
411248	AA551538	Hs.69321	KIAA1359 protein	TM	3.2
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-	SS,IL8	3.2
430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	TM	3.2
414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	SS	3.2
444471	AB020684	Hs.11217	KIAA0877 protein	TM	3.2
421674	T10707	Hs.296355	neuronal PAS domain protein 2	Ribosomal_L31e	3.2
434163	AW974720	Hs.25206	ESTs	TM	3.2
421991	NM_014918	Hs.110488	KIAA0990 protein	SS	3.2
409589	AW439900	Hs.256914	ESTs	TM	3.2
414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731	TM	3.2
414661	T97401	Hs.21929	ESTs	TM	3.2
437537	AA758974	Hs.121417	ESTs, Weakly similar to unnamed protein p	TM	3.2
439702	AW085525	Hs.134182	ESTs	A2M	3.1
420552	AK000492	Hs.98806	hypothetical protein	TM	3.1
441028	AI333660	Hs.17558	ESTs	ICE_p20,CARD	3.1
425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin indu	TM	3.1
422109	S73265	Hs.1473	gastrin-releasing peptide	SS,Bombesin	3.1
441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG	TM	3.1
415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMA	SS,Ephrin	3.1
447866	AW444754	Hs.211517	ESTs	homeobox	3.1
419978	NM_001454	Hs.93974	forkhead box J1	Fork_head	3.1
446219	AI287344	Hs.149827	ESTs	MIP	3.1
448428	AF282874	Hs.21201	nectin 3; DKFZP566B0846 protein	TM,ig	3.1
407615	AW753085		gb:PM1-CT0247-151299-005-a03 CT0247	TM	3.1

410518	AW976443	Hs.285655	ESTs	RasGEF,PH,RhoGEF	3.1
418396	AI765805	Hs.26691	ESTs	TM	3.1
427855	R61253	Hs.98265	ESTs	TM	3.1
429272	W25140	Hs.110667	ESTs	TM	3.1
450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	3.1
414774	X02419	Hs.77274	plasminogen activator, urokinase	SS,kringle,trypsin	3.1
422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38kD)	TM	3.1
420062	AW411096	Hs.94785	hypothetical protein LOC57163	TM	3.1
428698	AA852773	Hs.297939	ESTs; Weakly similar to neogenin [H.sapie	TM	3.1
427051	BE178110	Hs.173374	ESTs	TM	3.1
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic diffe	SS	3.1
452906	BE207039	Hs.75621	serine (or cysteine) proteinase inhibitor, cla	TM	3.1
429419	AB023226	Hs.202276	KIAA1009 protein	TM	3.1
417517	AF001176	Hs.82238	POP4 (processing of precursor , S. cerevisia	TM	3.1
406137	#(NOCAT)		0	TM	3.1
424800	AL035588	Hs.153203	MyoD family inhibitor	TM	3.1
410252	AW821182	Hs.61418	microfibrillar-associated protein 1	TM	3.1
420392	AI242930	Hs.97393	KIAA0328 protein	SS	3.1
423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone	voltage_CLC,CBS	3.1
429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone	Glyco_hydro_2	3.1
449802	AW901804	Hs.23984	hypothetical protein FLJ20147	TM	3.1
450506	NM_004460	Hs.418	fibroblast activation protein; alpha	SS,Peptidase_S9	3.0
433849	BE465884	Hs.280728	ESTs	TM	3.0
411984	NM_005419	Hs.72988	signal transducer and activator of transcript	SH2,STAT	3.0
422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	TM	3.0
422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033	TM	3.0
409757	NM_001898	Hs.123114	cystatin SN	SS,cystatin	3.0
418727	AA227609	Hs.94834	ESTs	TM	3.0
422244	Y08890	Hs.113503	karyopherin (importin) beta 3	TM	3.0
456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatidat	TM	3.0
432358	AI093491	Hs.72830	ESTs	SS	3.0
416896	AI752862	Hs.5638	KIAA1572 protein	BTB	3.0
447312	AI434345	Hs.36908	activating transcription factor 1	TM	3.0
445021	AK002025	Hs.12251	Homo sapiens cDNA FLJ11163 fis, clone P	TM	3.0
422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltran	SS	3.0
453597	BE281130	Hs.33713	myo-inositol 1-phosphate synthase A1	TM	3.0
401197	#(NOCAT)		0	arf,Ets	3.0
403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	TM	3.0
410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	TM,FG-GAP	3.0
413268	AL039079	Hs.75256	regulator of G-protein signalling 1	RGS	3.0
414080	AA135257	Hs.47783	ESTs, Weakly similar to T12540 hypotheti	TM	3.0
426882	AA393108	Hs.97365	ESTs	TM	3.0
427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone M	TM	3.0
439444	AI277652	Hs.54578	ESTs	TM	3.0
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	TM	3.0
444895	AI674383	Hs.301192	EST cluster (not in UniGene)	TM,ASC	3.0
441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone	TM	3.0
414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis, clone N	TM,7tm_1	3.0
434241	AF119913	Hs.283607	hypothetical protein PRO3077	SS	3.0
424962	NM_012288	Hs.153954	TRAM-like protein	TM	3.0
411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU7_HUMA	TM	3.0
421977	W94197	Hs.110165	ribosomal protein L26 homolog	TM	3.0
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conju	TM	3.0
407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	TM,7tm_2,Fz,Frizzled	3.0
442577	AA292998	Hs.163900	ESTs	TM	3.0
416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB5	TM	3.0
443775	AF291664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7tm_1	3.0
414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cd	TM	3.0
457590	AI612809	Hs.5378	spondin 1, (f-spondin) extracellular matrix	SS	3.0
418946	AI798841	Hs.132103	ESTs	TM	3.0
457940	AL360159	Hs.30445	Homo sapiens mRNA full length insert cDN	TM,SPRY,7tm_1	3.0

TABLE 15B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
407615	1005404_1	AW753085 AW753082 AW054744 AW753107 AW753087
409073	109851_1	AA063458 AA063018 AI444822
409745	115237_1	AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
410008	116812_1	AA079552 BE142525 BE142527
414147	142127_-1	BE091634
414315	143512_1	Z24878 AA494098 F13654 AA494040 AA143127
416120	1571266_1	H46739 H51513 H19779
419311	183793_1	AA689591 AW974261 AA236240 AI077451 AA631399 AW974262
419546	185766_1	AA244199 AA244272 H57440
422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
427072	274884_1	H36046 W69645 AA397968 H38047
428679	294049_1	AA431765 AA432015
438993	467651_1	AA828995 AA834879 AI926361
447197	711623_1	R36075 AI366546 R36167

TABLE 15C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400881	2842777	Minus	91446-91603,92123-92265
401197	9719705	Plus	176341-176452
401435	8217934	Minus	54508-55233
404440	7528051	Plus	80430-81581
404939	6862697	Plus	175318-175476
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405547	1054740	Plus	124361-124520,124914-125050
406137	9166422	Minus	30487-31058
406367	9256126	Minus	58313-58489
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 16A lists about 92 genes up-regulated in mucinous-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile amongst various mucinous-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 16A: ABOUT 92 UP-REGULATED GENES, MUCINOUS OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
Prot. Dom.: Predicted protein domain structure
ratio: ratio tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	Prot. Dom.	ratio
430691	C14187	Hs.103538	ESTs		34.9
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	START	28.0
418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitial collag	SS,Peptidase_M10	22.3
451181	AI796330	Hs.207461	ESTs		10.8
452838	U65011	Hs.30743	Preferentially expressed antigen in melanom		10.0
407638	AJ404672	Hs.288693	EST		9.3
450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN		9.2
426890	AA393167	Hs.41294	ESTs		9.1
421155	H87879	Hs.102267	lysyl oxidase	SS,Lysyl_oxidase	8.9
437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	7.6
453866	AW291498	Hs.250557	ESTs		7.6
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-rel		7.4
418738	AW388633	Hs.6682	solute carrier family 7, member 11		7.2
431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone P	RA	7.0
449579	AW207260	Hs.134014	prostate cancer associated protein 6		6.7
424586	NM_003401	Hs.150930	X-ray repair complementing defective repa		6.7
445891	AW391342	Hs.199460	ESTs		6.2
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	6.1
452705	H49805	Hs.246005	ESTs		6.1
421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	TM,p450	5.5
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote		5.3
420159	AI572490	Hs.99785	ESTs		5.3
451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo s		5.2
409049	AI423132	Hs.146343	ESTs		5.0
448674	W31178	Hs.154140	ESTs	TM	5.0
423811	AW299598	Hs.50895	homeo box C4		4.9
427469	AA403084	Hs.269347	ESTs		4.9
447033	AI357412	Hs.157601	EST - not in UniGene	PH	4.9
424433	H04607	Hs.9218	ESTs		4.9
448811	AI590371	Hs.174759	ESTs	TM	4.8
444330	AI597655	Hs.49265	ESTs		4.8
409041	AB033025	Hs.50081	KIAA1199 protein		4.7
418735	N48769	Hs.44609	ESTs		4.5
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	4.5
430073	U86136	Hs.232070	telomerase-associated protein 1	WD40	4.4
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotran	SS	4.4
422260	AA315993	Hs.105484	ESTs; Weakly similar to LITHOSTATHIN		4.4
421110	AJ250717	Hs.1355	cathepsin E	SS,asp	4.3
445676	AI247763	Hs.16928	ESTs		4.2
430704	AW813091		gb:RC3-ST0186-240400-111-d07 ST0186	Epimerase	3.8
414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	3.8
438078	AI016377	Hs.131693	ESTs		3.7
434032	AW009951	Hs.206892	ESTs		3.7
445657	AW612141	Hs.279575	ESTs	7tm_1	3.6
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN		3.5
455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318		3.5
448844	AI581519	Hs.177164	ESTs		3.5
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced g	SS	3.5
438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	3.4
458123	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004		3.4
407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMA		3.4
424894	H83520	Hs.153678	reproduction 8	SS,UBX	3.3

424639	AI917494	Hs.131329	ESTs		3.3
414083	AL121282	Hs.257786	ESTs		3.2
426471	M22440	Hs.170009	transforming growth factor, alpha	SS,EGF	3.2
428927	AA441837	Hs.90250	ESTs		3.1
406129	#(NOCAT)		0	TM,cNMP_binding	3.1
452699	AW295390	Hs.213062	ESTs		3.1
425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	homeobox	3.1
428976	AL037824	Hs.194695	ras homolog gene family, member I	ras	3.1
436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone H	wnt	3.0
454077	AC005952	Hs.37062	insulin-like 3 (Leydig cell)	SS,Insulin,pkinase	3.0
404253	#(NOCAT)		0	histone	2.9
452461	N78223	Hs.108106	transcription factor	G9a,PHD	2.9
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	TM	2.9
413289	AA128061	Hs.114992	ESTs		2.9
429703	T93154	Hs.28705	ESTs		2.9
407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fis, clone N		2.8
424796	AW298244	Hs.293507	ESTs		2.8
424086	AI351010	Hs.102267	lysyl oxidase	Lysyl_oxidase	2.8
408427	AW194270	Hs.177236	ESTs		2.7
450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain		2.7
446999	AA151520	Hs.279525	hypothetical protein PRO2605		2.7
428819	AL135623	Hs.193914	KIAA0575 gene product		2.7
422956	BE545072	Hs.122579	ESTs		2.7
428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-0		2.7
426300	U15979	Hs.169228	delta-like homolog (Drosophila)	TM,EGF	2.6
420380	AA640891	Hs.102406	ESTs		2.6
428651	AF196478	Hs.188401	annexin A10	TM,annexin	2.6
417849	AW291587	Hs.82733	Nidogen 2	EGF,ldl_recept_b	2.6
453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	TM	2.6
417975	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23186 fis, clone		2.6
448756	AI739241	Hs.171480	ESTs		2.6
425087	R62424	Hs.126059	ESTs		2.5
444153	AK001610	Hs.10414	hypothetical protein FLJ10748	Kelch	2.5
443211	AI128388	Hs.143655	ESTs		2.5
415263	AA948033	Hs.130853	ESTs	histone	2.5
432867	AW016936	Hs.233364	ESTs	GSHPx	2.5
438639	AI278360	Hs.31409	ESTs		2.5
455386	AW935875		gb:QV3-DT0019-120100-055-d06 DT0019		2.5
419092	J05581	Hs.89603	mucin 1, transmembrane	TM,SEA	2.5
452055	AI377431	Hs.293772	ESTs		2.5

TABLE 16B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
430704	322217_1	AW813091 AW206655 AA484440
451105	859083_1	AI761324 AW880941 AW880937
455386	1287756_1	AW935875 BE069116 BE160251
455666	1349545_1	BE065813 BE065788 BE065889 BE065832
458123	479942_1	AW892676 AA853877 D44747

TABLE 16C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
404253	9367202	Minus	55675-56055
406129	9160131	Plus	2567-3056

Table 17A lists about 183 genes up-regulated in endometrioid-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile amongst various endometrioid-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 17A: ABOUT 183 UP-REGULATED GENES, ENDOMETRIOID OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
Prot. Dom.: Predicted protein domains
ratio: ratio tumor vs. normal tissue

Pkey	Ex. Accn	UG ID	Title	Prot. Dom.	ratio
452838	U65011	Hs.30743	Preferentially expressed antigen in melanom		38.9
435094	AI560129	Hs.277523	EST		28.8
428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SR		24.1
428187	AI687303	Hs.285529	ESTs		23.9
449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapi		19.9
453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	TM,Fz,Frizzled	15.7

412925	AI089319	Hs.179243	ESTs		15.7
438817	AI023799	Hs.163242	ESTs		13.6
447033	AI357412	Hs.157601	EST - not in UniGene	PH	13.5
433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMA		13.1
422956	BE545072	Hs.122579	ESTs		12.9
450451	AW591528	Hs.202072	ESTs		11.9
453964	AI961486	Hs.12744	ESTs	homeobox	11.5
442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sa		11.4
431989	AW972870	Hs.291069	ESTs	SS	10.3
413623	AA825721	Hs.246973	ESTs		9.7
440901	AA909358	Hs.128612	ESTs		9.6
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	9.6
421478	AI683243	Hs.97258	ESTs		9.3
448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	SS,Tissue_fac	9.2
410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone P		8.7
438993	AA828995		Integrin; beta 8	SS,integrin_B	8.7
427121	AI272815	Hs.173656	KIAA0941 protein	C2,	8.4
420610	AI683183	Hs.99348	distal-less homeo box 5	homeobox	8.1
427356	AW023482	Hs.97849	ESTs		8.0
446577	AB040933	Hs.15420	KIAA1500 protein		8.0
431118	BE264901	Hs.250502	carbonic anhydrase VIII	carb_anhydrase	7.5
448112	AW245919	Hs.301018	ESTs, Weakly similar to ALU8_HUMAN		6.9
451106	BE382701	Hs.25960	N-myc	HLH,Myc_N_term	6.6
449433	AI672096	Hs.9012	ESTs		6.3
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (y		6.3
434636	AA083764	Hs.241334	ESTs		6.1
453688	AW381270	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C		5.9
422805	AA436989	Hs.121017	H2A histone family; member A	histone	5.8
400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic protein rec		5.7
443179	AI928402	Hs.6933	Homo sapiens cDNA FLJ12684 fis, clone N		5.6
418134	AA397769	Hs.86617	ESTs		5.5
452249	BE394412	Hs.61252	ESTs	homeobox	5.5
409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone O	TM,UPF0016	5.5
413335	AI613318	Hs.48442	ESTs		5.4
441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	5.4
428029	H05840	Hs.293071	ESTs		5.3
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitami	p450	5.3
409094	AW337237		gb:xw82f01.x1 NCI_CGAP_Pan1 Homo sa		5.2
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	START	5.1
410102	AW248508	Hs.279727	ESTs;	SS	5.1
447835	AW591623	Hs.164129	ESTs		5.1
438202	AW169287	Hs.22588	ESTs		5.0
423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H		5.0
425905	AB032959	Hs.161700	KIAA1133 protein	TM	5.0
452461	N78223	Hs.108106	transcription factor	G9a,PHD	4.9
430691	C14187	Hs.103538	ESTs		4.8
441675	AI914329	Hs.5461	ESTs		4.7
425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor	Band_41,Y_phosphatase	4.6
440340	AW895503	Hs.125276	ESTs		4.5
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	4.5
444783	AK001468	Hs.62180	ESTs	PH	4.4
451459	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMA		4.4
413395	AI266507	Hs.145689	ESTs		4.3
415263	AA948033	Hs.130853	ESTs	histone	4.2
413988	M81883	Hs.75668	glutamate decarboxylase 1 (brain, 67kD)	pyridoxal_deC	4.2
452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N		4.1
418852	BE537037	Hs.273294	hypothetical protein FLJ20069		4.1
446431	R45652	Hs.153486	ESTs		4.1
434891	AA814309	Hs.123583	ESTs		4.0
415139	AW975942	Hs.48524	ESTs	G-patch	4.0
453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN A		4.0
447112	H17800	Hs.7154	ESTs		3.9
420633	NM_014581	Hs.99526	odorant-binding protein 2B	TM,lipocalin	3.9
459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone N		3.9
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	Kunitz_BPTI,G-gamma	3.9
414083	AL121282	Hs.257786	ESTs		3.7
442006	AW975183	Hs.292663	ESTs		3.7
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma	Thymosin	3.7
424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein,		3.7
456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	homeobox	3.7
429125	AA446854	Hs.271004	ESTs		3.6
435538	AB011540	Hs.4930	low density lipoprotein receptor-related pro		3.6
458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Cells	PHD	3.5
418506	AA084248	Hs.85339	G protein-coupled receptor 39		3.5
423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; H	AIRS,AIRS	3.4
437960	AI669586	Hs.222194	ESTs		3.4
400298	AA032279	Hs.61635	STEAP1	TM	3.4
407162	N63855	Hs.142634	zinc finger protein		3.4
408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; feta		3.3
445829	AI452457	Hs.145526	ESTs		3.3
450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA		3.3
457979	AA776655	Hs.270942	ESTs	TM	3.3
402606	#(NOCAT)				3.2
426471	M22440	Hs.170009	transforming growth factor, alpha	SS,EGF	3.2

430294	AI538226	Hs.135184	ESTs	polyprenyl_synt	3.2
448027	AI458437	Hs.177224	ESTs		3.2
432619	AW291722	Hs.278526	related to the N terminus of tre	TBC	3.2
413627	BE182082	Hs.246973	ESTs		3.2
441377	BE218239	Hs.202656	ESTs		3.2
441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone N		3.2
433527	AW235613	Hs.133020	ESTs		3.2
450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	3.2
419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Hom		3.1
418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	homeobox	3.1
419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N		3.1
450480	X82125	Hs.25040	zinc finger protein 239	zf-C2H2	3.1
420149	AA255920	Hs.88095	ESTs		3.1
413415	AA829282	Hs.34969	ESTs		3.1
438966	AW979074		gb:EST391184 MAGE resequences, MAGP		3.1
431041	AA490967	Hs.105276	ESTs	Oxysterol_BP	3.1
415245	N59650	Hs.27252	ESTs		3.0
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6	kinesin	3.0
431707	R21326	Hs.267905	hypothetical protein FLJ10422		3.0
448816	AB033052	Hs.22151	KIAA1226 protein		3.0
447866	AW444754	Hs.211517	ESTs	homeobox	3.0
450221	AA328102	Hs.24641	cytoskeleton associated protein 2		3.0
406997	U07807	Hs.194762	Human metallothionein IV (MTIV) gene, c		3.0
433426	H69125	Hs.133525	ESTs	TM	3.0
420440	NM_002407	Hs.97644	mammaglobin 2	Uteroglobin	3.0
420181	AI380089	Hs.158951	ESTs		3.0
458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family pro		2.9
452055	AI377431	Hs.293772	ESTs		2.9
429663	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolas	C2,PLA2_B	2.9
415125	AF061198	Hs.301941	Homo sapiens mRNA for norepinephrine tr	TM,SNF	2.9
412708	R26830	Hs.106137	ESTs	TM,7tm_2,Rho_GDI	2.9
451389	N73222	Hs.21738	KIAA1008 protein		2.9
423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	DIX,RGS	2.9
435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase		2.9
428054	AI948688	Hs.266619	ESTs		2.9
448243	AW369771	Hs.77496	ESTs		2.9
425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	SS	2.9
432415	T16971	Hs.289014	ESTs		2.9
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)		2.9
400195			0		2.9
449874	AA135688	Hs.10083	ESTs		2.8
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	Hydrolase	2.8
428093	AW594506	Hs.104830	ESTs		2.8
409640	U78722	Hs.55481	zinc finger protein 165	TM,zf-C2H2,SCAN	2.8
424169	AA336399	Hs.153797	ESTs	mito_carr	2.8
409638	AW450420	Hs.21335	ESTs		2.8
440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [		2.8
426890	AA393167	Hs.41294	ESTs		2.8
452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat93		2.8
422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed ce		2.8
416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen 1NF	zf-C3HC4	2.8
445870	AW410053	Hs.13406	syntaxin 18	TM	2.7
441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone		2.7
447342	AI199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAM		2.7
421247	BE391727	Hs.102910	general transcription factor IIH, polypeptid		2.7
419752	AA249573	Hs.152618	ESTs		2.7
410658	AW105231	Hs.192035	ESTs		2.7
437698	R61837	Hs.7990	ESTs		2.7
458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34) f		2.7
438689	AW129261	Hs.250565	ESTs		2.7
439876	AI376278	Hs.100921	ESTs, Weakly similar to ALU7_HUMAN A	SCAN	2.7
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	pkinase	2.7
436406	AW105723	Hs.125346	ESTs		2.7
437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprote		2.7
419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E		2.7
434836	AA651629	Hs.118088	ESTs		2.7
448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709		2.7
444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	WD40	2.7
409757	NM_001898	Hs.123114	cystatin SN	SS,cystatin	2.6
443775	AF291664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7tm_1	2.6
427961	AW293165	Hs.143134	ESTs		2.6
426668	AW136934	Hs.97162	ESTs		2.6
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	2.6
434669	AF151534	Hs.92023	core histone macroH2A2.2	histone,A1pp,DUF27	2.6
417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	SS,TM,PTN_MK	2.6
451009	AA013140	Hs.115707	ESTs		2.6
429774	AI522215	Hs.50883	ESTs	pkinase	2.6
439951	AI347067	Hs.124636	ESTs	TM	2.6
417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfera	AIRS,formyl_transf	2.5
416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	WD40	2.5
420900	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C	2.5
457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	Dihydroorotase	2.5
459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sa		2.5
440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone T	PAX	2.5

446693	AW750373	Hs.42315	Homo sapiens cDNA FLJ13036 fis, clone N	TM	2.5
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone M		2.5
400882			0		2.5
431322	AW970622		gb:EST382704 MAGE resequences, MAGK		2.5
424081	NM_006413	Hs.139120	ribonuclease P (30kD)		2.5
451996	AW514021	Hs.245510	ESTs		2.5
403381	#(NOCAT)		0		2.5
419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	SS	2.5
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	TM,ABC_membrane	2.5

TABLE 17B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409094	1099611_1	AW337237 AW861642 AW861655 AW858008 AW857990 AW858007
416624	1604694_1	H69044 T47567 H75691 T50292
419807	188252_1	R77402 AA262462 AA250988 R06794
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438966	467436_1	AW979074 AA834841 AA828650
438993	467651_1	AA828995 AA834879 AI926361
442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
448404	761515_1	BE089973 AI498612 AW805032
449034	794817_1	AI624049 AW117770 AI858360
452771	930983_1	T05477 T07855 AI917711
458861	798085_1	AI630223 AI630470

TABLE 17C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400882	2842777	Minus	110431-110708
402606	9909429	Minus	81747-82094
403381	9438267	Minus	26009-26178

Table 18 lists lists 178 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various 149 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 18: ABOUT 178 UP-REGULATED GENES ENCODING SECRETED PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
ratio: ratio tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	30.5
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	29.4
427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	27.0
423739	AA398155	Hs.97600	ESTs	22.7
418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitial c	20.6
438993	M73780	Hs.52620	integrin; beta 8	16.7
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.5
439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	16.5
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	16.2
421155	H87879	Hs.102267	lysyl oxidase	16.1
431989	AW972870	Hs.291069	ESTs	15.9
426635	BE395109	Hs.129327	ESTs	15.9
424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	15.7
428976	AL037824	Hs.194695	ras homolog gene family, member I	15.1
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	15.0
439706	AW872527	Hs.59761	ESTs	14.7
452055	AI377431	Hs.293772	ESTs	13.2
410102	AW248508	Hs.279727	ESTs;	12.5
428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	12.4

402606	AA434329	Hs.36563	hypothetical protein FLJ22418	11.5
443715	AI583187	Hs.9700	cyclin E1	10.7
433496	AF064254	Hs.49765	VLCS-H1 protein	10.6
418601	AA279490	Hs.86368	calmegin	10.3
409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis,	10.1
445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	9.9
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	9.7
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.7
429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	9.5
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	9.4
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	9.4
435509	AI458679	Hs.181915	ESTs	9.3
408908	BE296227	Hs.48915	serine/threonine kinase 15	9.0
433764	AW753676	Hs.39982	ESTs	9.0
445413	AA151342	Hs.12677	CGI-147 protein	8.7
438078	AI016377	Hs.131693	ESTs	8.6
447342	AI199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFA	8.1
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	7.7
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	7.5
426320	W47595	Hs.169300	transforming growth factor, beta 2	7.5
424001	W67883	Hs.137476	KIAA1051 protein	7.4
458861	NM_007358	Hs.31016	DNA-BINDING PROTEIN M96	7.3
425465	L18964	Hs.1904	protein kinase C; iota	7.2
425776	U25128	Hs.159499	parathyroid hormone receptor 2	7.1
424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corn	7.0
409178	BE393948	Hs.50915	kallikrein 5	6.8
433159	AB035898	Hs.150587	kinesin-like protein 2	6.6
410530	M25809	Hs.64173	ESTs, Highly similar to VAB1	6.5
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.5
422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	6.4
425371	D49441	Hs.155981	mesothelin	6.4
448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin	6.4
447207	AA442233	Hs.17731	hypothetical protein FLJ12892	6.3
420440	NM_002407	Hs.97644	mammaglobin 2	6.2
457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.2
415139	AW975942	Hs.48524	ESTs	6.1
440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone TH	6.0
417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	6.0
437960	AI669586	Hs.222194	ESTs	6.0
410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.9
433447	U29195	Hs.3281	neuronal pentraxin II	5.9
437099	N77793	Hs.48659	ESTs, Highly similar to LMA1	5.9
427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.9
422867	L32137	Hs.1584	cartilage oligomeric matrix protein	5.8
444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	5.7
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	5.6
419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232	5.6
424539	L02911	Hs.150402	activin A receptor, type I	5.5
441645	AI222279	Hs.201555	ESTs	5.5
424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.4
426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	5.4
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.4
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.3
445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.2
452930	AW195285	Hs.194097	ESTs	5.2
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein	5.1
411571	AA122393	Hs.70811	hypothetical protein FLJ20516	5.1
432158	W33165	Hs.55548	ESTs, Weakly similar to unknown protein	5.0
447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.0
443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.9
448133	AA723157	Hs.73769	folate receptor 1 (adult)	4.9
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	4.8
428555	NM_002214	Hs.184908	integrin, beta 8	4.8
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.7
406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	4.7
439024	R96696	Hs.35598	ESTs	4.6
426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.6
448027	AI458437	Hs.177224	ESTs	4.6
404996	NM_001333	Hs.87417	Cathepsin L2	4.6
443933	AI091631	Hs.135501	ESTs	4.5
409459	D86407	Hs.54481	low density lipoprotein receptor-related	4.4
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	4.3
423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE	4.3
448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	4.2
419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.1
420736	AI263022	Hs.82204	ESTs	4.1
419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.1
414343	AL036166	Hs.75914	coated vesicle membrane protein	4.0
450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.0
445808	AV655234	Hs.298083	ESTs	3.9
417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor	3.9
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	3.8

430634	AI860651	Hs.26685	ESTs	3.8
431846	BE019924	Hs.271580	Uroplakin 1B	3.7
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.7
407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.7
420585	AW505139	Hs.279844	hypothetical protein FLJ10033	3.7
407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	3.6
421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.5
431958	X63629	Hs.2877	Cadherin 3, P-cadherin (placental)	3.5
410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.5
422278	AF072873	Hs.114218	ESTs	3.5
431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	3.4
408730	AV660717	Hs.47144	DKFZP586N0819 protein	3.4
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	3.3
421841	AA908197	Hs.108850	KIAA0936 protein	3.3
439864	AI720078	Hs.291997	ESTs	3.3
456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-related aci	3.2
410687	U24389	Hs.65436	lysyl oxidase-like 1	3.2
414774	X02419	Hs.77274	plasminogen activator, urokinase	3.2
420552	AK000492	Hs.98806	hypothetical protein	3.1
421991	NM_014918	Hs.110488	KIAA0990 protein	3.1
418140	BE613836	Hs.83551	microfibrillar-associated protein 2	3.1
458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.1
411789	AF245505	Hs.72157	Homo sapiens mRNA; cDNA DKFZp564I19	3.1
434241	AF119913	Hs.283607	hypothetical protein PRO3077	3.1
422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosy	3.1
409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase	3.1
416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	3.1
412604	AW978324	Hs.47144	DKFZP586N0819 protein	3.1
425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	3.0
431259	NM_006580	Hs.251391	claudin 16	3.0
418557	BE140602	Hs.246645	ESTs	3.0
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.0
419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.0
457590	AI612809	Hs.5378	spondin 1, (f-spondin) extracellular mat	2.9
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.9
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.9
417315	AI080042	Hs.180450	ribosomal protein S24	2.9
438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 [M.musculus	2.9
442295	AI827248	Hs.224398	ESTs	2.9
428248	AI126772	Hs.40479	ESTs	2.9
403019	AA834626	Hs.66718	RAD54 (S.cerevisiae)-like	2.8
436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis	2.8
419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.8
434288	AW189075	Hs.116265	ESTs	2.7
407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	2.7
431611	U58766	Hs.264428	tissue specific transplantation antigen	2.7
443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT	2.7
453779	N35187	Hs.43388	ESTs	2.7
433068	NM_006456	Hs.288215	sialyltransferase	2.7
426841	AI052358	Hs.193726	ESTs	2.7
428778	AK000530	Hs.193326	fibroblast growth factor receptor-like 1	2.7
451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein	2.6
443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	2.6
420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.6
447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	2.6
433656	AW974941	Hs.292385	ESTs	2.6
408210	N81189	Hs.43104	ESTs	2.6
430651	AA961694	Hs.105187	kinesin protein 9 gene	2.5
422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	2.5
421802	BE261458	Hs.108408	CGI-78 protein	2.5
446211	AI021993	Hs.14331	S100 calcium-binding protein A13	2.5
404029	W72881	Hs.266470	protocadherin beta 2	2.5
453012	T95804	Hs.31334	putative mitochondrial outer membrane pr	2.5
419981	AA897581	Hs.128773	ESTs	2.5
448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
419220	AA811938	Hs.291759	ESTs	2.5
432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	2.4
406850	AI624300	Hs.172928	collagen, type I, alpha 1	2.4
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.4
421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	2.4
409956	AW103364	Hs.727	H.sapiens activin beta-A subunit (exon 2	2.4
407584	W25945	Hs.18745	ESTs	2.4
448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.4

Table 19 lists about 17 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 19: ABOUT 17 GENES, AND COMBINATIONS THEREOF, USEFUL FOR DIAGNOSIS OF OVARIAN CANCER
UG ID: UniGene ID
Title: UniGene Title
% tumors: percent of tumors detected expressing gene

Single genes:

UG ID	Title	% tumors
Hs.5378	spondin 1, (f-spondin) extracellular matrix protein	77
Hs.12844	EGF-like-domain 6	86
Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	66
Hs.97644	mammaglobin 2	73
Hs.155981	mesothelin (cytokine)	57
Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	21
Hs.50915	kallikrein 5	27
Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)	54
Hs.79361	kallikrein 6 (neurosin, zyme)	38
Hs.83169	MMP 1 (interstitial collagenase)	23
Hs.72026	protease, serine, 21 (testisin)	16
Hs.39384	putative secreted ligand homologous to fjx1	46
Hs.2719	epididymis-specific; whey-acidic protein type; four-disulfide core	91
Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	11
Hs.1584	cartilage oligomeric matrix protein	25
Hs.169300	TGF beta 2	21
Hs.2250	leukemia inhibitory factor (cholinergic differentiation factor)	23

Exemplary Combinations:

	EGF-like-domain 6 + mammaglobin 2	93
	kallikrein 7 + mesothelin	71
	mammaglobin 2 + bone morphogenic protein 7	88
	EGF-like-domain 6 + bone morphogenic protein 7	91
	kallikrein 7 + bone morphogenic protein 7 + testisin	75
	kallikrein 7 + mammaglobin 2 + mesothelin	84
	mammaglobin 2 + bone morphogenic protein 7 + TGF beta 2	91
	EGF-like-domain 6 + bone morphogenic protein 7 + MMP 1	95

Table 20A lists about 1025 genes up-regulated in ovarian cancer compared to normal adult tissues. Genes associated with ovarian cancer were selected from the 53462 probesets such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens; the "average" normal adult tissue level was set to the 96th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Tables 20B-24B list accession numbers for Pkey's lacking UnigeneID's for tables 20A-24A. For each probeset is listed a gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 20C-24C list genomic positioning for Pkey's lacking Unigene ID's and accession numbers in tables 20A-24A. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 20A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: UniGene title
Pred. Protein Dom.: Predicted protein domain
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UniGene ID	Unigene Title	Pred. Protein Dom.	R1
421296	NM_002666	Hs.103253	perilipin	perilipin,SS	32.5
453028	AB006532	Hs.31442	RecQ protein-like 4	DEAD,helicase_C,Fork_head	27.6
422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS,TM,pkinase,fn3,ig	26.5
437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,zf-DHHC	26.3
446374	AA329256	Hs.24756	ESTs, Moderately similar to al		22.6
441021	AW578716	Hs.7644	H1 histone family, member 2		22.3
409518	BE384836	Hs.3454	KIAA1821 protein	SS	21.3
413436	AF238083	Hs.68061	sphingosine kinase 1	DAGKc	21.2
424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG,SS,TM,MAPEG	20.7
422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase,SS,Ets	20.7
422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.2
429556	AW139399	Hs.98988	ESTs	SS,pkinase,PMP22_Claudin	20.1
436485	X59135	Hs.156110	immunoglobulin kappa constant	SS,ig,SS	19.9
423652	AF052122	Hs.130712	Homo sapiens clone 23929 mRNA	ABC1,SS,PID,PID	19.8
431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH,SS,LIM,Troponin	19.4
422179	AF091619	Hs.112667	dynein, axonemal, intermediate	WD40,SS	19.3
420839	AI792682	Hs.282960	hypothetical protein MGC10870	SS,DS,UPF0139,Glyco_hydro	18.5
441356	BE384361	Hs.182885	ESTs, Weakly similar to JC5024	SS,TM,ank	18.5
424659	AW891298	Hs.331601	Homo sapiens, Similar to cyste	SS,Fork_head	18.4
439924	AI985897	Hs.125293	ESTs	SS	18.1
458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_H	SS,TM,ldl_recept_a,ldl_re	17.5
451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	17.2
439108	AW163034	Hs.6467	synaptogyrin 3	Synaptogyrin,SS,TM,PDZ,WD	16.9
432945	AL043683		hypothetical protein FLJ10803	SS	16.8

410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ldl_recept_a,trypsl	16.8
438424	AI912498	Hs.25895	hypothetical protein FLJ14996	SS,TM	16.7
409435	AI810721	Hs.95424	ESTs	SS	16.4
418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	16.2
421612	AF161254	Hs.106196	8D6 antigen	ldl_recept_a,SS,TM	16.0
456177	NM_012391	Hs.79414	prostate epithelium-specific E	Ets,SAM_PNT	15.7
414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	15.6
432631	H08379	Hs.165563	hypothetical protein DKFZp434N	TM,DnaJ,UBA,ArfGap,homeob	15.5
454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	15.5
401278			Target Exon	Band_41	15.4
444804	AI084452	Hs.22158	hypothetical protein FLJ21988	SS	15.4
410259	AK000337	Hs.61485	hypothetical protein	GFO_IDH_MocA,GFO_IDH_MocA	15.4
406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,l	15.1
423081	AF262992	Hs.123159	sperm associated antigen 4	TM	14.9
421495	AI583067	Hs.149152	ESTs, Weakly similar to RHOP M		14.7
416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rrm,SS	14.7
413244	AW955951	Hs.159265	kruppel-related zinc finger pr	SS,TM,BTB,Pep_M12B_propep	14.6
406901	M14624		gb:Human 4-beta-galactosyltran		14.6
416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	14.6
436186	BE390717	Hs.5074	similar to S. pombe dim1	DIM1,SS	14.5
455557	AW995839		gb:QV4-BN0044-110200-108-h07 B	Metallophos	14.4
434518	H56995	Hs.37372	Homo sapiens DNA binding pepti	SS	14.2
421489	AI922821	Hs.32433	ESTs	SS,PI-PLC-X,PI-PLC-Y,C2	14.1
444441	AW613841	Hs.301394	hypothetical protein MGC3101		14.0
435017	AA336522	Hs.12854	angiotensin II, type I recepto		14.0
446572	AV659151	Hs.282961	ESTs		13.9
434068	AA977935	Hs.127274	ESTs	SS	13.7
432481	AW451645	Hs.151504	Homo sapiens cDNA FLJ11973 fis	SS,Collagen,COLFI,TSPN	13.7
447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS,Peptidase_C2	13.6
421182	AA284855	Hs.104480	ESTs	SS,Topoisomerase_I,Topois	13.3
407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	13.3
456642	AW451623	Hs.109752	putative c-Myc-responsive		13.3
437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657	SQS_PSY	13.2
430178	AW449612	Hs.152475	ESTs	SS	13.1
430399	AI916284	Hs.199671	ESTs	Sec7,PH	12.9
436725	BE045223	Hs.136912	hypothetical protein MGC10796		12.9
410219	T98226	Hs.171952	occludin	SS,TM,Occludin,BIR	12.7
442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668	SS,RNA_pol_K	12.7
439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
425018	BE245277	Hs.154196	E4F transcription factor 1	zf-C2H2,LIM,SS,Exo_endo_p	12.6
423801	NM_015071	Hs.132942	GTPase regulator associated wi	RhoGAP,SH3,PH	12.6
417826	T85105	Hs.15471	ESTs	SS,cadherin,Cadherin_C_te	12.6
409261	BE315042	Hs.19210	hypothetical protein MGC11308		12.6
420568	F09247	Hs.247735	protocadherin alpha 10	cadherin,SS,TM,cadherin	12.6
411570	BE144584	Hs.314341	ESTs		12.5
430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.5
423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	12.4
441805	AA285136	Hs.301914	neuronal specific transcriptio	LIM,SS,LIM	12.3
402365			Target Exon	SS,SS,TM,ig	12.2
414371	AI905865		thymosin, beta 4, X chromosome	Thymosin	12.2
446780	R31107		gb:yh61g01.s1 Soares placenta		12.1
428782	X12830	Hs.193400	interleukin 6 receptor	SS,TM,fn3,ig,SS,TM	12.1
427695	R88483	Hs.172862	intron of Bicaudal D homolog 1		12.1
400460			C11002253*:gi|129091|sp|P23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_H	SS,TM	12.0
424049	AB014524	Hs.138380	KIAA0624 protein	SS	11.9
422872	BE326786	Hs.187646	ESTs	TM	11.9
450800	BE395161	Hs.1390	proteasome (prosome, macropain	SS	11.8
428648	AF052728	Hs.188021	potassium voltage-gated channe	cNMP_binding	11.7
432329	NM_002962	Hs.2960	S100 calcium-binding protein A	S_100,efhand,SS,efhand,S_	11.7
417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis	CTF_NFI	11.6
451195	U10492	Hs.438	mesenchyme homeo box 1	homeobox,SS	11.5
417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	11.5
426500	NM_014638	Hs.170156	KIAA0450 gene product	SS	11.4
433124	U51712	Hs.13775	hypothetical protein SMAP31		11.4
444001	AI095087	Hs.152299	ESTs, Moderately similar to S6		11.4
419298	AA853479	Hs.89890	pyruvate carboxylase	CPSase_L_chain,PYC_OADA,H	11.4
428593	AW207440	Hs.185973	degenerative spermatocyte (hom	SS	11.3
411408	U76666	Hs.69949	calcium channel, voltage-depen	ion_trans,SS,TM	11.2
404438			Target Exon		11.2
427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2
406230			Target Exon		11.2
432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis	Band_41,ERM	11.2
408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_H		11.1
400206			Eos Control	SS,SS,Glyco_tranf_43,COLF	11.1
450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	11.0
407605	W03512	Hs.6479	hypothetical protein MGC13272	SS,Sema,pkinase,TIG,PSI,e	11.0
432143	AL040183	Hs.123484	Homo sapiens, clone IMAGE:4178	SS,TM,cys_rich_FGFR	10.9
446839	BE091926	Hs.16244	mitotic spindle coiled-coil re	Troponin,SS,glycolytic_en	10.8
443559	AI076765	Hs.269899	ESTs, Moderately similar to AL	SS,TM,BIR,UQ_con	10.8
411298	AW835858		gb:PM0-LT0017-031299-001-h07 L		10.8
409557	BE182896	Hs.211193	ESTs		10.8
435158	AW663317	Hs.65588	DAZ associated protein 1	rrm,SS,rrm	10.8
444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	10.6

428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIP5K	10.6
424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema	10.6
416819	U77735	Hs.80205	pim-2 oncogene	pkinase,SS,TM,OTU,K_tetra	10.5
419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_H	SS,TM,UPF0016	10.5
444359	AI697160	Hs.143594	ESTs, Weakly similar to HS4L_H		10.5
404333			C7001735*:gi|7768636|dbj|BAA95	vwd	10.5
401210			C12000519:gi|7710046|ref|NP_05		10.5
457941	AI004525	Hs.14587	ESTs, Weakly similar to AF1518	SS,TM,SS,TM	10.4
401594			NM_024817:Homo sapiens hypothe		10.3
441790	AW294909	Hs.132208	ESTs		10.3
444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_H	SS,SS,SAC3_GANP	10.3
438185	Y19188	Hs.320461	ESTs	SS	10.2
432031	AF039196	Hs.272367	hairless protein (putative sin	jmjC	10.2
410471	T88872		gb:yd31a12.s1 Soares fetal liv		10.1
433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cadherin,	10.1
417371	N74613	Hs.269149	ESTs		10.0
428167	AA770021	Hs.16332	ESTs	SS,ig,fn3	10.0
419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis		10.0
412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand,SS,CAP_GLY	10.0
425863	U43604	Hs.159901	Human unidentified mRNA, parti		9.9
442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thio	Acyl-CoA_hydro,SS,TM	9.9
429469	M64590	Hs.27	glycine dehydrogenase (decarbo	GDC-P,GDC-P	9.9
420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	9.8
445625	BE246743		hypothetical protein FLJ22635	SS,TM	9.8
435339	AI358300		ESTs	SS,ras	9.8
407235	D20569	Hs.169407	SAC2 (suppressor of actin muta	SS,TM,Ribosomal_S13,Galac	9.8
428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	9.8
401349			inositol polyphosphate-1-phosp		9.7
437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D		9.7
424511	BE300512	Hs.193557	ESTs, Moderately similar to AL		9.7
423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	9.7
405143			NM_013432*:Homo sapiens nuclea	ank,SS,TM,CPSF_A	9.6
427497	AW139476	Hs.31240	ESTs		9.6
420423	AA827718	Hs.88218	ESTs	SS	9.6
431512	BE270734	Hs.2795	lactate dehydrogenase A	ldh,ldh_C,SS,ldh	9.6
450052	AI681298	Hs.236524	ESTs	zf-C3HC4,zf-B_box	9.5
412738	N34731	Hs.74562	siah binding protein 1; FBP in	homeobox	9.5
444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	9.5
451165	AI340575	Hs.286084	MRIP-1 protein		9.5
411450	H49619	Hs.127301	ESTs	SS,pkinase	9.5
405371			NM_005569*:Homo sapiens LIM do	pkinase,LIM,PDZ	9.5
435782	N49433	Hs.285737	Homo sapiens cDNA: FLJ20895 fi	SS,G6PD,Glucosamine_iso,G	9.5
416866	AA297356	Hs.80324	serine/threonine protein phosp	Metallophos,Metallophos	9.4
405474			NM_001093*:Homo sapiens acetyl	CPSase_L_chain,biotin_lip	9.4
412837	AI922293	Hs.58389	hypothetical protein MGC4090		9.3
448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.3
431081	AA491594	Hs.75813	polycystic kidney disease 1 (a	SS,TM	9.3
427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF,late_protein_L2,SS,GS	9.2
427435	AW938739	Hs.115412	hypothetical protein FLJ13881	SS	9.2
407688	W25317	Hs.37616	Human D9 splice variant B mRNA		9.2
407507	U73799		gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.2
400833			C11000890:gi|3746443|gb|AAC639	SS,TM,7tm_1	9.2
422064	AW452589	Hs.335742	ESTs	TM	9.2
452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	9.2
451752	AB032997		KIAA1171 protein	TBC,SS,TM,pkinase,laminin	9.2
432931	AF174487	Hs.293753	Bcl-2-related ovarian killer p		9.1
407893	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	9.1
427397	AI929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RrnaAD,SS,efhand	9.1
405159			ENSP00000243337*:CDNA FLJ13984		9.1
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45,	CDC45	9.1
407058	X94563		gb:H.sapiens dbi/acbp gene exo	SS	9.0
448045	AJ297436	Hs.20166	prostate stem cell antigen	SS,TM,UPAR_LY6,toxin,SS,T	9.0
400772			NM_003105*:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	9.0
427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp5	spectrin,SH3,PH,CH	9.0
414391	BE409872		gb:601299655F1 NIH_MGC_21 Homo		9.0
447867	AI525268	Hs.164303	ESTs	TM	9.0
422639	AI929377	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt	9.0
454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	8.9
428781	AF164799	Hs.193384	putatative 28 kDa protein		8.9
408645	AW245738	Hs.109274	hypothetical protein MGC4365	SS,TM	8.9
429527	AA454184	Hs.289014	ESTs		8.9
406651	AI559224		gb:tq32c02.x1 NCI_CGAP_Ut1 Hom		8.9
430893	BE502068	Hs.282067	ESTs		8.8
414413	BE294877		gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	8.8
432211	BE274530	Hs.273333	hypothetical protein FLJ10986		8.8
421694	BE387430	Hs.106880	bystin-like		8.8
453683	AL079854	Hs.118598	Homo sapiens mRNA for KIAA1878	SS	8.8
456741	W37608	Hs.184492	ESTs	SS,pkinase	8.7
442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fi		8.7
415898	Z43379	Hs.177193	gb:HSC1AE111 normalized infant		8.7
456977	AK000252	Hs.169758	hypothetical protein FLJ20245		8.7
439632	AW410714	Hs.334437	hypothetical protein MGC4248	SS,TM,transmembrane4	8.7
431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	8.7

400128			Eos Control	TM,E1-E2_ATPase,HMA,Hydro	8.7
438582	AI521310	Hs.283365	ESTs, Weakly similar to ALU5_H	SS	8.7
450958	AL137669	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4		8.7
410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	SNF2_N,helicase_C,SS	8.7
415126	D60945		gb:HUM141D04B Clontech human f	SS,TM	8.7
418736	T18979	Hs.87908	Snf2-related CBP activator pro	SS,helicase_C,AT_hook,SS,	8.6
431157	AI823969	Hs.132678	ESTs	SS,MAPEG,SS,MAPEG	8.6
418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	8.6
419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS	8.6
432343	NM_002960	Hs.2961	S100 calcium-binding protein A	S_100,SS,efhand,S_100,efh	8.6
458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombosp		8.6
407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	8.6
452851	AW173191	Hs.213117	ESTs	SS,Sema	8.6
422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	8.6
420836	AW958453	Hs.204959	hypothetical protein FLJ14886	SS,ras	8.6
455588	AI129903	Hs.74669	vesicle-associated membrane pr	synaptobrevin,SS,TM	8.5
431974	AW972689	Hs.200934	ESTs	bZIP	8.5
410720	AF035154	Hs.65756	regulator of G-protein signall	RGS,G-gamma,DEP,SS,RGS,DI	8.5
449751	AW207115	Hs.25555	ESTs		8.5
434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	8.5
405557			Target Exon	Ets,SAM_PNT	8.5
443780	NM_012068	Hs.9754	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	8.5
428860	U38291	Hs.194301	microtubule-associated protein	M	8.5
421901	AB014554	Hs.109299	protein tyrosine phosphatase,	SAM,SS,TM,rrm,PDZ	8.4
401885			Target Exon	kinesin,SS,TM	8.4
449382	AI650407	Hs.197875	ESTs	SS,rrm,zf-RanBP	8.4
432862	AW004958	Hs.236720	amnionless protein	SS,MATH,zf-TRAF,zf-C3HC4	8.4
441363	AW450211	Hs.126825	ESTs, Weakly similar to A46302	SS,TM,HSP20,7tm_1	8.4
407363	AF035032	Hs.181125	gb:Homo sapiens clone MCA1L my	SS,ig,SS,G_glu_transpept	8.4
425380	AA356389	Hs.32148	AD-015 protein	SS,TM,LRR,P,Peptidase_S8	8.4
424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis	SS,SAM,SS,TM,7tm_1	8.4
424080	AW189983	Hs.139119	Homo sapiens cDNA FLJ10967 fis		8.3
439772	AL365406	Hs.10268	Homo sapiens mRNA full length		8.3
431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2,SS,TM	8.3
404365			Target Exon	SS	8.3
424310	AA338648	Hs.50334	testes development-related NYD	SS,TM	8.3
401935			Target Exon	PH	8.3
434796	AA812046		ESTs	SS,myb_DNA-binding,myb_DN	8.3
423098	AA321980	Hs.204682	ESTs		8.3
434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	8.2
457082	AA470687	Hs.104772	ESTs	SS	8.2
432603	AA554920	Hs.105794	UDP-glucose:glycoprotein gluco	SS,TM	8.2
402445			Target Exon	fn3,SS,TM,BNR	8.2
422078	AW872378	Hs.120170	hypothetical protein FLJ21415	SS	8.2
418361	AW505368	Hs.12460	gb:UI-HF-BN0-alu-d-03-0-UI.r1		8.2
431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	SS,PWWP,PHD	8.2
403885			Target Exon	TM,Sulfate_transp,STAS,HM	8.2
450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	8.2
452512	AW363486	Hs.337635	ESTs	SS	8.2
420138	BE268854	Hs.177729	ESTs	SS	8.2
439786	N71241	Hs.119275	ESTs	UQ_con	8.2
423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	8.2
449656	AA002008	Hs.188633	ESTs	PIP5K	8.1
452295	BE379936	Hs.28866	programmed cell death 10	SS,serpin	8.1
448650	AW769385	Hs.204891	ESTs	SS,IL8	8.1
446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine pro .	KH-domain	8.1
444406	AI147237		immunoglobulin heavy constant	SS	8.1
437215	AL117488		Human clone 23564 mRNA sequenc	SS	8.1
408891	NM_006577	Hs.284284	ESTs, Highly similar to beta-1	SS,TM,DIX,PDZ,DEP,Disheve	8.1
400409	AF153341		Homo sapiens winged helix/fork	SS	8.0
443801	AW206942	Hs.253594	Intron of: trichorhinophalang	GATA	8.0
425281	AA444390	Hs.155482	hydroxyacyl glutathione hydrol	lactamase_B,SS	8.0
458216	AW024282	Hs.104938	hypothetical protein MGC15906		8.0
401507			C15000810*:gi|11131272|sp|P793		8.0
401180			eukaryotic translation elongat	SS,TM,ion_trans,IQ	8.0
454291	AW384847	Hs.213534	ESTs, Weakly similar to MUC2_H	SS,XRCC1_N,BRCT,lactamase	8.0
444014	AI095718	Hs.135015	ESTs		8.0
412128	AW894709		gb:CM1-NN0032-020500-212-d05 N	SCAN,zf-C2H2,KRAB	7.9
408363	NM_003389	Hs.44396	coronin, actin-binding protein	WD40	7.9
425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2,he	7.9
425263	NM_001197	Hs.155419	BCL2-interacting killer (apopt	SS,TM,TspO_MBR	7.9
447045	AW392394		sorting nexin 17	SS,IF-2B,PP2C	7.9
457613	AA598869	Hs.173770	ESTs		7.9
410338	W03445	Hs.38205	gb:za05g11.r1 Soares melanocyt	pkinase	7.9
402545			Target Exon		7.9
454246	AW245185	Hs.6996	ESTs		7.9
410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8	7.9
443678	AW009605	Hs.231923	ESTs	SS	7.9
404676			Target Exon		7.9
406649	AI569392		gb:tn86a02.x1 NCI_CGAP_Ut2 Hom		7.9
420230	AL034344	Hs.284186	forkhead box C1	Fork_head,SS,Fork_head	7.9
413534	BE146961		gb:QV4-HT0222-011199-019-b12 H	SS,TM	7.8
444628	U01120	Hs.242	glucose-6-phosphatase, catalyt	PAP2,SS,TM	7.8
410839	NM_006849	Hs.66581	protein disulfide isomerase	thiored,Rho_GDI,gntR,SS,T	7.8

444046	AI360834	Hs.135094	ESTs	SS,GTP_EFTU,EFG_C,GTP_EFT	7.8
439501	AF086321	Hs.287452	Homo sapiens cDNA FLJ11760 fis	TM	7.8
415441	R13977	Hs.9634	ESTs		7.8
450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS	7.8
448993	AI471630		KIAA0144 gene product		7.8
400923			Target Exon	SS,TM,DUF289	7.8
440546	AI491994		gb:to07g09.x1 NCI_CGAP_Ut2 Hom	SS,HATPase_c	7.8
419757	AA773820	Hs.63970	ESTs	SS,TM	7.8
451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocyt	spectrin,PH,CH,SS,Peptida	7.8
458834	AI566883	Hs.196446	ESTs		7.8
422633	X56832	Hs.118804	enolase 3, (beta, muscle)	enolase,SS,TM,kinesin,FHA	7.7
438452	AI220911	Hs.288959	hypothetical protein FLJ20920	SS	7.7
421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054	asp,SS,TM,ion_trans,K_tet	7.7
434743	AI363410		ribosomal protein S18	SS,TM	7.7
450635	AW403954	Hs.25237	mesenchymal stem cell protein	4HBT	7.7
442394	R62926	Hs.285193	ESTs		7.7
434333	AA186733	Hs.292154	stromal cell protein		7.7
427221	L15409	Hs.174007	von Hippel-Lindau syndrome	VHL,TM	7.7
429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	7.7
444670	H58373	Hs.332938	hypothetical protein MGC5370	SS,zf-RanBP,MDM2	7.7
449495	AI652833		gb:wb22c11.x1 NCI_CGAP_GC6 Hom	SS	7.7
444607	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PH,PI-PLC-Y,C	7.7
449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657	TIMP	7.7
447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	7.6
448626	W27670	Hs.55613	hypothetical protein FLJ22531		7.6
430432	AB037758	Hs.241419	KIAA1337 protein	TM,Patched,TM	7.6
401822			C17001422:gi|2695866|emb|CAA75		7.6
428909	AI190714	Hs.98945	ESTs		7.6
414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	7.6
421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214		7.6
441650	AI261960	Hs.132545	ESTs	SS,TM,KOW	7.6
442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	7.6
439539	BE348395	Hs.121589	ESTs	SS,Fork_head	7.5
400286			C16000922:gi|7499103|pir||T209	TM,ABC_tran,ABC_membrane	7.5
452833	BE559681	Hs.30736	KIAA0124 protein	WD40	7.5
417390	AA196552	Hs.85852	hypothetical protein MGC3169		7.5
427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	7.5
450716	T57758	Hs.10255	ESTs		7.5
407435	AF211976		gb:Homo sapiens LENG9 mRNA, pa		7.5
413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_H		7.5
427899	AA829286	Hs.332053	serum amyloid A1	SS,SAA_proteins,SS,SAA_pr	7.5
406495			Target Exon	SRCR,TM,Acetyltransf	7.5
430387	AW372884	Hs.240770	nuclear cap binding protein su	rrm,SS,TM,rrm	7.5
408601	U47928	Hs.86122	protein A	SS,7tm_1,SS,ig,WD40,zf-UB	7.5
424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763	SS,ras	7.4
409832	AW963293		gb:EST375366 MAGE resequences,	SS	7.4
448043	AI458653	Hs.201881	ESTs	PHD	7.4
421148	AF008936	Hs.102178	syntaxin 16	Syntaxin,SS,Peptidase_M17	7.4
420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	7.4
419295	BE397712	Hs.144027	ESTs	myb_DNA-binding,myb_DNA-b	7.4
448330	AL036449		ESTs		7.4
419639	AK001502	Hs.91753	hypothetical protein		7.4
431488	AB037785	Hs.257594	KIAA1364 protein	SS,CH,LIM,SS	7.4
456487	AF064804		suppressor of Ty (S.cerevisiae		7.4
448615	AI910868	Hs.212957	ESTs	SS	7.4
427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,pkinase	7.4
441076	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343		7.4
452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	7.4
411448	AA178955	Hs.271439	ESTs, Weakly similar to I38022	rrm,PDZ	7.4
442318	AI792199		ESTs	SS,zf-C2H2	7.4
425055	AW961959	Hs.96940	ESTs		7.4
412935	BE267045	Hs.75064	tubulin-specific chaperone c	SS,TM,transmembrane4	7.4
403748			Target Exon	TM	7.4
447282	AI989963	Hs.197505	ESTs	TM	7.3
422305	AI928242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.3
416472	AA180756	Hs.340316	ESTs, Moderately similar to AL	zf-C2H2	7.3
427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	7.3
412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
447859	AK002194	Hs.19851	peroxisomal biogenesis factor		7.3
432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.3
406727	AI219282	Hs.2186	eukaryotic translation elongat	SS,G-gamma	7.3
404199			ENSP00000211797*:Helicase SKI2	SS,RasGAP,PH,SS,PHD	7.3
445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,lipoc	7.2
428550	AW297880	Hs.98661	ESTs	SS,homeobox,homeobox	7.2
454718	AW815144		gb:QV4-ST0212-120100-075-d10 S	SS,ATP-synt_ab,ATP-synt_a	7.2
407686	AW901268	Hs.126043	chromosome 21 open reading fra	SS,TM,ISK_Channel	7.2
418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Ho	serpin	7.2
424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK,SS,TM,fn3,ig,R	7.2
407581	R48402	Hs.173508	P3ECSL	SS,TM,7tm_1	7.2
430746	AW977370	Hs.222012	ESTs	SS	7.2
402651			NM_000721*:Homo sapiens calciu	ion_trans	7.2
407323	AA181183	Hs.143504	gb:zp57c02.s1 Stratagene endot	SS,Ribosomal_S4e,ubiquitl	7.2
407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.2
434035	AI762074	Hs.204769	ESTs, Weakly similar to T28770	SS,TM	7.2

400419	AF084545		Target	EGF,ig,lectin_c,sushi,Xll	7.2
424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrog	SAM_PNT	7.2
445837	AI261700		ESTs		7.2
427725	U66839	Hs.180533	mitogen-activated protein kina	pkinase	7.1
421679	AW959607		gb:EST371677 MAGE resequences,		7.1
418285	H68616	Hs.293756	ESTs	SS,EMP24_GP25L	7.1
442893	H78133		gb:yu86c11.s1 Soares fetal liv		7.1
437829	AI358522	Hs.103834	ESTs		7.1
450873	BE464016	Hs.238956	ESTs	SS,zf-C2H2,rrm	7.1
433396	AI742071	Hs.133205	ESTs	SS,TM	7.1
415595	R54144	Hs.278707	chromosome 21 open reading fra	SS	7.1
436629	AA861011	Hs.249795	ESTs	TM	7.1
414593	BE386764		gb:601273249F1 NIH_MGC_20 Homo		7.1
422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIR,TK,SS,TM	7.1
419823	AW271708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS,TM	7.1
405247			Target Exon	SS	7.1
455778	BE088746		gb:CM2-BT0693-210300-123-d09 B		7.1
431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	WD40	7.1
435717	AF227905	Hs.105794	UDP-glucose:glycoprotein gluco	Glyco_transf_8	7.1
405113			Target Exon	SS	7.1
428070	T63918	Hs.182313	retinol-binding protein 2, cel	lipocalin,lipocalin,WD40	7.1
429029	AA443443	Hs.85524	for muscle specific ring finge	SS	7.1
430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,ig	7.0
412970	AB026436	Hs.177534	dual specificity phosphatase 1	Rhodanese,DSPc,SS,DSPc	7.0
438701	AA937112	Hs.207788	ESTs	TM,sushi	7.0
454756	AW819273		gb:CM2-ST0284-061299-046-a12 S		7.0
401264			C18000090*:gi|6678656|ref|NP_0	SS,laminin_Nterm,laminin_	7.0
408080	AW149754	Hs.248652	ESTs, Weakly similar to T00273	SS	7.0
418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	7.0
431402	AA743534	Hs.250861	ESTs		7.0
423790	BE152393		gb:CM2-HT0323-171199-033-a08 H	SS	7.0
450688	AW272352	Hs.60450	ESTs	TM	7.0
405928			Target Exon	SS,cystatin,Coprogen_oxid	7.0
454438	AA224053		cell division cycle 27	SS,TM,SPRY,7tm_3,ANF_rece	7.0
407281	AI307226	Hs.164421	ESTs	SS	6.9
423386	AW136098	Hs.314081	ESTs	SS,WD40,EPO_TPO	6.9
459360	BE384526	Hs.25734	gb:601277913F1 NIH_MGC_20 Homo		6.9
420187	AK001714	Hs.95744	hypothetical protein similar t	ank,TM	6.9
431549	AA507036	Hs.170673	ESTs		6.9
423384	AL133632	Hs.127808	Homo sapiens mRNA; cDNA DKFZp4		6.9
454577	AW809272		gb:MR4-ST0118-040100-034-c08_1		6.9
438118	AW753311		ESTs	SS,lipocalin	6.9
416233	AA176633		gb:zp13g01.s1 Stratagene fetal		6.9
417012	N38970	Hs.194214	ESTs		6.9
452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin	6.9
439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_Ib,Lipase_GDSL,SS,	6.9
418416	U11700	Hs.84999	ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hydrolas	6.9
404956			C1003210*:gi|6912582|ref|NP_03	PI3_PI4_kinase,PI3K_C2,PI	6.9
451606	AA018791	Hs.7945	AIE-75 binding protein protein	SS	6.9
438525	AW368528	Hs.100855	ESTs	SS	6.9
400906			C18000324:gi|12229928|sp|Q9PTW		6.9
411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA13	SS	6.8
406834	AI318680		gb:ta49g09.x1 NCI_CGAP_Lu25 Ho		6.8
414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/m	SS,COesterase,SS,COestera	6.8
424198	AB029010	Hs.143026	KIAA1087 protein	SS,TM,Na_Ca_Ex,Calx-beta,	6.8
445873	AA250970	Hs.251946	poly(A)-binding protein, cytop	SS,PABP,rrm,pkinase,14-3-	6.8
439605	AF086431	Hs.22380	ESTs	SS,TM	6.8
432284	AA532807	Hs.105822	ESTs	SS,TM,pkinase	6.8
421904	BE143533	Hs.109309	hypothetical protein FLJ20035		6.8
443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosin,SS,TM	6.8
421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	6.8
448148	NM_016578	Hs.20509	HBV pX associated protein-8	PHD,Virus_HS,SS,ICln_chan	6.8
400205			NM_006265*:Homo sapiens RAD21	SS	6.8
434315	AW196608		ESTs		6.8
418184	AA367375		Homo sapiens cDNA FLJ14015 fis		6.8
431898	AK000020	Hs.272018	hypothetical protein FLJ20013		6.7
438627	AI087335	Hs.123473	ESTs	TM,Reticulon	6.7
409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	6.7
429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidored_q6,SS,TM,rrm	6.7
456886	AW089093	Hs.144996	ESTs, Weakly similar to I38022		6.7
427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	6.7
434000	BE002846	Hs.112964	ESTs		6.7
432530	AF131786	Hs.278303	Homo sapiens clone 25220 mRNA	SS,proteasome	6.7
436141	AA970001	Hs.150319	Homo sapiens, clone IMAGE:3610	SS,TM	6.7
441794	AW197794		ESTs		6.7
450287	AW291483	Hs.255909	ESTs		6.7
441523	AW514263		ESTs, Weakly similar to ALUF_H	SS	6.7
452798	AI918771	Hs.257170	ESTs	SS,TM,TNFR_c6	6.7
451937	AF119664	Hs.27299	transcriptional regulator prot	SS,integrin_B,fn3,Calx-be	6.7
421417	AA291004	Hs.326088	ESTs		6.7
440317	BE561888		gb:601346093F1 NIH_MGC_8 Homo		6.7
421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2,SS,TM,LRR	6.7
444904	AW452054	Hs.161139	ESTs		6.7
449730	R72290	Hs.117557	ESTs, Weakly similar to I38022	RasGAP,thyroglobulin_1,RI	6.7

450622	AI660285	Hs.58210	ESTs, Highly similar to ITH4_H	SS,TM,vwa	6.7
425424	NM_004954	Hs.157199	ELKL motif kinase	pkinase,KA1,UBA,SS	6.7
435864	AL036499	Hs.188491	ESTs		6.7
410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23	6.7
454262	AW612232	Hs.254835	ESTs	SS,TM,voltage_CLC,CBS	6.7
453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	6.6
419157	AA234540	Hs.23871	ESTs	pkinase	6.6
412464	T78141	Hs.22826	ESTs, Weakly similar to I55214	SS,cadherin,crystall	6.6
407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis	SS,adh_short,Transglutami	6.6
456643	AW751497	Hs.98370	cytochrome P450, subfamily IIS		6.6
411490	R39474		gb:yh95b09.r1 Soares placenta	SS	6.6
455885	BE153524		gb:PM0-HT0339-241199-002-C03 H	SS,pkinase	6.6
438857	AI627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	6.6
420307	AW502869	Hs.66219	ESTs	SS,TM	6.6
453496	AA442103	Hs.33084	solute carrier family 2 (facil	sugar_tr,SS,TM	6.6
419182	AA234822	Hs.66147	ESTs	SS,TM,ion_trans,ion_trans	6.6
406301			Target Exon	TM	6.6
433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta	TM	6.6
448980	AL137527	Hs.289038	hypothetical protein MGC4126		6.6
454095	AW178110	Hs.191705	gb:IL3-HT0061-010999-013-H04 H	SS,TM,homeobox,trypsin,PD	6.6
459702	AI204995		gb:an03c03.x1 Stratagene schiz		6.6
422201	NM_001505	Hs.113207	G protein-coupled receptor 30	7tm_1,SS,TM	6.6
406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	6.6
404149			C6002509*:gi|5031885|ref|NP_00	SS,TM,kringle	6.6
418576	AW968159	Hs.302740	Epithelial calcium channel 2,	SS,TM	6.6
421363	NM_001381	Hs.103854	docking protein 1, 62kD (downs	PH,IRS,TM,PH,IRS,trypsin,	6.6
458919	AI681567	Hs.13349	KIAA0756 protein	TM	6.6
427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	6.5
412289	AW935967	Hs.170162	KIAA1357 protein	SS	6.5
447105	AW377610	Hs.11123	DKFZP564G092 protein	SS,TM	6.5
444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,laminin_G,EGF	6.5
429299	AI620463	Hs.347408	hypothetical protein MGC13102	SS,TM,gla	6.5
420003	AA256906	Hs.111364	ESTs, Weakly similar to ubiqui	SS,TM	6.5
431849	AI670823	Hs.85573	hypothetical protein MGC10911	SS,TM	6.5
430396	D49742	Hs.241363	hyaluronan-binding protein 2	trypsin,kringle,EGF,SS	6.5
437662	AA765387		ESTs	WD40,RCC1,SPRY	6.5
436543	NM_002212	Hs.5215	integrin beta 4 binding protei	eIF6	6.5
405375			CX000741*:gi|4885461|ref|NP_00	SS,TM	6.5
430116	AA465350	Hs.119400	ESTs	SS,TM,adh_short	6.5
406109			Target Exon		6.5
414871	BE549179	Hs.29008	gb:601078714F1 NIH_MGC_12 Homo		6.5
440656	AI979248	Hs.148221	ESTs		6.5
438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	6.5
405376			Target Exon	SS,TM	6.5
426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fi	SS	6.5
400500			Target Exon		6.5
408294	BE141732		gb:QV0-HT0101-061099-032-e07 H	Ammonium_transp	6.5
447904	AW206303		ESTs		6.4
439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fi	SS	6.4
426828	NM_000020	Hs.172670	activin A receptor type II-lik	pkinase,Activin_recp,SS,T	6.4
446100	AW967109	Hs.13804	hypothetical protein dJ462O23.	SS,TM	6.4
442146	R52599		gb:yg81g01.r1 Soares infant br	TM	6.4
425041	AI377150	Hs.150914	ESTs	SS	6.4
457584	AA147979	Hs.285005	mitochondrial import receptor	Josephin	6.4
435449	AA682379	Hs.303460	EST		6.4
406284			Homo sapiens mRNA full length		6.4
425944	AK000664	Hs.164256	hypothetical protein FLJ20657		6.4
453367	AW732847	Hs.70573	PKCI-1-related HIT protein	SS,TM	6.4
419725	U66048	Hs.92683	Homo sapiens clone 161455 brea		6.4
412452	AA215731		suppression of tumorigenicity	SS	6.4
421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,tRNA-synt_1,GST_C,G	6.4
432746	AA564512	Hs.24301	polymerase (RNA) II (DNA direc	SS,TM,EF1BD	6.4
429398	AA452239		KIAA0970 protein		6.4
404430			C8000066*:gi|10432395|emb|CAC1	SS	6.4
427339	AI734109	Hs.97984	SRY (sex determining region Y)		6.4
436389	AI811706		CHMP1.5 protein		6.4
428890	AA525226	Hs.303293	ESTs, Moderately similar to I5		6.4
445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
414756	AW451101	Hs.159489	ESTs, Moderately similar to JC	hexokinase2,hexokinase	6.4
423847	U16997	Hs.133314	RAR-related orphan receptor C	hormone_rec,zf-C4,SS,TM,h	6.4
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (mus	PGAM,BRCT,RNA_pol_L	6.4
439569	AW602166	Hs.222399	CEGP1 protein	CUB,EGF,SS	6.4
457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	6.4
444550	BE250716	Hs.87614	ESTs	SS	6.4
407198	H91679		gb:yv04a07.s1 Soares fetal liv	BIR	6.4
423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	6.4
422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	6.3
447887	AA114050	Hs.19949	caspase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	6.3
400137			Eos Control		6.3
408784	AW971350	Hs.63386	ESTs	SS	6.3
435028	AW193035	Hs.187370	ESTs		6.3
438113	AI467908	Hs.8882	ESTs	SS,TM,7tm_1	6.3
417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	6.3
436050	AI057205	Hs.14584	ESTs		6.3

403672			C4001244:gi|539933|pir||A61275	tubulin,TM	6.3
448269	BE622358	Hs.61260	hypothetical protein FLJ13164		6.3
430217	N47863	Hs.180450	ribosomal protein S24	Ribosomal_S24e	6.3
426675	AW084791	Hs.133122	hypothetical protein FLJ14524	SS,TM,aminotran_1_2	6.3
423510	AB000824	Hs.129712	trehalase (brush-border membra	Trehalase	6.3
428573	AA430651	Hs.209249	ESTs		6.3
457052	BE167242	Hs.47099	hypothetical protein FLJ21212	SS	6.3
445099	BE163341		gb:QV3-HT0458-230200-099-b01 H		6.3
450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2,SS	6.3
416000	R82342	Hs.79856	ESTs, Weakly similar to S65657	SS,TM,sugar_tr	6.3
427880	AA436011	Hs.98187	ESTs		6.3
426722	U53823	Hs.171952	occludin	Occludin,SS,TM,BIR	6.3
452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf,SS,PDEase	6.2
431161	AA493591		gb:nh01a12.s1 NCI_CGAP_Thy1 Ho	SS	6.2
413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450	6.2
431250	BE264649	Hs.251377	taxol resistance associated ge		6.2
406373			Target Exon	SS,TM,vwa,FG-GAP,integrin	6.2
403003			NM_024944*:Homo sapiens hypoth	TM	6.2
437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Ho	SS	6.2
406299			Target Exon		6.2
439327	AF086141	Hs.50760	ESTs, Highly similar to BimL [	SS	6.2
414246	BE391090	Hs.280278	EST		6.2
427812	AA770424	Hs.98162	ESTs	SS	6.2
420926	AA830402	Hs.221216	ESTs	UQ_con	6.2
443766	N91071	Hs.109650	ESTs		6.2
431082	AA491600		gb:ne80a11.s1 NCI_CGAP_Ew1 Hom		6.2
420530	AI218431		coagulation factor VIII-associ		6.2
407360	X13075		gb:Human 2a12 mRNA for kappa-i		6.2
449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)		6.2
409946	AW162263	Hs.312468	ESTs, Weakly similar to ALUC_H	RasGAP,C2,PH,BTK	6.2
413272	AA127923		ESTs	SS	6.2
445050	AW205483	Hs.147260	ESTs	SS,trypsin,kringle,fn2,EG	6.2
458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	6.2
449940	AW291126	Hs.187520	Homo sapiens, clone IMAGE:3834	SS,zf-C2H2	6.2
440390	AW207385	Hs.36475	KIAA0493 protein		6.2
423106	N52572	Hs.13702	ESTs, Moderately similar to AL		6.2
402501			sperm specific antigen 2	ig,MHC_I,SS	6.1
431470	AA832417	Hs.139650	ESTs	SS,ig,pkinase,LRR,LRRCT	6.1
416597	H66891		gb:yr71c03.r1 Soares fetal liv		6.1
412122	AW852707		G-rich RNA sequence binding fa	SS,WD40	6.1
415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1,SS,TM	6.1
400358	AF181286		Homo sapiens mutant dystrophin		6.1
405473			NM_001093*:Homo sapiens acetyl	CPSase_L_chain,biotin_lip	6.1
422625	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin	6.1
422262	AL022315	Hs.113987	lectin, galactoside-binding, s	Gal-bind_lectin	6.1
401121			C12001638*:gi|7291960|gb|AAF47		6.1
425188	AK002052	Hs.155071	hypothetical protein FLJ11190	TM	6.1
457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796	bZIP_Maf,SS,P5CR,EF1BD	6.1
456021	BE246628	Hs.250726	gb:TCBAP1D5030 Pediatric pre-B	SS,TM,SS	6.1
420319	AW406289	Hs.96593	hypothetical protein	ras,arf	6.1
410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	SS,HECT,phoslip	6.1
450593	AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,lactam	6.1
437050	AA766420		ESTs	SS	6.1
458835	AI868753	Hs.76372	ESTs	SS	6.1
412777	AI335773		ESTs		6.1
454364	BE263928	Hs.323806	gb:601191272F1 NIH_MGC_7 Homo	SS,TM	6.1
448877	AI583696	Hs.253313	ESTs		6.1
413045	X92121	Hs.75180	protein phosphatase 5, catalyt	Metallophos,TPR	6.1
408054	AW816490	Hs.8102	ESTs		6.1
417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.1
410445	AA199830		gb:zq75h01.r1 Stratagene hNT n		6.1
415870	H15578	Hs.21017	ESTs		6.1
438723	M34429		gb:Human PVT-IGLC fusion prote		6.1
441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	6.0
406575			Target Exon	SS,pkinase,pkinase_C,RFX_	6.0
401488			Target Exon	Glyco_hydro_1	6.0
437650	AA814338	Hs.292297	ESTs		6.0
439827	AA846538	Hs.187389	ESTs	pkinase,DAG_PE-bind,PH	6.0
456373	BE247706	Hs.89751	membrane-spanning 4-domains, s	SS,TM	6.0
454513	BE159271	Hs.109731	gb:MR0-HT0407-180100-004-h05 H		6.0
414944	C15044		gb:C15044 Clontech human aorta	SS,TM	6.0
451277	AK001123	Hs.26176	hypothetical protein FLJ10261	TM,SS,TM,death,DED	6.0
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobro	Cys_knot,vwc	6.0
401215			C12000457*:gi|7512178|pir||T30	trypsin,SS,TM	6.0
408117	AL138255		ESTs, Weakly similar to I38022	SS,zf-C3HC4,BIR	6.0
426357	AW753757	Hs.12396	gb:RC3-CT0283-271099-021-a08 C		6.0
418630	AI351311	Hs.251946	poly(A)-binding protein, cytop	SS,pkinase	6.0
400389	AL135841		olfactory receptor, family 2,	7tm_1,SS,TM,CSD	6.0
447128	AI271898		cyclin K		6.0
431297	AA651771	Hs.3076	ESTs		6.0
431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p	PARP,PARP_reg,SS,TM,Pepti	6.0
430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	6.0
453101	AW952776	Hs.94943	ESTs	TM	6.0
407383	AA532576		ESTs, Moderately similar to AL	SS,Patatin,ank	6.0

430132	AA204686	Hs.234149	hypothetical protein FLJ20647	SS,SS,TM,ig	6.0
459111	AU077013	Hs.28757	transmembrane 9 superfamily me	EMP70	6.0
405770			NM_002362:Homo sapiens melanom	MAGE	6.0
415611	T26376		gb:AB123C11R Infant brain, LLN	SS,TM,rrm,sushi	6.0
453413	AJ003294		gb:AJ003294 Selected chromosom	SS,Folate_carrier	6.0
424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase,SS,Atrophin-1,Atr	5.9
426048	AI768853	Hs.134478	ESTs	TM	5.9
435750	AB029012	Hs.4990	KIAA1089 protein	SS,TM	5.9
439469	W69836		gb:zd48a02.r1 Soares_fetal_hea	SS,pkinase,C2,pkinase_C,D	5.9
445664	AW968638	Hs.237691	ESTs, Weakly similar to KIAA06		5.9
418830	BE513731	Hs.88959	hypothetical protein MGC4816	TM,CDP-OH_P_transf	5.9
452113	AI859393		gb:wm11a02.x1 NCI_CGAP_Ut4 Hom	actin	5.9
449101	AA205847	Hs.23016	G protein-coupled receptor	7tm_1,SS,TM	5.9
437640	AA764893	Hs.272155	ESTs, Weakly similar to I38022		5.9
400748			NM_022122:Homo sapiens matrix	SS,Peptidase_M10,hemopexi	5.9
442370	AI143593	Hs.129419	ESTs		5.9
442419	AI749893	Hs.270532	ESTs, Weakly similar to I38022	Adaptin_N,Alpha_adaptinC2	5.9
439986	AW750272	Hs.128608	ESTs	SS,TM,ISK_Channel	5.9
407553	Z11168		gb:H.sapiens 5HT1A receptor re	SS,TM	5.9
431424	AI222969		ESTs	SS	5.9
442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-spe	PDEase	5.9
457845	H93040	Hs.297729	ESTs	SS,TM,WD40	5.9
446912	AI347650	Hs.128521	ESTs, Moderately similar to AL	SS	5.9
451381	BE241831	Hs.172330	hypothetical protein MGC2705	SS,Ribosomal_L28e	5.9
416024	AW886484	Hs.343522	ATPase, Ca transporting, plasm	E1-E2_ATPase,Hydrolase,Ca	5.9
446329	NM_013272	Hs.14805	solute carrier family 21 (orga	kazal,OATP_N,OATP_C	5.9
431321	AW136372	Hs.1852	acid phosphatase, prostate	SS,TM,acid_phosphat	5.9
420039	NM_004605	Hs.94581	sulfotransferase family, cytos	Sulfotransfer,SS,DAGKc	5.9
428223	AA424313	Hs.98402	ESTs	HECT	5.9
433333	AI016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina	5.9
450251	BE080483		gb:QV1-BT0630-280200-086-a05 B	SS	5.9
408511	AW206404	Hs.27268	ESTs		5.9
414348	AF041430	Hs.75922	brain protein I3	SS,SH3	5.9
456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	5.9
412173	T71071		gb:yc50b05.r1 Stratagene liver	CPSase_L_chain	5.8
404001			Target Exon		5.8
445263	H57646	Hs.42586	KIAA1560 protein	SS	5.8
441583	AI791499	Hs.205742	ESTs, Weakly similar to ALUA_H		5.8
430168	AW968343		DKFZP434I1735 protein	SS,TM,efhand,efhand	5.8
454682	AW816029		gb:MR3-ST0220-151299-027-b10 S	filament	5.8
453829	AL138200		gb:DKFZp547N052_r1 547 (synony	SS,TM,ATP-synt_C,Galactos	5.8
437372	AA323968	Hs.283631	hypothetical protein DKFZp547G	SS	5.8
421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	5.8
451045	AA215672		gb:zr96e09.s1 NCI_CGAP_GCB1 Ho	SS,Peptidase_C1,zf-C2H2	5.8
439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis	SS,TM	5.8
455679	BE066529		gb:RC3-BT0333-300300-017-a12 B	UBX	5.8
457125	AW444451	Hs.134812	ESTs	SS	5.8
430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	5.8
421707	NM_014921	Hs.107054	lectomedin-2	Latrophilin,OLF,7tm_2,Gal	5.8
436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	5.8
414347	BE275835		gb:601121639F1 NIH_MGC_20 Homo	SS	5.8
439910	H66765	Hs.339397	ESTs	SS	5.8
410382	AW664971	Hs.259546	ESTs	LIM	5.8
426391	AW161050	Hs.169611	second mitochondria-derived ac	SS	5.8
423358	AI815474	Hs.343866	gb:au47f10.y1 Schneider fetal	SS	5.8
440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fi	Peptidase_M1	5.8
402189			ENSP00000247423*:D-siglec prec		5.8
439949	AW979197	Hs.292073	ESTs, Weakly similar to ALU7_H		5.8
457978	AA776638		gb:ae78g04.s1 Stratagene schiz	SS,PH,IQ,RasGEF,RasGEFN,R	5.8
436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,pkinase,Activin_rec	5.8
411602	L01406	Hs.767	growth hormone releasing hormo	7tm_2,HRM	5.8
433357	T05639		gb:EST03528 Fetal brain, Strat	SS	5.8
404311			Target Exon	TM	5.8
428092	AW879141		ESTs	SS,TM	5.8
452620	AA436504	Hs.119286	ESTs	SS	5.8
401938			Target Exon	SS,PHD,proteasome	5.7
407202	N58172	Hs.109370	ESTs	SS,F5_F8_type_C,pkinase,E	5.7
458882	R34993	Hs.226666	ESTs, Moderately similar to I5	SS,CRAL_TRIO,PKI	5.7
452357	AI638176	Hs.283865	ESTs	SS,TM,SS,TM	5.7
452625	AA724771	Hs.61425	ESTs		5.7
430281	AI878842	Hs.237924	CGI-69 protein	mito_carr,SS,TM	5.7
430490	AW902951	Hs.301723	Homo sapiens cDNA FLJ12974 fis	TM	5.7
450122	BE313765	Hs.343443	ESTs, Weakly similar to I38022	SS,TM,Y_phosphatase,LON,A	5.7
450801	AI739013	Hs.203348	ESTs	SS,TM,Hint,HH_signal	5.7
413413	D82520	Hs.132390	zinc finger protein 36 (KOX 18	SS,rrm,DUF185	5.7
445631	AK001822		Homo sapiens cDNA FLJ10960 fis		5.7
419390	AI701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	5.7
423139	AW402725	Hs.288560	hypothetical protein FLJ21106		5.7
426221	AB007881		KIAA0421 protein	PI3_PI4_kinase,FATC,SS,TM	5.7
443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS pro		5.7
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,ig	5.7
446596	AW204515	Hs.156113	ESTs, Weakly similar to G01025		5.7
432353	NM_016558	Hs.274411	SCAN domain-containing 1	SCAN	5.7
427625	AF008216	Hs.285013	putative human HLA class II as		5.7

421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	5.7
418087	AA961613	Hs.127838	ESTs		5.7
432751	AF152099	Hs.278911	interleukin 17C	SS	5.7
433943	AA992805	Hs.44865	lymphoid enhancer-binding fact		5.7
414274	AW300961	Hs.334684	Homo sapiens, clone IMAGE:4127	SS,Vps26,Acyl-CoA_dh	5.7
431328	AA502999	Hs.291591	ESTs		5.7
451481	AA300228	Hs.295866	hypothetical protein DKFZp434N		5.7
430344	AA476827	Hs.171012	hypothetical protein FLJ22349	HLH	5.6
419516	H82550		ATP-binding cassette, sub-faml	SS,TM,ABC_tran,ABC_membra	5.6
413564	BE260120		gb:601146990F1 NIH_MGC_19 Homo		5.6
415958	H10942		gb:ym06c11.r1 Soares infant br	SS,TM	5.6
401402			Target Exon		5.6
456145	BE299427	Hs.21446	KIAA1716 protein	SS,DIX,PDZ,DEP,Dishevelle	5.6
431536	AL133066	Hs.341906	ESTs	TM,SAM_decarbox,SS,pkinas	5.6
456266	L29073	Hs.198726	cold shock domain protein A	CSD,homeobox,SS,TM,7tm_2,	5.6
435800	AI248285	Hs.118348	ESTs	TM,ECH,chromo	5.6
449285	AI912702	Hs.139135	ESTs		5.6
418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	5.6
417442	AA199940	Hs.124039	ESTs		5.6
405931			Target Exon		5.6
455286	BE144384		gb:MR0-HT0166-191199-004-c11 H	SS	5.6
446931	AI348856	Hs.21627	gb:tb05a05.x2 NCI_CGAP_Lu26 Ho		5.6
446548	AI769392	Hs.200215	ESTs	SS,TM,Ribosomal_S25,sugar	5.6
401984			C17000146*:gi|2143629|pir||A57	pkinase,SS,TM,P2X_recepto	5.6
404066			Target Exon	SS,tRNA-synt_2b,HGTP_anti	5.6
418363	AA218628	Hs.202977	ESTs		5.6
458198	AI286100		ESTs		5.6
432278	AL137506	Hs.274256	hypothetical protein FLJ23563	SS,TM,GNS1_SUR4,SS,TM,Rho	5.6
432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fruct	PGAM,6PF2K	5.6
421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	5.6
415514	F11301	Hs.138329	ESTs	SS,TM	5.6
426208	AI370379	Hs.132216	ESTs	SS,TM	5.6
429367	AB007867	Hs.278311	plexin B1	Sema,PSI,TIG,SS,TM,TIG,Se	5.6
405939			Target Exon		5.6
457331	AV647405	Hs.18443	aldehyde dehydrogenase 8 famil	GTP_EFTU	5.6
438705	AI049624	Hs.283390	ESTs, Weakly similar to 210926	SS,E2F_TDP,E2F_TDP	5.6
428624	AI125222	Hs.98712	hypothetical protein DKFZp434H	SS,TM,ras,MSP_domain	5.6
419389	AI074951	Hs.319095	ESTs	SS,DPPIV_N_term	5.6
447595	AW379130	Hs.18953	phosphodiesterase 9A	PDEase	5.6
408015	AW136771	Hs.244349	epidermal differentiation comp		5.6
413041	BE061580	Hs.61622	gb:MR0-BT0249-091299-201-c07 B	SS	5.5
452849	AF044924	Hs.30792	hook2 protein	bZIP,SS,AhpC-TSA	5.5
434357	AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases,SS,TM	5.5
455274	BE151622		gb:PM0-HT0302-271099-001-a08 H	SS,TM,RNA_pol_L	5.5
453904	AW003821		ESTs		5.5
424624	AB032947	Hs.151301	Ca2+dependent activator protei	Fork_head	5.5
426576	AA381720		gb:EST94853 Activated T-cells	vwa,integrin_A,FG-GAP	5.5
440682	AW362152	Hs.27181	nuclear receptor binding facto		5.5
419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	5.5
450207	T87615	Hs.14716	ESTs		5.5
405211			C7000900:gi|4508027|ref|NP_003	SS	5.5
413937	H65775	Hs.207915	ESTs		5.5
426793	X89887	Hs.172350	HIR (histone cell cycle regula	WD40,Clathrin,Clathrin_pr	5.5
412091	R06185		gb:ye94d03.r1 Soares fetal liv	SS,TM,IBR,IBR	5.5
446536	W74413	Hs.15251	hypothetical protein	SS	5.5
451117	AA015752	Hs.205173	ESTs		5.5
409547	AW409885	Hs.335877	Homo sapiens, clone MGC:4558,	TM	5.5
412673	AL042957	Hs.31845	ESTs		5.5
426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr	5.5
449225	R39108	Hs.6777	ESTs	SS,TM,Na_sulph_symp	5.5
403938			Target Exon	Ephrin	5.5
441197	BE244638	Hs.166	sterol regulatory element bind	HLH	5.5
455604	BE011183		gb:PM3-BN0218-100500-003-d09 B		5.5
457468	AW971345	Hs.292715	ESTs		5.5
447677	AI419235	Hs.344456	gb:tf21d02.x1 NCI_CGAP_Brn23 H	SS,zf-C2H2,SCAN,SCAN,zf-C	5.5
415473	R39986	Hs.12778	ESTs	TM,Ion_trans	5.5
408422	AW977031	Hs.143554	ESTs, Highly similar to B45036		5.5
442780	AI017521		ESTs	SS,TM,7tm_1	5.5
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-faml	ABC_tran,SRP54,SS,TM,ECH	5.5
439422	AW452791	Hs.249625	ESTs	SS,TM	5.5
423479	NM_014326	Hs.129208	death-associated protein kinas	pkinase	5.5
459558	AI539821	Hs.298799	ESTs, Weakly similar to 210926	SS	5.5
441187	AW195237	Hs.7734	hypothetical protein FLJ22174	SS,TM,tubulin	5.5
420894	AA744597	Hs.88854	ESTs	SS,ank	5.5
404710			C9001584:gi|7499208|pir||T2099		5.5
447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	5.5
448387	AI874402	Hs.292590	ESTs		5.5
419541	AW749617	Hs.280776	tankyrase, TRF1-interacting an		5.5
449686	AW072813	Hs.270868	ESTs, Moderately similar to AL		5.5
426315	AA854219	Hs.348137	Homo sapiens, clone IMAGE:3542	SS,crystall	5.5
451312	AI769831	Hs.337054	ESTs	SS	5.5
432538	BE258332	Hs.278362	mate-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5
446790	AW452105		ESTs	SS,zf-C2H2	5.5
448682	T09471	Hs.250820	hypothetical protein FLJ14827		5.5

425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022	SS	5.5
411219	AW832917		gb:QV2-TT0003-161199-013-h06 T		5.5
439742	AI827721	Hs.284298	Homo sapiens mRNA full length	SS	5.5
432004	BE018302	Hs.2894	placental growth factor, vascu	PDGF,SS	5.5
402916			ENSP00000202587*:Bicarbonate t	HCO3_cotransp,SS	5.5
405346			Rag C protein	RCC1	5.5
415976	R43144	Hs.21919	ESTs	TM	5.4
435064	T70740	Hs.31433	ESTs	SS,MDM2	5.4
440024	AA969333	Hs.160098	ESTs		5.4
431525	AA506656	Hs.6185	KIAA1557 protein		5.4
458644	AW270149		ESTs, Moderately similar to GG		5.4
410895	AW809679		gb:MR4-ST0124-261099-015-f05 S		5.4
441350	AB020690	Hs.7782	paraneoplastic antigen MA2		5.4
413034	BE392896	Hs.129126	Homo sapiens, clone MGC:10992,	SS	5.4
444664	N26362	Hs.11615	map kinase phosphatase-like pr	DSPc,Rhodanese,SS,TM	5.4
443887	NM_004729	Hs.9933	Ac-like transposable element	zf-BED	5.4
445871	AI702901	Hs.145582	ESTs, Weakly similar to FOR4 M	SS,TM,efhand,efhand	5.4
411992	AW816214	Hs.143055	ESTs	SS,TM	5.4
458341	AW373583	Hs.221994	gb:QV4-BT0534-281299-053-e08 B		5.4
451677	AA059222	Hs.33538	ESTs, Weakly similar to oxygen		5.4
432656	NM_000246	Hs.3076	MHC class II transactivator	LRR	5.4
417739	Z43995		gb:HSC1QB121 normalized infant	SS,ArfGap,vwa,TSPN,fn3,Co	5.4
424618	L29472	Hs.1802	major histocompatibility compl	TM,ig,MHC_II_beta,SS,TM,A	5.4
446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fi	SS,TM,BNR,fn3,ldl_recept_	5.4
436094	AI798701		ESTs		5.4
433168	AI085436		gb:ow84g06.s1 Soares_fetal_liv	SS,TM,PID	5.4
417359	T99264	Hs.191117	ESTs		5.4
436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	5.4
435154	AA668764	Hs.301637	ESTs	SS,TM	5.4
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	5.4
444064	W85970	Hs.16292	ESTs	SS,TM,Dihydroorotase	5.4
415970	H23333	Hs.29002	KIAA1706 protein		5.4
445303	AW362198	Hs.12503	interleukin 15 receptor, alpha	SS,sushi,SS	5.4
421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11	SS,SS	5.4
459704	AA719572	Hs.274441	Homo sapiens mRNA; cDNA DKFZp4		5.4
402285			sclerostin	SS,TM	5.4
431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	5.4
431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,ras	5.4
417516	AA203473	Hs.81529	ESTs	TM	5.4
423233	BE048021	Hs.11067	ESTs, Highly similar to T46395		5.4
420733	AW291446	Hs.88651	ESTs	SS	5.4
404807			Target Exon	UPF0027	5.4
436483	AJ272063	Hs.283010	vanilloid receptor subtype 1	SS,TM,ank,ion_trans,SS,TM	5.4
425316	AA354977	Hs.99010	ESTs, Moderately similar to T1	SS,pkinase,ig	5.4
425565	AA359485	Hs.173084	gb:EST68511 Fetal lung II Homo		5.4
413341	H78472	Hs.191325	ESTs, Weakly similar to T18967		5.4
401203			Target Exon	filament	5.4
422452	AL110255	Hs.116808	Homo sapiens mRNA; cDNA DKFZp5	SS,asp,PGAM	5.4
436718	AW015227	Hs.289053	hypothetical protein FLJ14733	SS,TM	5.4
428501	AL041162	Hs.98587	ESTs	TM	5.4
439695	W28548	Hs.285050	ESTs	TM,ion_trans,K_tetra,Kv2c	5.3
417514	AA203445	Hs.325819	ESTs		5.3
441358	AW173212		ESTs		5.3
401722			Target Exon	TM,PLAT,SS	5.3
408905	AV655783	Hs.661	Target CAT		5.3
454453	AW752781		hypothetical protein FLJ12614		5.3
410312	AW850953	Hs.75350	gb:IL3-CT0220-150200-068-A11 C	Vinculin	5.3
437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	5.3
458682	AV659151	Hs.282961	ESTs		5.3
411605	AW006831		ESTs	TM,synaptobrevin	5.3
409164	AA706639		gb:ag90e09.r1 Stratagene hNT n	SS,TM,Hint,HH_signal,tubu	5.3
438868	AW246243	Hs.334800	hypothetical protein FLJ20974		5.3
439034	AF075083		gb:Homo sapiens full length in	filament,filament	5.3
411426	BE141714		gb:QV0-HT0101-061099-032-c04 H	SS	5.3
428186	AW504300	Hs.295605	mannosidase, alpha, class 2A,	Glyco_hydro_38,SS,TM,Pept	5.3
438470	AW936329	Hs.227823	pM5 protein	SS,TM	5.3
427789	AA412428	Hs.48642	hypothetical protein FLJ23093		5.3
430230	BE257724	Hs.236361	seb4D	rrm,SS,2-Hacid_DH,WD40	5.3
434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf,SS	5.3
428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	5.3
414927	T83587	Hs.186476	ESTs	SS,Sulfatase	5.3
404596			Target Exon	SS	5.3
454151	AA047169	Hs.154088	hypothetical protein FLJ22756	SS,TM,Glycos_transf_4	5.3
431627	AW609720		HSPC042 protein		5.3
422379	AA932860	Hs.133864	ESTs		5.3
426765	AA743603	Hs.172108	nucleoporin 88kD	MAM33	5.3
433325	AW206986	Hs.143905	ESTs	SS	5.3
403128			KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_t	5.3
447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755	SS,Transglutamin_C,Transg	5.3
405085			Target Exon	SS,SS,SNF2_N,helicase_C	5.3
438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_H		5.3
439091	AA830144	Hs.135613	ESTs, Moderately similar to I3	KH-domain	5.3
427326	AI287878		gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	SS,TM,7tm_1,SS,TM	5.3
427859	AA416856	Hs.98170	ESTs	SS,TM,DUF60,trypsin,CUB,u	5.3

421779	AI879159	Hs.108219	wingless-type MMTV integration	SS,wnt,SS	5.3
408270	AW177805		gb:IL3-HT0059-180899-007-B06 H		5.3
418437	AA771738	Hs.348000	ESTs, Moderately similar to AL		5.3
409879	BE083422	Hs.56851	hypothetical protein MGC2668	SS,TM	5.3
428304	AI743177		ESTs	SS,TM	5.3
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	5.3
436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM	5.2
437161	AA054477	Hs.25391	ESTs	SS,TM	5.2
400171			ENSP00000211797:Helicase SKI2W	SS,proteasome	5.2
431461	BE299671	Hs.256310	likely ortholog of mouse ZFP28		5.2
402197			Target Exon	SS,TM,ATP1G1_PLM_MAT8,ig,	5.2
449514	AW970440	Hs.23642	protein predicted by clone 236	SS,PX,srf,lipocalin,PHD,z	5.2
442472	AW806859		gb:MR0-ST0020-081199-004-c03 S	SS,TM,Inos-1-P_synth,Occl	5.2
409679	BE250521		ras homolog gene family, membe	SS,homeobox,CUT	5.2
439150	AF086006		gb:Homo sapiens full length In	SS	5.2
412934	BE011437		gb:CM4-BN0220-080500-170-f03 B		5.2
435186	AL119470		ESTs	SS	5.2
400668			Target Exon	CARD,ICE_p20,SS,ICE_p20,I	5.2
409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	5.2
445904	AW449920	Hs.248855	ESTs	SS,homeobox	5.2
414567	BE281057	Hs.184519	hypothetical protein FLJ12949	SS,TM,ank,Adap_comp_sub	5.2
414551	AI815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH,Peptidase_U7,SS,TM	5.2
432872	AI908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	5.2
419492	AA243547	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb,Metalloph	5.2
407478	L77559		gb:Homo sapiens DGS-B partial		5.2
457892	AA744389		gb:ny51e10.s1 NCI_CGAP_Pr18 Ho		5.2
457228	U15177	Hs.206984	Human cosmid CRI-JC2015 at D10	6PF2K,PGAM	5.2
437536	X91221	Hs.144465	ESTs	SS,TM,Na_Ca_Ex	5.2
420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN		5.2
431275	T56571	Hs.10041	ESTs	SS,HLH	5.2
428021	AI022287	Hs.111991	ESTs, Weakly similar to T33900	SS	5.2
422400	AA974434	Hs.128353	ESTs		5.2
446442	BE221533	Hs.257858	ESTs		5.2
415585	R59946	Hs.184852	KIAA1553 protein	SS	5.2
438429	D16918	Hs.12547	Homo sapiens cDNA: FLJ23388 fi	TM	5.2
401677			BAI1-associated protein 3	SS,TM,zf-C2H2,kinesin,Vau	5.2
405637			Target Exon		5.2
450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	5.2
408215	BE614290		syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	5.2
452666	AW194601	Hs.13219	ESTs	PI-PLC-X,PI-PLC-Y,C2,PH	5.2
401553			Target Exon		5.2
447541	AK000288	Hs.18800	hypothetical protein FLJ20281	zf-CCHC	5.2
453434	AJ271378	Hs.333243	ESTs		5.2
450351	BE547267	Hs.59791	hypothetical protein MGC13183	SS,TM	5.2
411456	AW847588		gb:IL3-CT0213-161299-038-G09 C	SS,TM	5.2
445634	AI624849	Hs.344612	ESTs, Weakly similar to NEL1_H	vwd	5.2
453740	AL120295	Hs.311809	ESTs, Moderately similar to PC		5.2
426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fi	SS,TM,EPH_lbd,pkinase,fn3	5.1
416470	N90464	Hs.303023	beta tubulin 1, class VI	SS,tubulin,SS	5.1
432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp7		5.1
457579	AB030816	Hs.36761	HRAS-like suppressor	TM	5.1
438484	AW021671	Hs.293330	ESTs, Weakly similar to p40 [H		5.1
422802	NM_004278	Hs.27008	phosphatidylinositol glycan, c	DUF158,ank	5.1
401724			C16001374:gi|6755086|ref|NP_03	TM,PLAT,SS	5.1
438670	AI275803	Hs.123428	ESTs		5.1
414757	U46922	Hs.77252	fragile histidine triad gene	HIT	5.1
425098	AW295349	Hs.8038	ESTs	SS,TM	5.1
431896	AW297844	Hs.101428	ESTs	SS	5.1
416732	H81066	Hs.285017	hypothetical protein FLJ21799	SS	5.1
404571			NM_015902*:Homo sapiens proges	HECT,zf-UBR1,PABP	5.1
433675	AW977653	Hs.75319	ribonucleotide reductase M2 po	SS	5.1
426358	AA376438		gb:EST88856 HSC172 cells II Ho	TM	5.1
456767	AI086412	Hs.129064	Homo sapiens chromosome 19, co	SS,TM,trypsin,kringle,UPA	5.1
412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH de		5.1
443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran,SS	5.1
415886	Z42737		gb:HSC0SE081 normalized infant	SS	5.1
401674			C16001417*:gi|7500345|pir||T21	FAD-oxidase_C,FAD_binding	5.1
424266	AA337810	Hs.149152	ESTs, Weakly similar to RHOP M		5.1
455035	AW851734		gb:MR2-CT0222-011199-007-e10 C		5.1
408567	S72921		ciliary neurotrophic factor	CNTF	5.1
436616	AW799109	Hs.226755	ESTs	14-3-3	5.1
409078	AW327515		ESTs		5.1
447976	AW972653	Hs.293691	ESTs, Highly similar to CR2_HU		5.1
457720	AA992835	Hs.186776	ESTs		5.1
400528			NM_020975*:Homo sapiens ret pr	cadherin,pkinase,SS	5.1
407757	BE048414	Hs.165215	hypothetical protein MGC5395	SS,EF1G_domain,GST_C,GST_	5.1
452446	AA086123	Hs.297856	ESTs	rrm,NTF2	5.1
450807	AI739262		gb:wl17b08.x1 NCI_CGAP_Co16 Ho		5.1
432540	AI821517	Hs.105866	ESTs	SS,TM	5.1
449324	AI638706		ESTs, Weakly similar to A47582		5.1
426434	M17755	Hs.2041	thyroid peroxidase	EGF,sushi,An_peroxidase,p	5.1
407652	W27953	Hs.292911	ESTs, Highly similar to S60712	Troponin	5.1
443952	AI149106		ESTs	SS,pkinase	5.1
448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_H	SS,TM	5.1

422837	U25441	Hs.121478	dopamine receptor D3	7tm_1,SS,TM,7tm_1	5.1
407143	C14076	Hs.332329	EST	SS,TM	5.1
442296	NM_007275	Hs.8186	lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	5.1
407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB,SS	5.1
427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	5.1
447960	AW954377	Hs.26412	ring finger protein 26	SS,TM,Cbl_N,Cbl_N2,Cbl_N3	5.1
400863			C11002296:gi|11692557|gb|AAG39	SS,TM	5.1
409034	AI684149	Hs.172035	hypothetical protein similar t	SS	5.1
421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA		5.1
427587	BE348244	Hs.284239	ESTs, Weakly similar to I78885	SS,UDPGT	5.1
407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	5.1
454219	X75042	Hs.44313	v-rel avian reticuloendothelio	RHD,TIG	5.1
430513	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	5.1
435902	AA701867	Hs.297726	ESTs		5.1
442743	AI801351	Hs.302110	ESTs, Weakly similar to MUC2_H	SS,fibrinogen_C,Rhodanese	5.1
454923	AW897236		gb:CM0-NN0057-150400-335-c06 N	SS,Caldesmon	5.1
440518	AA888046	Hs.233235	ESTs	SS,TM	5.1
448237	AI471790	Hs.309386	ESTs	TM,Ribosomal_S7	5.1
428924	AI016405	Hs.98959	ESTs, Weakly similar to JC5314	SS,TM,lectin_c	5.1
412081	Z24895	Hs.293818	gb:HS867F122 STRATAGENE Human	SS,TM,SQS_PSY,GATA	5.1
437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	5.1
421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	5.1
423467	AK000214	Hs.129014	hypothetical protein FLJ20207	SS,TM,GDPD,SS,TM,SH3,PDZ,	5.0
417151	AA194055	Hs.293858	ESTs	PH	5.0
408307	AI761786	Hs.204674	ESTs	Armadillo_seg	5.0
404752			NM_024778:Homo sapiens hypothe		5.0
453126	AA032155	Hs.61622	ESTs		5.0
413983	BE348384	Hs.279194	ESTs		5.0
405366			NM_003371*:Homo sapiens vav 2	SS	5.0
412425	AW949156		gb:QV4-FT0005-110500-205-b06 F		5.0
437036	AI571514	Hs.133022	ESTs	SS,TM,Glycos_transf_2	5.0
448455	AI252625	Hs.269860	ESTs, Moderately similar to S6	SS,TM	5.0
411413	BE379438	Hs.211573	heparan sulfate proteoglycan 2	ig,laminin_B,laminin_EGF,	5.0
432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD,SS,HSF_DNA-bind,E2F_	5.0
424874	AA347951		Homo sapiens cDNA FLJ20812 fis	SS	5.0
408023	BE018269	Hs.279688	ESTs		5.0
411758	AW860667		gb:QV0-CT0383-210400-204-d03 C	homeobox,homeobox	5.0
410660	AI061118	Hs.65328	Fanconi anemia, complementatio		5.0
427411	AA402242		ESTs		5.0
437018	AA889078		ESTs	SS,TM,ERG4_ERG24	5.0
427029	AA397596		ESTs	SS,ras	5.0
452047	N35953	Hs.43510	ESTs, Weakly similar to BOX B	SS	5.0
432093	H28383		gb:yl52c03.r1 Soares breast 3N	Band_41,ERM	5.0
453099	H62087	Hs.31659	thyroid hormone receptor-assoc	SS	5.0
441456	AI458911	Hs.127765	ESTs		5.0
414356	AW505085	Hs.335147	gb:UI-HF-BN0-als-a-10-0-UI.r1	SS,TM	5.0
434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis		5.0
436393	AW022213		ESTs	Galactosyl_T_2	5.0
409227	AA806165	Hs.130323	Homo sapiens, clone IMAGE:3960		5.0
448680	AW245890	Hs.21753	JM5 protein	WD40,SS,TM,KOW,HLH	5.0
439343	AF086161	Hs.114611	hypothetical protein FLJ11808		5.0
428079	AA421020	Hs.208919	ESTs	SS,TM,trypsin	5.0
421951	BE327432	Hs.109804	H1 histone family, member X		5.0
427204	AA405404	Hs.215725	ESTs	SS,SS	5.0
409690	W45393	Hs.55888	activating transcription facto		5.0
436574	AW293527	Hs.126465	ESTs		5.0
457761	AW401809	Hs.4779	KIAA1150 protein	SS,LIM,SS	5.0
435294	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis	HMG_box	5.0
445372	N36417	Hs.144928	ESTs	SS,PID,PDZ	5.0
440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE,Ribosomal_S17,	5.0
424437	BE244700	Hs.147049	cut (Drosophila)-like 1 (CCAAT	CUT,homeobox,beta-lactama	5.0
401539			NM_002675:Homo sapiens promyel	zf-B_box,zf-C3HC4,SS	5.0
417903	NM_002342	Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6,SS	5.0
442451	AI498080	Hs.129616	ESTs	SS	5.0
450536	AI699529		gb:tt17a02.x1 NCI_CGAP_GC6 Hom	SS,G-alpha,arf	5.0
425169	AW292500	Hs.128514	ESTs	SS	5.0
435262	AA677088		ESTs		5.0
444855	BE409261	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	5.0
433507	AI817336	Hs.191791	ESTs	pkinase	5.0
432396	AW295956	Hs.11900	hypothetical protein FLJ14972	SS	5.0
438395	AA017514	Hs.6211	methyl-CpG binding domain prot	MBD,zf-CXXC,SS,zf-CXXC	5.0
446603	NM_014835	Hs.15519	oxysterol-binding protein-rela	Oxysterol_BP,SS	5.0
400762			Target Exon		5.0
440133	AI056255	Hs.133349	ESTs		5.0
445903	AI347487	Hs.132781	class I cytokine receptor	SS,TM,EF1BD	5.0
412940	BE295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	5.0
419269	AA235838		gb:zs41b04.s1 Soares_NhHMPu_S1	TM	5.0

TABLE 20B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408117	104000_1	AL138255 BE380045 AA047314 D82381 T18585 H64978 T10798
408215	10478_1	BE614290 AA307674 N35629 AA338538 AI193603 AA781096 AI680061 AI613258 AW276647 BE221263 AI348910 AI985031 AI090078 AI359617 AA666391 AI160210 AI446461 AI355345 AI343638 AI343640 AI275091 M78746 AW262795 AW250002 AA503756 AI934519 AW272086 N26520 AA626639
408270	1049980_1	AW177805 AW177895 AW177816 AW177901 BE141597 BE141584 AW177822 AW177818 AW177899
408294	1050553_1	BE141732 U75823 BE141331 AW178416 AW178430 BE141343 BE141298 BE141702 BE141285
408567	10663_1	S72921 NM_000614 X55889 X60542 X60477
409078	1098756_1	AW327515 AW327774 AW327571
409164	110421_1	AA706639 AA064707 AL036920 AI651598
409679	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
409832	115564_1	AW963293 AI866310 AA077791 AA362540
410445	120374_2	AA199830 AI143895 AW961629 AA322482
410471	1204721_1	T88872 AW749857
410895	1226051_1	AW809679 AW809678 AW810113 AW810182 AW809900 AW809851 AW810110 AW810228 AW810342 AW810181 AW809632 AW809745 AW810372 AW809681 AW809792 AW809806 AW810452 AW809675 AW809964 AW810033 AW810111 AW809846 AW809847 AW809717
411219	1236055_1	AW832917 AW832913 AW832906 AW832788 AW832915 AW832776
411298	1237955_1	AW835858 AW835836 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW835835 AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838
411426	1245515_1	BE141714 AW845993 AW845989
411456	1246706_1	AW847588 AW847716 AW847664 AW847592
411490	1247426_1	R39474 AW848420 R76943
411605	125123_2	AW006831 AA678298 R12579 W86152 AI123683 AA699780 AI672156 BE092587 AA094230 AI633815 AA526153 W86151
411758	1256751_1	AW860667 AW860665
412091	1276564_1	R06185 AW891805 AW901892 AW901895
412122	127838_2	AW852707 N57282 AA725075 AI703492 AW612137 AI696372 AI879394 AI653605 W26914
412128	1278726_1	AW894709 N78140
412173	1280870_1	T71071 AW902279 AW897608
412425	1293726_1	AW949156 AW949003 AW949008
412452	129707_1	AA215731 N48523 AA307559 AA130794 BE296746 BE378396 AA190411 AI904194 AA311805 AI356291 AA446714 AI818924 AI609152 AW771476 BE298184 AA295023 AA130708 AI078381 AA114156 AI198283 AA215665 AI201085 AI694848 AI077572 AA102778 AW016425 AI923123 AA577072 AI671
412777	132672_1	AI335773 AI288496 AA120880
412934	1337389_1	BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011406
413272	135718_1	AA127923 AA127846 AA534131 N53566 AA533669 AW511251 AI174441 AA127875 AI685293 AA127913 N72525 AW770386 N69010 AW070312 H80275 H80289 AA972923
413534	1375357_1	BE146961 BE146780 BE146788 BE146967 BE146774 BE146963 BE146907
413564	1376722_1	BE260120 BE148538
414347	1437406_1	BE275835 BE390063 BE388764 BE409101
414371	14388_8	AI905865 BE294801 BE562308 BE297957 AW157051 AI815883 AW162529 BE439610 AW157225 AW157210 AW162675 AW161998 AI816168 AW162599 AI816004 AI815820 AW162158 AW162339 M17733 AW157639 AI879416 BE258811 AW157436 AW162433 AW161633 AW162155 AW157410 AW157269 AW162
414391	1441921_1	BE409872 BE281460
414413	1443696_1	BE294877 BE294759
414593	1464909_1	BE386764 BE387560
414944	1509480_1	C15044 D80943 C15696
415126	1523506_1	D60945 D61346 D81568 D80539
415611	1540555_1	T26376 F12852 T75058
415886	1560411_1	Z42737 T08986 H07956
415958	1563222_1	H10942 Z42911 R60453
416233	158010_1	AA176633 AW961842 AA309418
416597	1603081_1	H66891 R98149 H68467
417739	1696198_1	Z43995 R12357 R34740
418184	172744_1	AA367375 AA486701 BE152479 BE152800 AW816961 AA214097
418304	173658_2	AA215702 AA368006 AA215703 BE066555 BE006876
419269	183444_1	AA235838 BE180775
419516	185533_1	H82550 N43802 AA243820 AL040762 N24315 U66692
420530	19446_1	AI218431 AA432232 AW183040 X86012 AA868831 AI191788 AA912999 AI204297 AI205744 AI218259 AA428596 AA993742 AA703660 AI018669 AA879431
421879	208649_1	AW959607 AA299654 AA579966
423790	232031_1	BE152393 AA330984 BE073904
424874	244523_1	AA347951 AI688463 AA883123
426221	26281_1	AB007881 U32581 AW131202 AW995994 W31964 N24261 AI033045 H98694 AW364848 AI222031 AA907216 AI215730 AA776981 AW473826 W31373
426358	265504_1	AA376438 AA376324 AW963848 AW834782
426576	269378_1	AA381720 AA382040 AW963564
427029	274544_1	AA397596 AI198827 AA435832
427326	277229_1	AI287878 AI804160 AA400787
427411	278474_1	AA402242 AA813659 AI150316 AA412054
428092	286920_1	AW879141 AA421182 AI734104 AI733923 AA430600
428304	289603_1	AI743177 AA425743 AI804283 AI743189
428948	29737_1	BE514362 AI879343 BE272870 BE616390 AW163444 AW161588 AW378754 AW238803 BE267205 BE047746 BE207213 BE312782 BE266301 BE266413 BE278348 BE280885 BE278833 BE281417 BE407786 BE378176 BE392818 AW377597 BE395951 BE393978 AW327483 BE394175 BE385795 BE275663 BE3
429398	303954_1	AA452239 AI262173 AI925886 AI469041 H96628 AI768463 AI671422 AI915624 AA766891 AA521087 AA814103 AW993151 AW005927
430168	313927_1	AW968343 AA468507 AI478223 AW513008 AI762122 AI554512 AA862642 AA468976
431082	327710_1	AA491600 AA491645 AI920986
431161	328713_1	AA493591 AA829120 AA533792
431424	333110_1	AI222969 AA806560 AA504839 AA805261
431627	33581_1	AW609720 AW609735 AA082767 N88831 R23418 N55837 BE549484 AW816584 AW816947 AW816897
432093	341283_1	H28383 AW972670 H28359 AA525808
432945	356589_1	AL043683 AA570698 AA907496 AL043682 AW362288
433168	360235_1	AI085436 AA579438 AA579002
433357	36402_1	T05639 AF024702

434315	383402_1	AW196508 AA884617 AA758108 AI126321 AA629291 AW196549 AI208031
434743	3925_1	AI363410 AI356019 H00141 T78748 AL049365 AL079911 AI750972 Z42602 AW452523 AI223826 AA215407 AI633829 AA292122 N42783 AW505595 AF086096 N90340 N63271 AA131836 AW607273 AA527132 T32315 AA421961 T34951 AW966080 M78807 N31947 AA521151 AA278866 AA044784 AA700
434796	393400_1	AA812046 AW974514 AA764999 AA649302
435186	402143_1	AL119470 AA669492 AI628351 AI263835 AL119498
435262	403605_1	AA677088 AI022246 AA677107
435339	404485_1	AI358300 AI762981 AA678073 AA988621
436094	414444_1	AI798701 AW008826 AA704731
436389	41894_1	AI811706 AW297940 AJ227887 AA875850 AA228803 AI610234 AI921618 AI768606 N37039 AA081104 BE172693 D56503 Z28585 T95651 AA292389 AA293502 N28751
436393	41903_1	AW022213 AI274032 AJ227898 AI160412 AI084451
437018	431333_1	AA889078 AA907263 AA742199
437050	432210_1	AA766420 AA743319 AW976442
437215	43473_1	AL117488 AL044479
437662	440374_1	AA765387 AA832241 AI222134 AI216405 AI685043
437834	443674_1	AA769294 AW749299 AW749302 AW749295 AW749304 AW749293 AW749298 AW749294 AW749288 AW749291 AW749297 AW749292 AW749296 AW749289 AW749287 BE535498
438118	450293_1	AW753311 AW663081 AA778411
438723	46392_1	M34429 M34431 M34432 M25802 AW938720
439034	46802_1	AF075083 H52291 H52528
439150	46919_1	AF086006 H64722 H65212 H66282
439469	47274_1	W69836 AF086287 W69657
440317	49187_1	BE561888 BE560615 BE562102
440546	496976_2	AI491994 AW139809 AA889258 AI700895
441358	515468_1	AW173212 AA983948 AI080705 AA931334
441523	519049_1	AW514263 AI567908 AI299828 AI299043 N51706 AA936483
441794	526289_1	AW197794 AW195867 AW197787 AA968466
442146	533972_1	R52599 T65201 F11984 F13186 AA977679 T77028 H12167
442318	538584_1	AI792199 AI733491 AA991378
442472	543371_1	AW806859 AW806852 AF049582
442780	551405_1	AI017521 AI017613 AW511133
442893	553987_1	H78133 H90849 AI023482
443952	586524_1	AI149106 AI500318 AI334156 AI093029 AI765679 AI769652 AI167308 AI128885
444406	605004_1	AI147237 AI800517
445099	629785_1	BE163341 AI207756 BE171477
445625	64558_1	BE246743 AA436942 AW024744 AW242177 AA975476 AW385185 R07536 R73462 AV654529 T57442 AI399986 R50073 R48743 AI769689 AI863005 AA317806 AI678000 AW189963 AI986207 AW471273 R73463 AI335104 AI590161 AI469257 AI954604 H21954 T25141 AA856793 R50074 AI708253 AI2
445631	6457_1	AK001822 AW860325 AA335296 AW965531 AW130957 AW193951 AI347975 AW081323 AW662527 AI343924 AI380749 AA938153 T66966 AI655000 AW418837 AI380485 AA410698 AI520726 BE501355 AI637925 AW779200 AI524755 AW593995 AI336927 AI336928 AI357036 R60592 H19058 R11124 T1
445837	652068_1	AI261700 AI793196 AI469160 AI793007
446780	692897_1	R31107 AI341136 AI653198 H04953
446790	693032_1	AW452105 AI341280 AI917445
447045	70510_1	AW392394 AW579531 AW382131 AA010316 BE146145 AW579562 AW579577 BE146152 BE146040 BE145972 BE146099 AW003280 AA868470 BE146306 T85009 AI087294 BE146299 BE146319 BE146307 W44912 AI703134 AW026017 BE382873 AA903733 AI655933 BE551223 AA847664 AW173582 AW57240
447128	70934_1	AI271898 BE048502 AI452509 AI244810 X84721 AI858001 AI553937 AA149853 H00719 AI765259 AW973696 F25787 F35749 AI568815 AW015380 AA554539 C00201 AA961610 AW059537 R77127
447904	741913_1	AW206303 AW207644 AI765705
448330	758690_1	AL036449 AW016705 AI492482
448993	79225_1	AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265 AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245 AA730380 AA394063 AA454
449324	804806_1	AI638706 BE550292 R11026
449495	808345_1	AI652833 AI695904 AW888916
450251	829987_1	BE080483 BE080416 AI689298
450536	837848_1	AI699529 BE161564 BE077251
450807	847591_1	AI739262 R28418
451045	85673_1	AA215672 AI696628 AA013335 H86334 AA017006
451752	8835_1	AB032997 N74056 BE467119 AW237035 AI141678 AA934774 AW978722 AI761408 H09497 AI934521 AA716567 H62600 AI479668 Z40632 AA832081 Z44858 H09496 BE395335 AW295901 BE465977 AI621269 BE465983 M79058 H62533 AA325444
452113	899664_1	AI859393 BE177742
453413	966269_1	AJ003294 AJ003315 AJ003293
453829	982731_1	AL138200 T71830 T71828
453904	986581_1	AW003821 AW027475 AW025661
454438	120132_1	AA224053 AA114150 AA214275 AA224027 T58431 AA211908 AA669657 AA199744 AA630511 AA164864 T58463 AA214394 AA161378 AA161386 AA205211 AA167824 AA084940 AA223625 AA191190 AA309486 AW961804
454453	1206827_1	AW752781 BE143749 AW752727 AW752559 AW752578 AW752584 R45742
454577	1225673_1	AW809272 AW809169 AW809179 AW809192 AW809166 AW809172 AW809191 AW809165 AW809197 AW809181 AW809237 AW809226 AW809250 AW809199 AW809259 AW809239 AW809273 AW809270 AW809147 AW809188 AW809245
454682	1228976_1	AW816029 AW813292 AW816156 AW813333 AW816159 AW813302 AW813344 AW813172
454718	1230532_1	AW815144 AW815150 AW861007
454756	1233646_1	AW819273 AW819283 AW819287 AW819281 AW819274 AW819282 AW819277 AW819286
454923	1245024_1	AW897236 AW845406
455035	1249762_1	AW851734 AW851676 AW851693 AW851713 AW851722 AW851616 AW851731 AW851618 AW851648 AW852215
455274	1272212_1	BE151622 BE151636 AW885648
455286	1273576_1	BE144384 AW887474 AW887403 BE144386
455557	1325974_1	AW995839 AW995907
455604	1337197_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
455679	1349914_1	BE066529 BE066274 BE066390 BE066356 BE066419 BE066345 BE066298 BE066292 BE066359
455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
455885	1380385_1	BE153524 BE153576 BE153583

456487	19270_1	AF064804 AA320309 N89343 AA564588 AF069734 AA349248 AW964366 T98541 AW511100 T98542 AW070452 AA013172 AI767005 T32140 W05727 T30969 T30970 N74883 AA903211 AI392796 AI434622 AA829283
457892	432926_1	AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698
457978	448900_1	AA776638 BE439540
458198	504834_1	AI286100 AA952934 AA918305
458644	670856_1	AW270149 AW664628 AI285912

TABLE 20C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400460	8389428	Plus	35559-36295
400500	9796136	Minus	120238-120495
400528	6981824	Plus	472381-472528,474170-474277,475328-475542,475878-476000
400668	8118719	Plus	121756-122043
400748	8119063	Plus	84237-84398
400762	8131616	Plus	7235-7605
400772	8131629	Minus	34896-35021,41078-41197
400833	8705148	Minus	187599-188138
400863	9798616	Plus	21575-22330
400906	9966290	Plus	112863-112989,120162-120286
400923	7637836	Minus	94518-94659
401121	8570296	Plus	57211-57525
401180	9438648	Minus	150981-152128
401203	9743387	Minus	172961-173056,173868-173928
401210	7712287	Plus	166969-167133,169760-169877,171563-171733
401215	9858408	Plus	103739-103919
401264	9797154	Plus	130810-130927,133367-133504
401278	9799936	Plus	98428-98573
401349	9930791	Plus	72440-73030
401402	7710964	Plus	75730-76077
401488	7341775	Plus	54523-54686,55364-55451,55737-55846,58047-58175,58261-58356
401507	7534110	Plus	71055-71259
401539	8072433	Minus	62028-62608
401553	8099284	Minus	83990-84161
401594	7230963	Plus	7997-8170
401674	7689903	Plus	138786-138927,139157-139298,139440-139599,139960-140159
401677	9965537	Minus	62856-63086,63603-63884
401722	7656694	Plus	143861-144054
401724	7656694	Plus	150063-150241
401822	6730824	Plus	88400-89959
401885	8140731	Plus	148234-148321,150365-150559
401935	3808091	Plus	46329-46473
401938	6102666	Plus	151891-152032
401984	4454511	Plus	103825-104024
402189	8576043	Minus	128318-129601
402197	8576113	Plus	199466-199585
402285	2689079	Minus	92386-92634
402365	9454515	Minus	70928-71185
402445	9796614	Plus	90925-91064,91172-91331
402501	9797862	Plus	8601-8876
402545	9838114	Minus	48547-48678,50604-50737,51384-51467
402651	7960391	Plus	174215-174380
402916	7406502	Minus	361-474,541-687
403003	5441423	Minus	79403-79560,79712-80021
403128	7331426	Plus	122884-123018,123134-123283,123372-123695,123779-123940,124059-124256
403672	7283286	Minus	96600-96881,96951-97280,97393-97594
403748	7658423	Minus	129503-130344
403885	7710403	Minus	53259-53524
403938	7711795	Plus	48636-48822
404001	8655948	Minus	137995-138317
404066	3367505	Minus	71040-71288
404149	7534008	Plus	121831-121951,124044-124150
404199	6010176	Minus	1669-2740
404311	8570412	Minus	149189-149303
404333	9802821	Minus	137948-138024,138111-138300
404365	9964977	Plus	50151-50319,50859-51098
404430	7407979	Plus	42921-43109
404438	6984205	Plus	63413-63553
404571	7249169	Minus	112450-112648
404596	9958262	Minus	104807-105043
404676	9797204	Minus	56167-56342,58066-58189,58891-59048,60452-60628
404710	9801097	Minus	45190-45339,47509-47622,48137-48264,48805-48946,50073-50345,51467-51588
404752	7109522	Minus	120168-120326
404807	4165210	Minus	124246-124422
404956	7387343	Plus	55883-56203
405085	8072509	Minus	44045-44230
405113	8096927	Plus	170073-170894
405143	9438278	Plus	5894-5983,7355-7427
405159	9966252	Plus	79659-79804

405211	6692345	Minus	31340-32609
405247	7249301	Minus	65578-65778,68088-68234
405346	2981263	Plus	101982-102171
405366	2182280	Plus	22478-22632
405371	2078469	Minus	47657-47766,48461-48596
405375	1552539	Plus	11646-12050,12207-12485
405376	1552533	Plus	28875-29099
405473	8439781	Plus	153074-153343,154501-154598,156879-156999,158863-159051,159910-160053,161109-161229,163035-163131,165163-165259,165868-166003,167375-167552,169252-169364,171127-171281
405474	8439781	Plus	172005-172175
405557	1621108	Plus	39883-40047
405637	6289229	Plus	189852-189978
405770	2735037	Plus	61057-62075
405928	7717155	Minus	2923-3209
405931	6758795	Minus	148233-148705
405939	6758795	Plus	170500-170654
406109	9127147	Minus	58328-58485
406230	4760409	Plus	71716-72515
406284	7549620	Plus	74002-74199
406299	5686278	Minus	35655-36119
406301	8575868	Plus	57291-57494
406373	9256130	Plus	188922-189152
406495	7711328	Minus	174661-174978
406575	7711679	Plus	142034-142473

Table 21A lists about 933 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0, the "average" ovarian cancer level was set to the 96th percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 75th percentile value amongst variou non-malignant tissues, the "average" ovarian cancer value was greater than or equal to 400 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., Ig, fn3, efg, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

TABLE 21A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UG ID: Unigene number
Title: UniGene gene title
Pred. Protein Dom.: Predicted protein domain
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UG ID	Title	Pred. Protein Dom.	R1
407223	H96850		gb:yw03b12.s1 Soares melanocyt	SS,TM,SS,TM,DDOST_48kD	58.9
421296	NM_002666	Hs.103253	perilipin	perilipin,SS	47.6
430281	AI878842	Hs.237924	CGI-69 protein	mito_carr,SS,TM	46.7
410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ldl_recept_a,trypsi	41.0
431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH,SS,LIM,Troponin	37.1
428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	35.6
438424	AI912498	Hs.25895	hypothetical protein FLJ14996	SS,TM	35.3
450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS	34.4
437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,zf-DHHC	33.9
452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	32.5
422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS,TM,pkinase,fn3,ig	30.5
452849	AF044924	Hs.30792	hook2 protein	bZIP,SS,AhpC-TSA	29.6
407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB,SS	28.2
416819	U77735	Hs.80205	pim-2 oncogene	pkinase,SS,TM,OTU,K_tetra	27.9
430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	27.7
427725	U66839	Hs.180533	mitogen-activated protein kina	pkinase	27.5
454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	27.2
445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,lipoc	26.8
452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin	26.5
419451	AI907117	Hs.90535	syntaxin binding protein 2	Sec1,SS,TM	25.1
424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG,SS,TM,MAPEG	25.1
407893	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	25.0
412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand,SS,CAP_GLY	24.4
430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	24.3
444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,laminin_G,EGF	24.0
413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	23.1
438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	23.0
429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	23.0
422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase,SS,Ets	22.4
427899	AA829286	Hs.332053	serum amyloid A1	SS,SAA_proteins,SS,SAA_pr	22.2
407117	AA146625		gb:zo71c07.s1 Stratagene pancr	SS	21.3
402916			ENSP00000202587*:Bicarbonate t	HCO3_cotransp,SS	20.8
425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase,SS,TM	20.7
422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.6
442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	20.1
453157	AF077036	Hs.31989	DKFZP586G1722 protein	SS,Tropomyosin	20.0
422179	AF091619	Hs.112667	dynein, axonemal, intermediate	WD40,SS	20.0
419444	NM_002496	Hs.90443	Target CAT	fer4,SS,TM,V_ATPase_sub_a	19.5
416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rrm,SS	19.2
434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	19.1
411813	NM_014931	Hs.72172	KIAA1115 protein	SS,TM,Y_phosphatase	18.9
422305	AI928242	Hs.293438	ESTs, Highly similar to AF1984	SS	18.8

419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS	18.6
406663	U24683		Immunoglobulin heavy constant	SS	18.5
429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidored_q6,SS,TM,rrm	18.5
425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	GST_C,GST_N,Tropomyosin,S	18.4
447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	18.4
413343	BE392026	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	18.2
450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	17.7
427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,Integrin_B,	17.6
443780	NM_012068	Hs.9754	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	17.2
421612	AF161254	Hs.106196	8D6 antigen	ldl_recept_a,SS,TM	17.1
444607	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PH,PI-PLC-Y,C	16.7
406621	X57809	Hs.181125	immunoglobulin lambda locus	SS	16.6
443496	AJ006973	Hs.9482	target of myb1 (chicken) homol	VHS,GAT,TM,Heme_oxygenase	16.6
440104	AA132838	Hs.239894	hypothetical protein MGC2803	SS,DS	16.3
427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF,late_protein_L2,SS,GS	16.2
445625	BE246743		hypothetical protein FLJ22635	SS,TM	16.1
427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	15.9
423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	15.7
409017	T86957	Hs.272299	hypothetical protein RP4-622L5	SS,TM	15.6
428167	AA770021	Hs.16332	ESTs	SS,ig,fn3	15.5
420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	15.5
400460			C11002253*:gi|129091|sp|P23267	SS,TM,SCAN,zf-C2H2,KRAB	15.4
407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	15.4
406918	M88357		gb:Homo sapiens DNA-binding pr	zf-C2H2,SS	15.4
435158	AW663317	Hs.65588	DAZ associated protein 1	rrm,SS,rrm	15.3
407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	15.3
421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,tRNA-synt_1,GST_C,G	15.1
402365			Target Exon	SS,SS,TM,ig	14.9
450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	14.8
427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	14.6
432872	AI908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	14.5
439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	14.5
416897	M78146	Hs.324700	hypothetical protein MGC2663	SS	14.3
447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS,Peptidase_C2	14.2
431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	14.0
447544	AA401573	Hs.288284	hypothetical protein FLJ22378	SS,TM	14.0
417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	13.8
436127	W94824	Hs.11565	RIKEN cDNA 2010100O12 gene	Corona_7,SS,TM	13.8
412623	R28898	Hs.74170	metallothionein 1E (functional	SS,TM,metalthio,DEAD,meta	13.7
448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	13.5
453367	AW732847	Hs.70573	PKCI-1-related HIT protein	SS,TM	13.5
431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	13.2
408724	AI685842	Hs.294143	ESTs, Weakly similar to T22914	SS,pkinase,tubulin	13.2
423464	NM_016240	Hs.128856	CSR1 protein	Collagen,SS	13.1
428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	13.0
436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	12.9
438857	AI627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	12.8
444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	12.8
427527	AI809057	Hs.153261	immunoglobulin heavy constant	SS,TM,ig	12.6
430168	AW968343		DKFZP434I1735 protein	SS,TM,efhand,efhand	12.5
437543	H16443	Hs.7117	glutamate receptor, ionotropic	SS,TM,lig_chan,ANF_recept	12.4
413711	AW291765	Hs.75486	heat shock transcription facto	NA,SS,E2F_TDP	12.3
422625	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin	12.2
443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosin,SS,TM	12.1
407143	C14076	Hs.332329	EST	SS,TM	12.1
424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema	12.1
425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	12.0
421572	AA531607		hypothetical protein FLJ22678	SS,TM,TGF-beta,ASC	12.0
447946	AI566164	Hs.165827	ESTs	SS,PTN_MK,7tm_1,DAGKc,DAG	11.9
425954	AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	11.7
427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	11.7
427397	AI929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RmaAD,SS,efhand	11.7
424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase,SS,Atrophin-1,Atr	11.7
417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	11.6
447451	AI379925	Hs.207525	ESTs	SS,pkinase,PH,pkinase_C	11.5
410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23	11.4
430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,ig	11.3
419390	AI701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	11.3
422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	11.3
422178	AL122083	Hs.112645	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	11.2
450122	BE313765	Hs.343443	ESTs, Weakly similar to I38022	SS,TM,Y_phosphatase,LON,A	11.1
453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	11.1
444744	BE394732	Hs.147562	ESTs	SS	10.9
423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_recp,pkin	10.9
417116	Z43916	Hs.7634	hypothetical protein FLJ12287	SS,TM,filament,IF_tail	10.9
406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	10.8
450593	AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,lactam	10.7
406837	R70292	Hs.156110	Immunoglobulin kappa constant	SS	10.7
452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	10.7
440150	AW975738	Hs.7001	Homo sapiens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	10.6
418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	10.6
414313	NM_004371	Hs.75887	coatomer protein complex, subu	WD40,SS,WD40,Ribosomal_S2	10.6
420307	AW502869	Hs.66219	ESTs	SS,TM	10.6

414918	AI219207	Hs.72222	hypothetical protein FLJ13459	SS,TM,efhand	10.6
446562	BE272686	Hs.15356	hypothetical protein FLJ20254	hormone,SS,pfkB	10.5
419846	NM_015977	Hs.285681	Williams-Beuren syndrome chrom	SS,HLH,SS,TM,WD40	10.4
453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	10.4
438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	10.3
431275	T56571	Hs.10041	ESTs	SS,HLH	10.3
407241	M34516		gb:Human omega light chain pro	SS,ig,PH,ig,PH	10.3
441238	AI372555	Hs.322456	hypothetical protein DKFZp761D	homeobox,SS,TM,Rho_GDI,th	10.3
436325	AL390088	Hs.7393	hypothetical protein from EURO	SS,Synapsin_C,SS	10.3
435605	AF151815	Hs.4973	hypothetical protein	SS,TM,SS,TM,ABC_tran,ABC_	10.3
444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	10.3
425597	U28694	Hs.158324	chemokine (C-C motif) receptor	7tm_1	10.3
415200	AL040328	Hs.78202	SWI/SNF related, matrix associ	SNF2_N,helicase_C,bromodo	10.2
446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	Nol1_Nop2_Sun,SS,SNF2_N,h	10.2
414874	D26351	Hs.77515	inositol 1,4,5-triphosphate re	TM,RYDR_ITPR,ion_trans,MI	10.2
423524	AF055989	Hs.129738	potassium voltage-gated channe	ion_trans,K_tetra,thaumat	10.2
434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	10.2
406836	AW514501	Hs.156110	immunoglobulin kappa constant	SS	10.1
420233	AA256714	Hs.194864	hypothetical protein FLJ22578	SS	10.1
427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU p	SS,F5_F8_type_C,EGF,TGT	10.1
427672	AA356615	Hs.336916	death-associated protein 6	SS,BTB,abhydrolase_2,RasG	10.0
423218	NM_015896	Hs.167380	BLu protein	zf-MYND,SS,TM,Glyco_hydro	10.0
403028			Target Exon	SS,trefoil	10.0
412790	NM_014767	Hs.74583	KIAA0275 gene product	kazal,thyroglobulin_1,zf-	10.0
419823	AW271708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS,TM	10.0
433886	AA613596	Hs.28412	ESTs	SS	9.9
428092	AW879141		ESTs	SS,TM	9.8
450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	9.7
420423	AA827718	Hs.88218	ESTs	SS	9.7
452302	AF173867	Hs.28906	glucocorticoid modulatory elem	SAND,SS	9.7
444681	AJ243937	Hs.288316	chromosome 6 open reading fram	notch,EGF,ank,GoLoco,SS,T	9.7
414249	AI797994	Hs.279929	gp25L2 protein	SS,TM,EMP24_GP25L,SS,TM,G	9.6
424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK,SS,TM,fn3,ig,R	9.6
438627	AI087335	Hs.123473	ESTs	TM,Reticulon	9.6
407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	9.6
441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	9.6
409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	9.6
424487	T08754	Hs.6259	KIAA1698 protein	SS,SS,TM,Glyco_hydro_31,G	9.5
444633	AF111713	Hs.286218	junctional adhesion molecule 1	ig,SS,TM,HLH	9.4
427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase,SS,TM,synaptobrev	9.4
450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	9.4
415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,SS,TM,CH,Filam	9.4
400201			NM_006156*:Homo sapiens neural	ubiquitin,SS,TM,Transglut	9.4
454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	9.4
421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,rrm,zf-RanBP,rrm,GA	9.4
445143	U29171	Hs.75852	casein kinase 1, delta	pkinase,SS	9.4
407507	U73799		gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.4
450883	NM_001348	Hs.25619	death-associated protein kinas	pkinase,GTP_EFTU,EFG_C,GT	9.4
411674	AW861123		gb:RC3-CT0297-120200-014-a05 C	SS	9.3
414625	AA335738	Hs.76686	glutathione peroxidase 1	GSHPx,SS,ras,HLH	9.3
456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	9.3
445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	9.2
407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	9.1
412338	AA151527	Hs.69485	hypothetical protein FLJ12436	SS,TM,TIG,Sema,PSI	9.1
439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_Ib,Lipase_GDSL,SS,	9.1
412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN	SS,TM	9.1
443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran,SS	9.1
448984	AW751955	Hs.22753	hypothetical protein FLJ22318	SS	9.0
418776	AI401004	Hs.88411	lymphocyte antigen 117	SS,TNF,TNF	9.0
418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	9.0
419244	AI436567	Hs.89761	ATP synthase, H transporting,	ATP-synt_DE,SS,rrm,Ephrin	8.9
451855	R54913	Hs.175804	ESTs	SS,TM,vwa	8.9
424825	AF207069	Hs.153357	procollagen-lysine, 2-oxogluta	2OG-FeII_Oxy,Glycos_trans	8.9
447374	AF263462	Hs.18376	KIAA1319 protein	SS,Myosin_tail,M	8.9
430167	Y08976	Hs.234759	FEV protein	Ets,SS,crystall	8.8
409936	AK001691	Hs.57655	hypothetical protein FLJ10829	SS,TM	8.7
437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	8.7
430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	8.7
424919	BE314461	Hs.153768	U3 snoRNP-associated 55-kDa pr	WD40,SS,KH-domain	8.7
414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	8.7
433333	AI016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina	8.7
423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	8.7
419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI,SS,CDK5_activator	8.7
420160	AI492840		ESTs	SS,TM	8.6
421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	8.6
447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	8.6
417193	AI922189	Hs.288390	hypothetical protein FLJ22795	SS	8.6
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	8.5
458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat hom	ras,SS,Peptidase_M10,hemo	8.5
406868	AA505445	Hs.300697	immunoglobulin heavy constant	SS,TM,ig	8.3
434105	AW952124	Hs.13094	presenilins associated rhombol	TM,Rhomboid,SS,TM	8.3
421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	8.3
421707	NM_014921	Hs.107054	lectomedin-2	Latrophilin,OLF,7tm_2,Gal	8.2
453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	SS,TM,lipoxygenase,PLAT,s	8.2

456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327,	SS,PK,PK_C,myosin_head,Rh	8.2
421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila)	homeobox,SS	8.2
409829	M33552	Hs.56729	lymphocyte-specific protein 1	Caldesmon,SS,Ribosomal_S2	8.1
444341	AI142027	Hs.146650	ESTs	SS,TM,Reprolysin,Pep_M12B	8.0
413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR,SS	8.0
436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,pkinase,Activin_rec	8.0
420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697	SS,bZIP_Maf	8.0
431493	AI791493	Hs.129873	ESTs, novel cytochrome P450	SS,p450,SS	7.9
447598	AI799968	Hs.199630	ESTs	SS,TM	7.9
415758	BE270465	Hs.78793	protein kinase C, zeta	pkinase,DAG_PE-bind,pkina	7.8
457022	AW377258		gb:MR2-CT0222-261099-003-a10 C	SS,Ribosomal_L7Ae	7.8
426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr	7.8
432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.8
441084	W24563	Hs.9911	hypothetical protein FLJ11773	SS,TM,hormone_rec,zf-C4	7.8
424443	AI751281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	7.7
424198	AB029010	Hs.143026	KIAA1087 protein	SS,TM,Na_Ca_Ex,Calx-beta,	7.6
430513	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	7.6
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,Ig	7.6
432891	AF161483	Hs.279761	HSPC134 protein	SS,TM,ubiquitin,Transglut	7.5
432234	AA531128	Hs.115803	ESTs	SS	7.5
453485	BE620712	Hs.33026	hypothetical protein PP2447	SS,TM	7.5
441327	AK001706	Hs.7778	hypothetical protein FLJ10751	SS,TM,7tm_1	7.5
436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM	7.5
418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	7.5
457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	7.5
437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	7.5
425428	AL110261	Hs.157211	DKFZP586B0621 protein	C1q,Collagen,SS	7.4
431934	AB031481	Hs.272214	STG protein	SS	7.4
418349	NM_001383	Hs.84183	diptheria toxin resistance pro	Diphthamide_syn,SS	7.4
430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	7.3
421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	7.3
412841	AI751157	Hs.101395	hypothetical protein MGC11352	SS,TM	7.3
418313	BE244231	Hs.84038	CGI-06 protein	SS,wap	7.3
429367	AB007867	Hs.278311	plexin B1	Sema,PSI,TIG,SS,TM,TIG,Se	7.3
418837	U48263	Hs.89040	prepronociceptin	Opiods_neuropep,SS	7.2
423015	U18548	Hs.123034	G protein-coupled receptor 12	TM	7.2
440188	AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK,SS,TM	7.2
421975	AW961017	Hs.6459	hypothetical protein FLJ11856	SS,TM,ACAT	7.2
423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	7.2
446143	BE245342	Hs.306079	sec61 homolog	secY,SS,TM	7.2
417704	NM_001747	Hs.82422	capping protein (actin filamen	Gelsolin,SS,Gelsolin	7.2
440869	NM_014297	Hs.7486	protein expressed in thyroid	lactamase_B,SS,XRCC1_N,BR	7.1
435099	AC004770	Hs.4756	flap structure-specific endonu	XPG_N,XPG_I,5_3_exonuclea	7.1
438856	N40027	Hs.7473	ESTs	SS,TM,connexin	7.1
426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	pkinase,pkinase	7.1
418373	AW750770	Hs.84344	CGI-135 protein	SS,TM,PMP22_Claudin,2OG-F	7.1
445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	7.1
421748	NM_014718	Hs.107809	KIAA0726 gene product	cadherin,TM,TPR	7.1
413837	AW163525		titin-cap (telethonin)	SS,Methyltransf_3	7.0
426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	pkinase,SS,UCH-2,UCH-1,rr	7.0
409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	7.0
424251	AA677466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,helicase_C,brom	7.0
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	7.0
428156	BE269388	Hs.182698	mitochondrial ribosomal protei	SS	7.0
459255	AI493244	Hs.239500	hypothetical protein MGC13114	SS	7.0
441323	AA928413	Hs.159089	ESTs, Weakly similar to ALU7_H	SS,Peptidase_C1,zf-C2H2	6.9
455928	BE170313		gb:QV4-HT0536-040500-193-g02 H	SS	6.9
420856	BE513294	Hs.205736	HLA class II region expressed	kazal,SS,TM,ig,pkinase	6.9
421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	6.9
442296	NM_007275	Hs.8186	lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	6.9
445937	AI452943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2,SS,TM,tsp_	6.9
439732	AW629604	Hs.167641	hypothetical protein from EURO	SS,TM,SS,TM,A2M,A2M_N,NTR	6.8
429542	AF038660	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2,Ig,SS,TM,A	6.8
420190	AI816209	Hs.95867	hypothetical protein EST00098	SS,dynamin_2,dynamin,PH,G	6.8
408215	BE614290		syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	6.7
410277	R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	6.7
419667	AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	6.7
448677	AI560769		ESTs	SS,TM	6.7
425228	NM_005253	Hs.301612	FOS-like antigen 2	bZIP,SS	6.6
432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	6.6
421864	BE387198	Hs.108973	dolichyl-phosphate mannosyltra	SS,TM,SS,TM	6.6
429962	M69113	Hs.226795	glutathione S-transferase pi	GST_C,GST_N,SS,efhand	6.6
406867	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	6.6
426068	AF029778	Hs.166154	jagged 2	DSL,EGF,vwc,granulin,SS,T	6.5
419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bi	6.5
424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK,SS,TM,7tm_	6.5
417903	NM_002342	Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6,SS	6.5
423876	BE502835	Hs.15463	Homo sapiens, clone IMAGE:2959	SS,efhand	6.4
433439	AA431176	Hs.133230	ribosomal protein S15	TM,SS,TM,TPR,ras	6.4
441379	AW175787	Hs.334841	selenium binding protein 1	SS,RFX_DNA_binding	6.4
432968	BE614192	Hs.279869	melanoma-associated antigen re	SS,TM,RGS,DIX	6.4
456863	T16837	Hs.4241	ESTs	fusion_gly,homeobox,TM	6.4
432269	NM_002447	Hs.2942	macrophage stimulating 1 recep	pkinase,Sema,PSI,TIG,A4_E	6.4
425676	AW410656	Hs.159161	Rho GDP dissociation inhibitor	Rho_GDI,homeobox,SS,Cytid	6.4

443420	R06846	Hs.191208	ESTs	SS	6.4
436322	AL355092	Hs.120243	parvin, gamma	CH,SS,TM,CTF_NFI	6.4
440088	BE559877	Hs.183232	hypothetical protein FLJ22638	SS,zf-C3HC4,SPRY,zf-B_box	6.4
447665	BE044245	Hs.30011	hypothetical protein MGC2963	SS,TM	6.3
431785	AA292385	Hs.268763	Breakpoint cluster region prot	BAF,kazal,TM	6.3
422714	AB018335	Hs.119387	KIAA0792 gene product	DUF221,SS,TM,TGFb_propept	6.3
434916	AF161383	Hs.284207	Homo sapiens, Similar to RIKEN	TM	6.3
414551	AI815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH,Peptidase_U7,SS,TM	6.3
413254	U40272	Hs.75253	isocitrate dehydrogenase 3 (NA	isodh,SS	6.3
458367	AA088470	Hs.83135	Homo sapiens, Similar to RIKEN	SS,tRNA-synt_2d	6.3
415010	NM_004203	Hs.77783	membrane-associated tyrosine-	pkinase,SS,PMP22_Claudin	6.3
410076	T05387	Hs.7991	ESTs	SS	6.3
412940	BE295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	6.2
440042	AI073387	Hs.133898	ESTs	SS	6.2
414023	BE243628		gb:TCBAP1D1053 Pediatric pre-B	SS	6.2
414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C,SS,	6.2
446662	NM_013323	Hs.15827	sorting nexin 11	PX,SS	6.2
409882	AJ243191	Hs.56874	heat shock 27kD protein family	HSP20,SS,TM,zf-C2H2,BTB,E	6.2
414576	AK000405	Hs.76480	ubiquitin-like 4	ubiquitin,SS,TM,G6PD,G6PD	6.2
447507	H59696	Hs.18747	POP7 (processing of precursor,	SS,TM,WD40,vwd,MAM,EPO_TP	6.2
453447	AW771318	Hs.326586	hypothetical protein MGC11134	SS,TPR	6.1
435968	AW161481	Hs.111577	integral membrane protein 3	TM	6.1
424441	X14850	Hs.147097	H2A histone family, member X	histone,CBFD_NFYB_HMF,SS,	6.1
434558	AW264102	Hs.39168	ESTs	SS,TM,LRRCT,LRR	6.1
434202	BE382411	Hs.3764	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
432183	AW151952	Hs.46679	hypothetical protein FLJ20739	SS	6.0
444416	AW288085	Hs.11156	hypothetical protein	zf-C3HC4,SpoA,PHD,TM,syna	6.0
447205	BE617015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRRCT,Sema	6.0
407704	BE315072	Hs.78768	malignant cell expression-enha	TM,MBOAT,SS,TM	6.0
453190	AB002354	Hs.32312	KIAA0356 gene product	PH,PHD,RUN,SS	6.0
439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Ham1p_like,SS	6.0
449514	AW970440	Hs.23642	protein predicted by clone 236	SS,PX,arf,lipocalin,PHD,z	6.0
432805	X94630	Hs.3107	CD97 antigen	SS,TM,7tm_2,GPS,EGF,SS,TM	6.0
414362	AI347934	Hs.75932	N-ethylmaleimide-sensitive fac	NSF,SS,TM	6.0
417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0
427988	AA789333	Hs.181349	hypothetical protein 628	SS,SS	6.0
423473	H49104	Hs.129888	hypothetical protein FLJ14768	zf-C2H2,SS,rrm,ENTH	6.0
406773	AA812424	Hs.76067	heat shock 27kD protein 1	HSP20,SS	5.9
409938	AW974648		gb:EST386752 MAGE resequences,	SS,Adap_comp_sub,GYF	5.9
424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	pkinase,SH3	5.9
453082	H18835	Hs.31608	hypothetical protein FLJ20041	SS,TM,ion_trans	5.9
452094	AF049105	Hs.27910	centrosomal protein 2	bZIP,5_3_exonuclease,M,SS	5.9
451524	AK001466	Hs.26516	hypothetical protein FLJ10604	SS,SS,TM,pkinase,pkinase_	5.9
427438	AW328515	Hs.178011	hypothetical protein FLJ20257	SS,TM	5.9
439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_H	SS,PWWP,TSC22	5.9
440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE,Ribosomal_S17,	5.9
417334	AA337572	Hs.157240	hypothetical protein MGC4737	SS,TM,ion_trans	5.9
425976	C75094	Hs.334514	NG22 protein	SS,TM,pkinase,SH2,SH3,BNR	5.8
433173	Z35093	Hs.3196	surfeit 1	SURF1,SS,TM,SURF1,SURF4	5.8
437891	AW006969	Hs.6311	hypothetical protein FLJ20859	TM,SET	5.8
410239	AI568350	Hs.61273	hypothetical protein MGC2650	SS,ART,TM	5.8
458060	R95860	Hs.293629	hypothetical protein MGC3121	SS	5.8
409591	AA532963	Hs.9100	Homo sapiens cDNA FLJ13100 fis	SS,TM,LIM,homeobox	5.8
409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp4	SS,ABC_tran,SS,TM	5.8
450778	U81375	Hs.25450	solute carrier family 29 (nucl	Nucleoside_tran,SS,TM,HSP	5.8
423612	NM_002067	Hs.1686	guanine nucleotide binding pro	G-alpha,arf,SS,G-alpha	5.8
422701	NM_014699	Hs.119273	KIAA0296 gene product	zf-C2H2,GST_C,PHD,SS,TM,H	5.8
412958	BE391579	Hs.75087	Fas-activated serine/threonine	SS,pkinase	5.8
436957	AA902488	Hs.122952	ESTs	SS,DAGKc,DAGKa,RA,DAG_PE-	5.8
423158	H97991	Hs.193313	Target CAT	MoaA_NifB_PqqE,SS,TM	5.8
414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	5.8
420904	AL035964	Hs.100221	nuclear receptor subfamily 1,	hormone_rec,zf-C4,SS,DNA_	5.7
410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA	pkinase	5.7
420508	AJ270993	Hs.98428	homeo box B6	homeobox,SS,homeobox,home	5.7
435593	R88872	Hs.4964	DKFZP586J1624 protein	Herpes_HEPA,SS	5.7
433064	D79991	Hs.30002	SH3-containing protein SH3GLB2	TM	5.7
451920	AA224483	Hs.27239	DKFZP586K0524 protein	SS,TM,SS,TM	5.7
453054	AI878908	Hs.31547	Target CAT	SS	5.7
415117	AF120499	Hs.78016	polynucleotide kinase 3'-phosp	Viral_helicase1,SS,Amino_	5.7
413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3,ig,Y_phosphatase,SS,T	5.7
425246	AI085561	Hs.155321	serum response factor (c-fos s	SRF-TF,flavodoxin,SS,TM,p	5.7
433271	BE621697	Hs.14317	nucleolar protein family A, me	SS,TM	5.7
448484	BE613340	Hs.334725	Homo sapiens, Similar to RIKEN	TM,SS,TM,Kunitz_BPTI	5.7
449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-	neur,SS,zf-C2H2,DNase_II	5.7
449181	X96783	Hs.23179	synaptotagmin V	C2,SS,TM,Y_phosphatase,Tr	5.6
414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	ATP-synt_C,SS,TM,pkinase	5.6
424964	AW161271	Hs.153961	ARP1 (actin-related protein 1,	actin,SS	5.6
415193	AL048891	Hs.12185	hypothetical protein MGC14333	SS,TM,aminotran_1_2,LRR	5.6
407754	AA527348	Hs.288967	Homo sapiens cDNA FLJ14105 fis	SS,TM,SS,TM,TSPN,tsp_3,SE	5.6
413049	NM_002151	Hs.823	hepsin (transmembrane protease	trypsin,SS,TM,ATP1G1_PLM_	5.6
454252	H50256	Hs.63236	ribosomal protein S15a	SS	5.6
431787	AW972024	Hs.343661	ret finger protein	SS,WD40,pkinase	5.6
431607	AB033097	Hs.183669	KIAA1271 protein	SS,TM	5.6
406782	AA430373		gb:zw20f11.s1 Soares ovary tum	SS	5.6

444364	AL137294	Hs.10964	hypothetical protein FLJ22351	SS,TM,pkinase	5.6
427834	AA506101	Hs.285813	hypothetical protein FLJ11807	SS,TM	5.5
443759	BE390832	Hs.134729	FXYD domain-containing ion tra	SS,TM,ATP1G1_PLM_MAT8,ATP	5.5
416322	BE019494	Hs.79217	pyrroline-5-carboxylate reduct	P5CR,Octopine_DH_N,SS,thi	5.5
406673	M34996	Hs.198253	major histocompatibility compl	SS,TM,MHC_II_alpha,ig,SS,	5.5
415351	U44755	Hs.78403	small nuclear RNA activating c	SS,TM,pkinase	5.5
411030	BE387193	Hs.67896	7-60 protein	SS,Collagen,Collagen	5.5
410653	BE383768	Hs.65238	95 kDa retinoblastoma protein	zf-C3HC4,SS,SNF2_N,helica	5.5
433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, y	HMA,SS,TM	5.5
437741	BE561610	Hs.5809	putative transmembrane protein	SS,TM,SS,TM,RA,VPS9,SH2	5.5
421883	X55079	Hs.1437	glucosidase, alpha; acid (Pomp	trefoil,Glyco_hydro_31,SS	5.4
427361	AW732480	Hs.7678	cellular retinoic acid-binding	SS,TM,aminotran_1_2,LRR	5.4
411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF,SS,TM	5.4
457313	AF047002	Hs.241520	transcriptional coactivator	SS,rrm,SS,Cytidylyltransf	5.4
428345	AI242431	Hs.118282	PAP-1 binding protein	SS,TM	5.4
434845	BE267057	Hs.325321	hypothetical protein R32184_1	SS,TM,CH,calponin,ARID	5.4
427162	AB011133	Hs.173864	KIAA0561 protein	SS,pkinase,PDZ,SS,SH2,Rho	5.4
447402	H54520	Hs.18490	hypothetical protein FLJ20452	SS,TM	5.4
433676	AW371389	Hs.250173	hypothetical protein FLJ13158	SS	5.4
424373	AJ133798	Hs.146219	copine VII	C2,SS	5.4
423402	BE167615	Hs.141556	Homo sapiens cDNA FLJ12976 fis	SS	5.4
409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch,SS,TM	5.4
450184	W31096	Hs.237617	Homo sapiens, clone IMAGE:3447	SS	5.3
431629	AU077025	Hs.265827	interferon, alpha-inducible pr	pkinase,SH2,SH3	5.3
430413	AW842182	Hs.241392	small inducible cytokine A5 (R	IL8,SS	5.3
440333	AI378424	Hs.288761	hypothetical protein FLJ21749	SS,TM,IP_trans,pkinase,pk	5.3
424927	AW973666	Hs.153850	hypothetical protein C321D2.4	SS,TM	5.3
412276	BE262621	Hs.73798	macrophage migration inhibitor	MIF,SS,TM,MIF,sugar_tr	5.3
416181	AA174126	Hs.332163	ESTs	SS,TM,GalP_UDP_transf,Gal	5.3
440609	AI287585	Hs.7301	G protein pathway suppressor 2	SS,Acyl-CoA_dh,Acyl-CoA_d	5.3
435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	SS,HLH,Myc_N_term,Myc-LZ,	5.2
421139	AW953933	Hs.301372	KIAA1552 protein	SS,TM	5.2
453449	W16752	Hs.32981	sema domain, immunoglobulin do	SS,Sema,ig,PSI,SS,TM,G-al	5.2
414411	X54079	Hs.76067	heat shock 27kD protein 1	HSP20,SS	5.2
440906	AW161556	Hs.240170	hypothetical protein MGC2731	SS,TM,Furin-like,pkinase,	5.2
421899	AJ011895	Hs.109281	Nef-associated factor 1	Virus_HS,bZIP,G-gamma,Myo	5.2
439473	AI215529	Hs.144787	ESTs	SS	5.2
451585	AK001171	Hs.326422	hypothetical protein MGC4549	SS,Metallophos	5.2
407191	AA608751		gb:ae56h07.s1 Stratagene lung	SS,Peptidase_C1	5.2
427515	T79526	Hs.179516	integral type I protein	EMP24_GP25L,SS	5.2
405325			C14000786*:gi|7023514|dbj|BAA9	SS	5.2
434119	AF193844	Hs.3758	COP9 complex subunit 7a	SS	5.1
413052	BE249841		gb:600942857F2 NIH_MGC_15 Homo	TM,SS,TM	5.1
445109	AF039916	Hs.12330	ectonucleoside triphosphate di	SS,TM,GDA1_CD39,SS,TM,pho	5.1
409323	H28855	Hs.53447	Homo sapiens mRNA; cDNA DKFZp7	TPR,SS,TM,pkinase,ig	5.1
438707	L08239		amino acid system N transporte	SS,TM,ACAT,MBOAT,SS,TM,TB	5.1
442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank,SS,TM,HHH,ig	5.1
420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535	SS	5.1
436576	AI458213	Hs.77542	ESTs	SS,TM,7tm_1,DnaJ	5.1
439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	AAA,DnaB,UPF0079,SS,Cys_k	5.1
418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH,SS,TM,aminotran_3,ABC	5.1
414849	AW372721	Hs.291623	ESTs, Weakly similar to unname	TM,pkinase	5.1
425743	BE396495	Hs.159428	BCL2-associated X protein	Bcl-2,SS,ferritin,Bcl-2,e	5.1
418231	AA326895	Hs.83848	triosephosphate isomerase 1	TIM,SS,TM,zf-UBP,UCH-2,UB	5.0
419238	AW959538	Hs.321214	hypothetical protein DKFZp564D	SS,TM,WH2	5.0
441917	AI989925	Hs.24891	ESTs, Highly similar to unknow	SS,TM,Ammonium_transp	5.0
437617	AI026701	Hs.5716	KIAA0310 gene product	SS,zf-C3HC4,Peptidase_M16	5.0
412867	AU076861	Hs.74637	testis enhanced gene transcrip	UPF0005,SS,TM	5.0
419579	W49529	Hs.296200	hypothetical protein AF053356_	MSP_domain,SS,TM,CUB,NTR,	5.0
425824	AI939563	Hs.159589	ESTs, Moderately similar to RE	SS,PHD	5.0
439414	NM_001183	Hs.6551	ATPase, H transporting, lysoso	SS,SS,TM,GDI,Sema,TIG,PSI	5.0
436042	AF284422	Hs.119178	cation-chloride cotransporter-	SS,TM,aa_permeases,SS,TM,	5.0
410775	AB014460	Hs.66196	nth (E.coli endonuclease III)-	HhH-GPD,SS,TM,REJ,PLAT,PK	5.0
453350	AI917771	Hs.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	4.9
400300	X03363		HER2 receptor tyrosine kinase	pkinase	4.9
426811	BE259228	Hs.172609	nucleobindin 1	efhand,SS,TM,GFO_IDH_MocA	4.9
421179	U72664	Hs.148495	proteasome (prosome, macropain	UIM,SS,TM,PMP22_Claudin,P	4.9
429762	AI346255	Hs.216354	ring finger protein 5	SS,zf-C3HC4,Palm_thioest	4.9
419250	AW770185		U5 snRNP-specific protein, 116	SS,TM,7tm_1,BAH,zf-CXXC,D	4.9
426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase,SS	4.9
442103	AA333367	Hs.8088	similar to S. cerevisiae Sec6p	SS	4.9
414820	AA371931	Hs.77422	proteolipid protein 2 (colonic	SS	4.9
426347	AA454912	Hs.169407	SAC2 (suppressor of actin muta	SS,RasGEF,RA,RasGEFN,horm	4.9
423880	BE278111	Hs.134200	DKFZP564C186 protein	UPF0120,SS,TM	4.9
429545	AI824164		lymphocyte antigen 6 complex,	SS,TM	4.9
443044	N28522	Hs.8935	quinolinate phosphoribosyltran	QRPTase,QRPTase_N,SS,TM	4.9
417080	BE392846	Hs.1063	small nuclear ribonucleoprotei	SS,S10_plectin	4.8
441455	AJ271671	Hs.7854	zinc/iron regulated transporte	Zip,SS,TM,Cytidylyltransf	4.8
410182	NM_001983	Hs.59544	excision repair cross-compleme	HHH,SS,SH3,ank	4.8
456062	AI866286	Hs.71962	ESTs, Weakly similar to B36298	SS	4.8
439270	BE268278	Hs.28393	hypothetical protein MGC2592	SS,TM,HCO3_cotransp	4.8
408985	BE267317	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	4.8
416976	BE243985	Hs.80680	major vault protein	Vault,SS,TM,kinesin,zf-C2	4.8
436057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding,SS,TM,cNMP_b	4.8

424501	AI470163	Hs.323342	actin related protein 2/3 comp	SS,HhH-GPD	4.8
409214	AW405967	Hs.333388	Homo sapiens, clone IMAGE:3957	SS,EF1BD,P5CR	4.8
432716	AI762964	Hs.205180	ESTs	SS,TM	4.8
414460	L00727	Hs.898	dystrophia myotonica-protein k	pkinase,SS,WD40	4.8
443329	BE262943	Hs.9234	hypothetical protein MGC1936	SS,TM,SS,TM,gpdh,gpdh_C	4.7
426120	AA325243	Hs.166887	copine I	C2,SS,aminotran_5	4.7
405356			ENSP00000247029*:SEBOX.	SS,TM,hemopexin,Somatomed	4.7
437118	AB037857	Hs.300591	CD9 partner 1	TM,Ig,SS,TM	4.7
430609	AA302921	Hs.247362	dimethylarginine dimethylamino	SS,TM,GST_C,abhydrolase	4.7
447131	NM_004585	Hs.17466	retinoic acid receptor respond	SS,TM,pkinase	4.7
428469	BE549205	Hs.184488	flotillin 2	Band_7,Flotillin,TM	4.7
405189			Target Exon	SS	4.7
404256			NM_024018*:Homo sapiens butyro	SS,TM,SPRY,SPRY,Ig	4.7
457955	AI208986	Hs.121647	ESTs	SS,zf-B_box,SPRY,SS,Nol1_	4.7
413201	BE275378	Hs.13972	hypothetical protein MGC12972	SS,SH2,RhoGAP,SH3,GILT	4.7
431115	AB015427	Hs.250493	zinc finger protein 219	zf-C2H2,SS	4.7
442414	BE408758	Hs.8297	ribonuclease 6 precursor	ribonuclease_T2,SS,ribonu	4.7
418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome	SS	4.6
436730	AA045767	Hs.5300	bladder cancer associated prot	SS	4.6
444596	BE560662	Hs.11417	Rab acceptor 1 (prenylated)	SS,TM,lig_chan,ANF_recept	4.6
433019	AI208513	Hs.279915	translocase of inner mitochond	zf-Tim10_DDP,SS	4.6
431522	AI625859	Hs.258609	protein tyrosine phosphatase,	fn3,Y_phosphatase,SS,TM	4.6
400846			sortilin-related receptor, L(D	ldl_recept_a,fn3,ldl_rece	4.6
422154	T79045	Hs.168812	ESTs	SS	4.6
420321	D78761	Hs.96657	hypothetical protein	SS,tsp_1,SS	4.6
439921	AL110209	Hs.6770	LCAT-like lysophospholipase	SS,LACT,SS,TM,aa_permease	4.6
427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase	pkinase,Furin-like,Recep_	4.6
426899	AL043221	Hs.172825	KIAA1037 protein	WD40,TPR,SS,TM	4.6
408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN	SS,TM	4.6
412974	R18978	Hs.75105	emopamil-binding protein (ster	SS,TM,SS,TM,TBC,rrm,FtsJ	4.6
426510	AW861225	Hs.110613	BANP homolog, SMAR1 homolog	TM	4.6
414702	L22005	Hs.76932	cell division cycle 34	UQ_con,SS,trypsin,ig	4.6
408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4,SS,p450,Ge	4.6
445637	W58459	Hs.8949	hypothetical protein MGC4172	SS	4.6
452190	H26735	Hs.91668	Homo sapiens clone PP1498 unkn	SS	4.6
409680	W31092	Hs.55847	mitochondrial ribosomal protei	SS,TM,synaptobrevin	4.6
421140	AA298741	Hs.102135	signal sequence receptor, delt	Herpes_UL3,SS,TM,Sema,pkl	4.6
413407	AI356293	Hs.75339	inositol polyphosphate phospha	SH2,SAM,SS,Folate_rec	4.6
402463			NM_014624:Homo sapiens S100 ca	efhand,S_100,SS,efhand,S_	4.5
426402	BE387327	Hs.80475	polymerase (RNA) II (DNA direc	SS,PGAM	4.5
406939	M34515		gb:Human omega light chain pro	SS,Ig,PH	4.5
417891	W79410	Hs.82887	protein phosphatase 1, regulat	SS,TFIIS	4.5
426207	BE390657	Hs.30026	HSPC182 protein	SS	4.5
423664	NM_004714	Hs.130988	dual-specificity tyrosine-(Y)-	pkinase,SS,Fibrillarin,CK	4.5
432562	BE531048	Hs.278422	DKFZP586G1122 protein	zf-C2H2,SS,TM,FG-GAP,Inte	4.5
427391	W60675		hypothetical protein FLJ10350	SS,SS	4.5
432893	NM_016154	Hs.279771	Homo sapiens clone PP1596 unkn	ras,arf,SS,2OG-FeII_Oxy,2	4.5
424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni	P53,SS	4.5
413815	AL046341	Hs.75562	discoidin domain receptor fami	F5_F8_type_C,pkinase,SS,T	4.5
448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610	SS,TM	4.5
416297	AA157634	Hs.79172	solute carrier family 25 (mito	mito_carr,SS	4.5
421962	D82061	Hs.288354	FabG (beta-ketoacyl-[acyl-carr	SS,adh_short,SS,TM,zf-C3H	4.5
426726	AA488915	Hs.171955	trophinin associated protein (	SS	4.5
414427	L19711	Hs.76111	dystroglycan 1 (dystrophin-ass	SS,TM	4.5
435891	AW249394	Hs.5002	copper chaperone for superoxid	sodcu,HMA,SS,TM,spectrin,	4.5
453997	AW247615	Hs.37003	v-Ha-ras Harvey rat sarcoma vi	ras,SS	4.5
449029	N28989	Hs.22891	solute carrier family 7 (catio	aa_permeases,SS,TM,bZIP	4.5
432078	BE314877	Hs.24553	hypothetical protein FLJ12541	SS,TM	4.5
409650	T08490	Hs.288969	HSCARG protein	SS,SS,WD40	4.5
412833	AW960547	Hs.298262	ribosomal protein S19	SS,TM,Ig,ITAM,Ribosomal_S	4.4
424133	AA335721	Hs.213628	ESTs	SS,TM	4.4
414787	AL049332	Hs.77311	BTG family, member 3	SS,Anti_proliferat	4.4
433046	AA229553	Hs.279945	HSPC023 protein	SS	4.4
417068	AA451910	Hs.85852	hypothetical protein MGC3169	SS,TM	4.4
414814	D14697	Hs.77393	farnesyl diphosphate synthase	polyprenyl_synt,SS,TM	4.4
418267	BE389537	Hs.83919	glucosidase I	Glyco_hydro_63,SS,PH	4.4
439902	AF174499	Hs.6764	histone deacetylase 6	Hist_deacetyl,zf-UBP,SS,G	4.4
448847	AI587180	Hs.110906	Homo sapiens, Similar to RIKEN	TM,SS	4.4
452160	BE378541		cysteine sulfinic acid decarbo	SS	4.4
416121	X92762	Hs.79021	tafazzin (cardiomyopathy, dila	Acyltransferase,SS,TM,GDI	4.4
449717	AB040935	Hs.23954	cerebral cell adhesion molecul	SS,SS	4.4
425069	AA687465	Hs.298184	potassium voltage-gated channe	SS,aldo_ket_red	4.4
413380	AI904232	Hs.75323	prohibitin	Band_7,SS,Band_7,SH3	4.4
452911	AA541537	Hs.112619	metallothionein 1E (functional	SS,SS,TM,Sec1	4.4
436415	BE265254	Hs.343258	proliferation-associated 2G4,	Peptidase_M24,SS,TM,Pepti	4.4
429218	AA225065	Hs.198269	Target CAT	SS,Nop	4.4
447987	BE621544	Hs.157160	hypothetical protein MGC2616	SS,NDK,LRRNT,LRRCT,LRR	4.4
407230	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	4.3
448886	AL137291	Hs.22451	hypothetical protein FLJ10357	SS,PH,RhoGEF,SS,rnaseA	4.3
421178	BE267994	Hs.102419	zinc finger protein	zf-C2H2,SS,TM	4.3
454031	R36772	Hs.71941	hypothetical protein MGC15677	TM	4.3
450126	BE018138	Hs.24447	sigma receptor (SR31747 bindin	SS,Ig,fn3	4.3
446557	U68566	Hs.15318	HS1 binding protein	SS,TM,MIP,UBA	4.3
413781	J05272	Hs.850	IMP (inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD,S	4.3

433251	AB040955	Hs.322735	KIAA1522 protein	SS,SS,zf-C3HC4,SPRY	4.3
420531	AI652069	Hs.98614	ribosome binding protein 1 (do	bZIP,SS	4.3
432179	X75208	Hs.2913	EphB3	EPH_lbd,fn3,pkinase,SAM	4.3
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
426626	AI124572	Hs.323879	inhibitor of kappa light polyp	zf-C2H2,SS	4.3
432956	AL037895	Hs.279861	CGI-31 protein	thiored,SS,TM	4.3
428970	BE276891	Hs.194691	retinoic acid induced 3	7tm_3,SS,TM	4.3
428953	AA306610	Hs.348183	tumor necrosis factor receptor	TNFR_c6,SS	4.2
401128			C12000644:gi|5729785|ref|NP_00	SS	4.2
446899	NM_005397	Hs.16426	podocalyxin-like	SS,TM,SS,TM	4.2
407151	H25836	Hs.301527	ESTs, Moderately similar to un	SS,TNF	4.2
426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydro	adh_short,SS	4.2
408616	R51604	Hs.300842	KIAA1608 protein	SS,DENN,DENN	4.2
446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_H	SS,Zn_carbOpept	4.2
414467	AW903820	Hs.85752	copine II	SS	4.2
455857	T70192		gb:yc18d03.s1 Stratagene lung	SS,TM,isodh	4.2
401751			RAN binding protein 3	SS,Orexin,SH2,STAT	4.2
400563			Target Exon	SS,Pep_M12B_propep	4.2
430237	AI272144	Hs.236522	DKFZP434P106 protein	abhydrolase,TM	4.2
406101			C11000273*:gi|12656107|gb|AAK0	SS,TM,7tm_1	4.2
421661	BE281303	Hs.299148	hypothetical protein FLJ21801	SS,VHP	4.2
444590	AA457456		hypothetical protein FLJ20435	SS	4.2
408187	AF034373	Hs.43509	ataxin 2 related protein	SS	4.2
437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	SS,Hydrolase,SS,Gal-bind_	4.2
400278			ENSP00000243264:Dolichyl-dipho	SS,TM	4.2
407394	AF005081		gb:Homo sapiens skin-specific	SS	4.2
447407	BE387301	Hs.18528	Sjogren's syndrome nuclear aut	SS,HLH,ras,GSHPx	4.2
410237	AI750589	Hs.61258	argininosuccinate lyase	lyase_1,SS	4.1
415410	AF037332	Hs.278569	sorting nexin 17	PX,fn3,pkinase,SAM,EPH_lb	4.1
457757	AA434109	Hs.12271	f-box and leucine-rich repeat	SS,F-box,SS,TM,HSF_DNA-bi	4.1
446388	AA292979	Hs.7788	NPD007 protein	SS,TM	4.1
412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ13625 fis	SS	4.1
439737	AI751438	Hs.41271	Homo sapiens mRNA full length	SS,C1q,Collagen	4.1
422256	M64673	Hs.1499	heat shock transcription facto	NA,SS,TM,F-box	4.1
441164	AB023180	Hs.7724	KIAA0963 protein	helicase_C,SS,RNA_pol_H	4.1
401727			Target Exon	A_deamin,SS	4.1
411142	NM_014256	Hs.69009	transmembrane protein 3	Galactosyl_T,SS,Ribosomal	4.1
458176	AI961519	Hs.140309	Homo sapiens, clone IMAGE:3677	SS,pkinase,pkinase_C	4.1
432178	BE265369	Hs.272814	hypothetical protein DKFZp434E	SS,serine_carbpept	4.1
421537	BE383488	Hs.105547	neural proliferation, differen	SS,TM,Glyco_hydro_47	4.1
421380	D31833	Hs.1372	arginine vasopressin receptor	7tm_1	4.1
422702	AJ011373	Hs.119285	chromosome 9 open reading fram	SS,TM,SS,TM	4.1
434142	U47927	Hs.3759	ubiquitin specific protease 5	zf-UBP,UCH-2,UBA,UCH-1,SS	4.1
423696	Z92546		Sushi domain (SCR repeat) cont	SS,TPR,vwd,sushi,Somatome	4.1
427407	BE268649	Hs.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,PARP_re	4.1
413749	AI929320	Hs.75516	tyrosine kinase 2	pkinase,SS,TM,ig	4.1
411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1,SS	4.1
433320	D60647	Hs.250879	ESTs, Highly similar to CTXN R	SS,TM,rrm	4.1
433890	AF103801	Hs.16361	hypothetical protein	DAO,SS	4.1
452603	AW410601	Hs.30026	HSPC182 protein	SS	4.1
444496	BE302472	Hs.11314	DKFZP564N1363 protein	SS,GKAP,Band_41	4.1
422556	NM_006245	Hs.118244	protein phosphatase 2, regulat	B56,SS,TM,Atrophin-1,Exo_	4.1
447347	AA570056	Hs.122730	ESTs, Moderately similar to KI	TM,SS	4.1
428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH de	SS,TM,Josephin,UIM,Joseph	4.1
426551	AA381268	Hs.323947	ESTs	SS,sushi	4.0
417782	T10149	Hs.4243	hypothetical protein FLJ12650	SS,TM	4.0
443639	BE269042	Hs.9661	proteasome (prosome, macropain	proteasome,SS,TM,LACT,try	4.0
410039	AF207989	Hs.58014	Homo sapiens, Similar to G pro	SS,TM,7tm_3,SS,TM	4.0
452715	Z21093	Hs.30352	ribosomal protein S6 kinase, 5	pkinase	4.0
442549	AI751601	Hs.8375	TNF receptor-associated factor	zf-C3HC4,MATH,zf-TRAF,SS,	4.0
430603	AA148164	Hs.247280	HBV associated factor	SS,zf-C3HC4,zf-RanBP,pkin	4.0
427239	BE270447		ubiquitin carrier protein	UQ_con,SS,TM	4.0
402665			Target Exon	SS,TM,ig,DSPc	4.0
413818	BE161405	Hs.79	hypothetical protein MGC15429	SS,KH-domain,WD40,Ribosom	4.0
406919	M88359		gb:Homo sapiens DNA-binding pr	SS,rrm	4.0
412656	AF006011	Hs.74375	dishevelled 1 (homologous to D	SS,PDZ,DEP,DIX,Dishevelle	4.0
437546	AW074836	Hs.173984	T-box 1	SS,TM,T-box,GTP_CDC,LRRCT	4.0
419489	AW411280	Hs.90693	replication initiation region	zf-C2H2,LIM,TM	4.0
410043	D30612	Hs.58167	zinc finger protein 282	zf-C2H2,KRAB,SS,zf-C2H2,K	4.0
430067	U79458	Hs.231840	WW domain binding protein 2	GRAM,SS	4.0
408449	NM_004408	Hs.166161	dynamin 1	PH,GED,dynamin,dynamin_2,	4.0
448099	BE621839	Hs.61976	Homo sapiens cDNA FLJ12947 fis	SS	4.0
436656	N35568	Hs.5245	hypothetical protein FLJ20643	SS,TM,sugar_tr,PID	4.0
424512	X53002	Hs.149846	integrin, beta 5	integrin_B,EGF,SS,TM	4.0
440346	AI923985	Hs.59621	ESTs, Weakly similar to A40815	SS,TM,ig,pkinase	3.9
420065	AW140093	Hs.129926	ESTs	SS,TM	3.9
426636	BE242634	Hs.2055	ubiquitin-activating enzyme E1	ThiF,UBACT,SS,pkinase,UCH	3.9
421579	NM_002975	Hs.105927	stem cell growth factor; lymph	lectin_c,SS,TM	3.9
427498	NM_003926	Hs.178728	methyl-CpG binding domain prot	SS,HLH	3.9
457820	AA341497	Hs.31408	RAR (RAS like GTPASE)	SS,TM,Rhomboid	3.9
439998	BE559554	Hs.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	3.9
438662	AA223599	Hs.6351	cleavage and polyadenylation s	zf-CCHC,zf-CCCH,thaumatin	3.9
414303	NM_004427	Hs.165263	early development regulator 2	SAM,SS	3.9
435406	F26698	Hs.4884	calcium/calmodulin-dependent p	pkinase,SS,hexokinase,hex	3.9

414168	AW793296	Hs.103845	ESTs, Moderately similar to I5	SS	3.9
451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp5	SS	3.9
418181	U37012	Hs.83727	cleavage and polyadenylation s	CPSF_A,SS,TM	3.9
402793			Target Exon	SS,TM,cyclin,cyclin_C	3.9
418681	AA287786	Hs.23449	insulin receptor tyrosine kina	SS,SH3	3.9
412621	L40397	Hs.74137	transmembrane trafficking prot	EMP24_GP25L,SS,TM	3.9
420631	AW976530	Hs.28355	hypothetical protein FLJ22402	SS,TM	3.9
438483	AW966735	Hs.321635	ESTs, Weakly similar to A46302	SS,TM,IP_trans	3.9
431472	AK001023	Hs.256549	nucleotide binding protein 2 (	fer4_NifH,ParA,APS_kinase	3.9
447800	AL080092	Hs.19610	DKFZP564N1362 protein	SS,TM,SS,TM	3.8
436686	AW450205	Hs.305890	BCL2-like 1	TM,Bcl-2,BH4	3.8
408815	AW957974	Hs.25485	hypothetical protein FLJ22341	SS,TM	3.8
441196	BE397802	Hs.7744	NM_007103*:Homo sapiens NADH d	Complex1_51K,SNF2_N,helic	3.8
433030	AW068857	Hs.279929	gp25L2 protein	SS,TM,EMP24_GP25L,SS,TM,G	3.8
408721	BE515274	Hs.47062	polymerase (RNA) II (DNA direc	RNA_POL_M_15KD,SS,COX7a	3.8
435049	AL122067	Hs.4746	hypothetical protein FLJ21324	SS,pfkB	3.8
431347	AI133461	Hs.251664	insulin-like growth factor 2 (	SS,insulin,insulin	3.8
450835	BE262773	Hs.25584	hypothetical protein FLJ10767	ArfGap,SS,vwa,TSPN,fn3,Co	3.8
414134	X60188	Hs.861	mitogen-activated protein kina	pkinase,SS,pkinase,T-box	3.8
418090	U57059	Hs.83429	tumor necrosis factor (ligand)	TNF,SS	3.8
448832	AW245212	Hs.22199	ECSIT	SS,rrm	3.8
447256	AW593008	Hs.6126	hypothetical protein dJ1141E15	SS,TM,SS,TM	3.8
448107	D45853	Hs.20313	protein tyrosine kinase 2 beta	Focal_AT,pkinase,SS,Pepti	3.8
426433	L38969	Hs.169875	thrombospondin 3	TSPN,tsp_3,SS,TM,SEA,TSPN	3.8
431626	AL035681	Hs.265327	hypothetical protein DKFZp761I	SS	3.8
430956	AI183529	Hs.2706	glutathione peroxidase 4 (phos	GSHPx,SS,TM,ABC_tran	3.8
450998	BE387614	Hs.25797	splicing factor 3b, subunit 4,	SS,TM,sugar_tr,histone	3.8
434899	BE613631	Hs.283565	FOS-like antigen-1	bZIP,SS,bZIP,cofilin_ADF,	3.8
444734	NM_001360	Hs.11806	7-dehydrocholesterol reductase	ERG4_ERG24,SS,TM	3.8
411090	BE165650	Hs.339697	VPS28 protein	SS,TM,CPSF_A	3.8
452135	AI492175	Hs.21446	KIAA1716 protein	SS,DIX,PDZ,DEP,Dishevelle	3.8
421339	AA070224	Hs.103561	SRp25 nuclear protein	SS	3.7
406535			Target Exon	SS,TM,Ribosomal_S19e,ig,I	3.7
447281	AA017018	Hs.18021	hypothetical protein FLJ20446	SS,SS,Tektin,Piwi,PAZ	3.7
433126	AB021262	Hs.99816	beta-catenin-interacting prote	SS,TM	3.7
425215	AF030291	Hs.155165	zinc finger protein-like 1	PHD,SS,TM,DnaJ,ERG4_ERG24	3.7
420536	AL117455	Hs.275438	histone deacetylase 7A	Hist_deacetyl,SS,Hist_dea	3.7
417998	AW957420		gb:EST379495 MAGE resequences,	SS,TM	3.7
430890	X54232	Hs.2699	glypican 1	Glypican,SS	3.7
427863	AF189712	Hs.181002	MLL septin-like fusion	SS,GTP_CDC,SS,TM	3.7
448606	BE613362		Homo sapiens ubiquitin conjuga	SS,TM	3.7
421961	AB032993	Hs.109929	likely homolog of rat GRIP-ass	TM,K_tetra,ion_trans,HLH,	3.7
410293	AK000047	Hs.61960	hypothetical protein	K_tetra,SS	3.7
425233	Z17861	Hs.155218	E1B-55kDa-associated protein 5	SPRY,SAP,SS,TM,SPRY,SAP,p	3.7
423683	BE388699	Hs.4188	hypothetical protein MGC10812	SS,Peptidase_C15,TGF-beta	3.7
415697	AI365603	Hs.78605	DKFZP566I1024 protein	SS,cpn60_TCP1	3.7
415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3	SS	3.7
418052	AA350659	Hs.83347	angio-associated, migratory ce	WD40,Bacterial_PQQ,TM,UPF	3.7
444706	AK000398	Hs.11747	hypothetical protein FLJ20391	SS,SS,TM	3.7
407381	AA420659	Hs.183110	ESTs, Weakly similar to ALUC_H	SS,TM	3.7
423432	BE252996	Hs.44067	ESTs	TM	3.7
444982	AK002182	Hs.12211	GDP-fucose transporter 1	SS,TM,DUF6,SS,TM	3.7
407777	AA161071	Hs.71465	squalene epoxidase	SS,TM,Monooxygenase	3.7
422715	AA332178	Hs.119403	hexosaminidase A (alpha polype	Glyco_hydro_20,Glyco_hydr	3.7
422609	Z46023	Hs.118721	sialidase 1 (lysosomal sialida	SS,TM,BNR,SS,TM,SET,HSP70	3.7
414732	AW410976	Hs.77152	minichromosome maintenance def	MCM,RIP,SS,zf-C2H2,KRAB	3.7
452579	AA131657	Hs.23830	ESTs	SS,CN_hydrolase	3.7
419032	W81330	Hs.58643	ESTs, Highly similar to JAK3B	SS,pkinase,SH2,insulin,pk	3.6
411165	NM_000169	Hs.69089	galactosidase, alpha	Melibiase,Ribosomal_L44,z	3.6
444000	AI095034	Hs.135528	ESTs	SS,HLH	3.6
441174	BE312775	Hs.294005	Homo sapiens, clone IMAGE:3050	SS,TM	3.6
429491	NM_012111	Hs.204041	chromosome 14 open reading fra	SS	3.6
438433	AB018274	Hs.6214	KIAA0731 protein	SS	3.6
425162	BE514851	Hs.154886	choline kinase-like	Carn_acyltransf,Choline_k	3.6
429671	BE379335	Hs.211594	proteasome (prosome, macropain	AAA,NB-ARC,TM	3.6
421018	AI569028	Hs.129888	hypothetical protein FLJ14768	zf-C2H2,SS,rrm,ENTH	3.6
433604	NM_013442	Hs.3439	stomatin-like 2	Band_7,SS,TM,AAA,cdc48_N,	3.6
451544	AK000429	Hs.26570	hypothetical protein FLJ20422	SS,TM,COX3,SS,TM,SRF-TF	3.6
444369	AV649296	Hs.282793	ESTs	SS	3.6
406660	X65371	Hs.172550	polypyrimidine tract binding p	rrm,beta-lactamase,SS,try	3.6
456503	AW977779	Hs.194613	ESTs	SS,TM,bromodomain,abhydro	3.6
451711	AK000461	Hs.26890	cat eye syndrome chromosome re	SS,SS,TM,A_deaminase	3.6
425394	AA356730	Hs.323949	kangai 1 (suppression of tumor	SS,TM,transmembrane4	3.6
428011	BE387514	Hs.181418	KIAA0152 gene product	Acyl-CoA_dh,SS,efhand	3.6
407627	AI419020	Hs.62620	chromosome 6 open reading fram	SS	3.6
436437	F12200	Hs.5811	chromosome 21 open reading fra	SS,Syja_N,Exo_endo_phos	3.6
419418	X75621	Hs.90303	tuberous sclerosis 2	Rap_GAP,Tuberin,Peptidase	3.6
440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN	SS	3.6
448136	AA036680	Hs.20447	protein kinase related to S. c	pkinase,PBD	3.6
435977	AL138079	Hs.5012	brain-specific membrane-anchor	SS,TM,SS,TM,ubiquitin,Rib	3.6
419095	AA234009	Hs.188715	ESTs	pkinase,PH,pkinase_C	3.6
447267	AL360143	Hs.17936	DKFZP434H132 protein	SS	3.6
418054	NM_002318	Hs.83354	lysyl oxidase-like 2	SRCR,Lysyl_oxidase,SS,TM,	3.6
444354	AA847582	Hs.10927	hypothetical protein R33729_1	SS	3.6

429098	AF030249	Hs.196176	enoyl Coenzyme A hydratase 1,	ECH,Herpes_V23,SS,Gal-bin	3.6
430622	BE616971	Hs.247478	Homo sapiens, Similar to DNA s	G-patch,SS,TM,ubiquitin,a	3.6
440675	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_H	pkinase	3.6
409678	NM_005632	Hs.55836	small optic lobes (Drosophila)	TM,Peptidase_C2	3.6
413097	BE383876	Hs.75196	ankyrin repeat-containing prot	ank,SET,SS,TM,pkinase,SH2	3.6
427579	AA366143	Hs.179669	hypothetical protein FLJ20637	HECT,SS,HECT	3.6
409154	U72882	Hs.50842	interferon-induced protein 35	SS,ras,Ribosomal_L27e,KOW	3.5
448528	BE613248	Hs.172084	Homo sapiens, clone IMAGE:3627	SS,PID,SH2	3.5
444426	AL121105	Hs.11170	RNA binding motif protein 14	rrm,SS,spectrin,PH,rrm,so	3.5
409297	R34662	Hs.53066	hsp70-interacting protein	SS	3.5
441138	T56785	Hs.10101	hypothetical protein FLJ12875	SS	3.5
435169	AF148509	Hs.279881	mannosidase, alpha, class 1B,	TM,Glyco_hydro_47	3.5
422575	AK000546	Hs.118552	hypothetical protein FLJ20539	TM,SS,TM,SRCR,Glyco_trans	3.5
403325			C2000428*:gi|7705383|ref|NP_05	SS	3.5
437895	AB014568	Hs.5898	KIAA0668 protein	TM,UL21,Lipoprotein_6,GBP	3.5
449030	AI365582	Hs.57100	Homo sapiens mRNA for FLJ00016	SS,Synuclein	3.5
426542	AF190746	Hs.170310	cat eye syndrome chromosome re	A_deaminase,SS,TM,Hydrola	3.5
439873	BE159253	Hs.300638	ESTs	SS	3.5
428950	BE311879	Hs.194673	phosphoprotein enriched in ast	DED,SS,TM,Calsequestrin	3.5
421564	AB007864	Hs.105850	KIAA0404 protein	SS	3.5
441094	U33819	Hs.7647	MYC-associated zinc finger pro	SS,zf-C2H2,LIM,PHD,TFIIS,	3.5
450007	BE270693	Hs.24301	polymerase (RNA) II (DNA direc	NA,SS	3.5
422898	AL043101	Hs.127401	DKFZP434A163 protein; selectiv	SS,TM	3.5
444914	AA046947	Hs.12142	WD repeat domain 13	WD40,SS,TBC,rrm	3.5
420178	D50550	Hs.95659	lethal giant larvae (Drosophil	WD40,SS,TM	3.5
418984	AA421401		ribosomal protein L18	SS,TM	3.5
414166	AW888941	Hs.75789	N-myc downstream regulated	Ndr,abhydrolase,SS	3.5
409944	BE297925	Hs.57687	four and a half LIM domains 3	LIM,SS	3.5
421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate	SS	3.5
423599	AI805664	Hs.31731	peroxiredoxin 5	AhpC-TSA,SS,hormone_rec,z	3.5
427715	BE245274	Hs.180428	KIAA1181 protein	TM,SS,TM,KOW	3.5
405496			Target Exon	SS,tubulin,SS	3.5
417911	AA333387	Hs.82916	chaperonin containing TCP1, su	cpn60_TCP1,SS,cpn60_TCP1	3.5
433620	AA604520	Hs.269468	ESTs, Moderately similar to AL	SS,UCH-2,UCH-1	3.5
430053	AF052155	Hs.227949	SEC13 (S. cerevisiae)-like 1	WD40,SS,TM,E1-E2_ATPase,C	3.5
458687	AW024815	Hs.170088	GLUT4 enhancer factor	SS	3.5
424679	AL117477	Hs.119960	*DKFZP727G051 protein*	*chromo*,SS	3.5
417360	AW651703	Hs.82023	hypothetical protein similar t	SS,TM,GDA1_CD39,GDA1_CD39	3.5
439641	AI251317	Hs.33184	ESTs	SS,TM,GYF,actin,PA	3.5
426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E	UQ_con,SS,TM,Armadillo_se	3.5
427117	BE258946	Hs.173611	Target CAT	complex1_49Kd,SS,TM,ITAM,	3.4
422051	AW327546	Hs.111024	solute carrier family 25 (mito	SS;mito_carr,SS,mito_carr	3.4
422759	AA316582	Hs.224571	ESTs	SS	3.4
417230	U40998	Hs.81728	unc119 (C.elegans) homolog	SS,glycolytic_enzy	3.4
450158	AK001999	Hs.24545	hypothetical protein FLJ11137	SS,zf-C2H2,SCAN,TFIIS,SS	3.4
425421	L11669	Hs.157145	tetracycline transporter-like	SS,TM,SS,TM	3.4
415515	F11327	Hs.167406	gb:HSC2VD101 normalized infant	SS	3.4
427868	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (bra	PGAM,SS,TM,ldh	3.4
413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glu	SS,HSP70,homeobox,Hydanto	3.4
413014	AW250533	Hs.75139	partner of RAC1 (arfaptin 2)	SS,hemopexin,Filamin,NHL,	3.4
457655	AA622968	Hs.71574	hypothetical protein FLJ14926	SS,P5CR,EF1BD	3.4
419432	AK001459	Hs.90375	hypothetical protein FLJ10597	PEP-utilizers,PEP-utilize	3.4
421066	AU076725	Hs.101408	branched chain aminotransferas	aminotran_4,TM	3.4
428038	AW134756	Hs.192477	ESTs	SS,Exonuclease,zf-C2H2	3.4
430352	AW750535	Hs.50742	Homo sapiens cDNA: FLJ23331 fi	TM	3.4
432647	AI807481	Hs.278581	fibroblast growth factor recep	ig,pkinase,SS,TM,ig,pkina	3.4
421310	AW630087	Hs.103315	trinucleotide repeat containin	TM,zf-C2H2,SS,PHD	3.4
420999	AA338903	Hs.100915	peroxisomal biogenesis factor	SS	3.4
409561	U58048	Hs.183138	procollagen (type III) N-endop	SS,TM	3.4
419727	AW160796	Hs.92700	DKFZP564O243 protein	Herpes_env,SS,TM,Peptidas	3.4
421267	BE314724	Hs.103081	ribosomal protein S6 kinase, 7	pkinase,pkinase_C,SS	3.4
411501	AB002368	Hs.70500	KIAA0370 protein	SS,TM,SS,TM	3.4
448741	BE614567	Hs.19574	hypothetical protein MGC5469	SS	3.4
407103	AA424881	Hs.256301	hypothetical protein MGC13170	SS,TM,trypsin	3.4
422808	AA449014	Hs.121025	chromosome 11 open reading fra	SS,TM,trypsin,CUB,ubiquit	3.4
448173	N95657	Hs.6820	ESTs, Moderately similar to YO	SS	3.4
416535	H61851		gb:yr80e10.r1 Soares fetal liv	SS,TM,homeobox,LIM	3.4
406656	M16714	Hs.181392	major histocompatibility compl	MHC_I,Ig,SS,TM	3.4
435669	AI867781	Hs.31819	HT014	SS,abhydrolase_2	3.4
411077	AW977263	Hs.68257	general transcription factor I	SS,TM,TGF-beta	3.4
427062	AW327785	Hs.173421	KIAA1564 protein	SS,Peptidase_M24	3.4
421890	AW959486	Hs.21732	ESTs	SS,zf-C3HC4,SPRY	3.4
412968	AW500508	Hs.75102	alanyl-tRNA synthetase	DHHA1,SS,tRNA-synt_2c,DHH	3.4
439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN	SS	3.4
433659	AK001301	Hs.3487	hypothetical protein FLJ10439	WD40,SS,TM,Syntaxin,Synta	3.3
447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314	SS	3.3
441722	AW960504	Hs.173103	FE65-LIKE 2	SS,TM	3.3
452345	AA293279	Hs.29173	hypothetical protein FLJ20515	DSPc,SS,jmjC,F-box	3.3
451714	AK000344	Hs.26898	hypothetical protein FLJ20337	SS,TBC,FHA,zf-C3HC4	3.3
410633	BE546789	Hs.346742	hypothetical protein MGC3260	SS,TM	3.3
410609	BE298441	Hs.287361	ADP-ribosylation factor relate	arf,ras,SS,arf,Stathmin	3.3
414775	AA992036	Hs.172702	ESTs, Weakly similar to (defi	SS,PCI	3.3
428495	NM_013279	Hs.184640	hypothetical protein MGC10781	SS,TM,XPG_N,XPG_I,5_3_exo	3.3
429215	NM_005341	Hs.2364	GLI-Kruppel family member HKR3	zf-C2H2,BTB,TP2,K_tetra,S	3.3

446618	AL110307	Hs.15591	COP9 subunit 6 (MOV34 homolog,	Mov34,SS,zf-C2H2,SCAN	3.3
444868	BE560471	Hs.12101	hypothetical protein	SS,PCI	3.3
430041	AW247237	Hs.227835	KIAA1049 protein	SS,TM,7tm_1,tubulin	3.3
416950	AL049798	Hs.80552	dermatopontin	SS	3.3
431203	AW248421	Hs.250758	proteasome (prosome, macropain	AAA,Sigma54_activat,SS,TP	3.3
432714	Y12059	Hs.278675	bromodomain-containing 4	bromodomain,SS,TM,SNF2_N,	3.3
415674	BE394784	Hs.78596	proteasome (prosome, macropain	SS,proteasome,SS,TM,Cadhe	3.3
426152	BE299190	Hs.167246	P450 (cytochrome) oxidoreducta	flavodoxin,FAD_binding,SS	3.3
418440	NM_006936	Hs.85119	SMT3 (suppressor of mif two 3,	ubiquitin,SS,UQ_con	3.3
410545	U32324	Hs.64310	interleukin 11 receptor, alpha	ig,fn3,SS,TM,GalP_UDP_tra	3.3
409428	M33680	Hs.54457	CD81 antigen (target of antipr	transmembrane4,cyclin,SS,	3.3
443121	Z19267	Hs.9006	VAMP (vesicle-associated membr	TM,MSP_domain	3.3
453856	AA804789	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb	3.3
430137	NM_005456	Hs.234249	mitogen-activated protein kina	SS,SH3,PID,SS,PID	3.3
446427	AW295863	Hs.119632	ESTs	SS	3.3
400747			Target Exon	fn3,Ig	3.3
445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	SS,SS	3.3
452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp5	SS,rrm,Ephrin,pkinase,ATP	3.3
418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via d	death,DED,SS,TM	3.3
401655			Target Exon	SS	3.3
429460	D56263	Hs.203238	phosphodiesterase 1B, calmodul	PDEase,SS,PDEase	3.3
416448	L13210	Hs.79339	lectin, galactoside-binding, s	SRCR,SS,TM	3.3
433038	AF192559	Hs.279939	mitochondrial carrier homolog	TM,mito_carr,TM	3.3
440251	AW796016	Hs.332012	Homo sapiens, clone IMAGE:3687	SS,TM,SS,TM,IRK	3.3
412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo b	SS,homeobox,SS	3.3
432941	W04803	Hs.279851	hypothetical protein FLJ10241	SS,RNase_PH,RNase_PH_C	3.3
441244	BE612935	Hs.184052	PP1201 protein	SS,TM,WD40	3.3
438175	AI376727	Hs.122110	ESTs	SS,TM,trypsin,kringle,fn2	3.3
423024	AA593731	Hs.325823	ESTs, Moderately similar to AL	SS,TM,CD36,CD36	3.3
430120	AW675298	Hs.233694	hypothetical protein FLJ11350	SS	3.3
419571	AW674962	Hs.91146	protein kinase D2	pkinase,DAG_PE-bind,PH,DC	3.3
413019	BE281604	Hs.75140	low density lipoprotein-relate	SS	3.3
400299	X07730	Hs.171995	kallikrein 3, (prostate specif	trypsin,SS,trypsin,trypsi	3.3
433519	BE263901		ESTs, Weakly similar to S37431	SS,TM	3.2
434702	AL039734	Hs.4099	nardilysin (N-arginine dibasic	Peptidase_M16,HCO3_cotran	3.2
422242	AJ251760	Hs.273385	guanine nucleotide binding pro	G-alpha,arf,SS,G-alpha	3.2
430480	AL079399	Hs.241543	DKFZP586F1524 protein	SS,TM,hemopexin,Somatomed	3.2
452438	BE514230	Hs.29595	JM4 protein	SS,TM,KOW,HLH	3.2
456939	AA431633	Hs.163867	NM_002488*:Homo sapiens NADH d	SS,tRNA-synt_2b,WHEP-TRS,	3.2
421009	AL049709	Hs.343357	Human DNA sequence from clone	TM	3.2
411969	X12458	Hs.72980	Protein P3	SBF,SS,TM,G6PD,G6PD_C,hex	3.2
409197	N54706	Hs.303025	chromosome 11 open reading fra	SS	3.2
417896	AA379770	Hs.82890	defender against cell death 1	DAD,SS,TM	3.2
418026	BE379727	Hs.83213	fatty acid binding protein 4,	lipocalin,SS,lipocalin	3.2
409057	AA702305	Hs.180060	ESTs	SS,TGFb_propeptide,TGF-be	3.2
437869	W91976	Hs.290834	ESTs	SS,TM,SH3,zf-C3HC4	3.2
413211	AW967107	Hs.109274	hypothetical protein MGC4365	SS,TM	3.2
425080	AI393498		inositol 1,4,5-triphosphate re	SS,CTF_NFI	3.2
445363	NM_005993	Hs.12570	tubulin-specific chaperone d	ATP-synt_B,HEAT_PBS,SS,TM	3.2
421943	BE616520	Hs.343912	Homo sapiens, Similar to RIKEN	SS,TM,SS,TM	3.2
443337	Y07604	Hs.9235	non-metastatic cells 4, protei	NDK,SS,adh_short,NDK	3.2
418885	D17530	Hs.89434	drebrin 1	cofilin_ADF,SS,cofilin_AD	3.2
411817	BE302900	Hs.72241	mitogen-activated protein kina	pkinase,SS	3.2
413891	BE271020		tumor suppressor deleted in or	SS,TM	3.2
449455	T60748	Hs.278408	hypothetical protein	TM	3.2
419193	D29643	Hs.34789	dolichyl-diphosphooligosacchar	SS,TM,DDOST_48kD,VP7,SS,T	3.2
406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	SS,TM,UDPGT	3.2
436467	AW450278	Hs.91681	ESTs, Weakly similar to DCHUO	SS,tRNA-synt_1b,tRNA_bind	3.2
446334	U52427	Hs.14839	polymerase (RNA) II (DNA direc	S1,SS	3.2
410270	AF279142	Hs.195727	tumor endothelial marker 1 pre	SS,TM,EGF,lectin_c,sushi,	3.2
445411	AL137255	Hs.12646	hypothetical protein FLJ22693	SS,hormone_rec,zf-CCCH	3.2
458018	AI199575	Hs.37716	ESTs	SS,TM,Oxysterol_BP	3.2
426530	U24578	Hs.278625	complement component 4A	SS,A2M,NTR,A2M_N,prenyltr	3.2
445604	T08566	Hs.12956	Tax interaction protein 1	PDZ,SS,TM,P2X_receptor,FG	3.2
443402	U77846		elastin (supravalvular aortic	SS,PDZ,LIM,pkinase	3.2
432416	BE410937	Hs.2985	emerin (Emery-Dreifuss muscula	LEM,SS,Ribosomal_L10e,Acy	3.2
429662	AI929701	Hs.211588	phosphoinositide-3-kinase, reg	SH2,SH3,RhoGAP,SS,GILT,SH	3.2
429150	AF120103	Hs.197366	smoothened (Drosophila) homolo	SS,TM,Fz,Frizzled,7tm_2,S	3.2
427729	AB033100	Hs.300646	KIAA1274 protein (similar to m	SS	3.2
418151	AA864238.comp	Hs.83583	actin related protein 2/3 comp	RhoGEF,REV,PH,SS,TM,Ribos	3.2
448250	NM_016034	Hs.20776	mitochondrial ribosomal protei	Ribosomal_S2,SS,lipocalin	3.2
431158	AW859138	Hs.136280	Homo sapiens cDNA: FLJ22288 fi	SS,Exonuclease	3.2
414292	BE388407	Hs.75875	ubiquitin-conjugating enzyme E	UQ_con,SS,TM,SAM_PNT	3.2
406307			Target Exon	SS,TM,7tm_2,SS,TM,7tm_2,G	3.2
423325	R55565	Hs.347286	hypothetical protein FLJ22427	SS,TM,Surp,ubiquitin,TBC	3.2
427584	BE410293	Hs.179718	v-myb avian myeloblastosis vir	NA,SS	3.1
419069	AA233801		ESTs, Weakly similar to CA13_H	SS	3.1
431717	BE396150	Hs.6945	mitochondrial ribosomal protei	SS,TM	3.1
448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp4	RhoGAP,SS,TM,SET,zf-CXXC,	3.1
419394	AB011124	Hs.90232	KIAA0552 gene product	SS,Ig	3.1
436240	BE388673	Hs.5086	hypothetical protein MGC10433	SS,TM,Ets,COX6B,transmemb	3.1
413900	AW409747	Hs.75612	stress-induced-phosphoprotein	TPR,SS,TM,DnaJ	3.1
417920	S47833	Hs.82927	adenosine monophosphate deamin	A_deaminase,SS,G-alpha,GS	3.1
421819	NM_013403	Hs.108665	zinedin	WD40,pkinase,pkinase	3.1

426362	BE267158	Hs.169474	DKFZP586J0119 protein	IF-2B,SS,PP2C	3.1
408917	AW249025	Hs.7768	fibroblast growth factor (acid	SS,bZIP,cofilin_ADF,EGF	3.1
443099	AI372836	Hs.9003	hypothetical protein FLJ13868	TM	3.1
427022	AW245839	Hs.173255	small nuclear ribonucleoprotei	rrm,SS,rrm,SH3,ras,2OG-Fe	3.1
452711	AW967047	Hs.293224	ESTs, Weakly similar to T00375	SS	3.1
407236	W79485	Hs.173980	nuclear matrix protein NMP200	WD40,SS,TM,PTR2,7tm_1	3.1
452537	AW247390	Hs.77735	hypothetical protein FLJ11618	SS,SNF2_N,helicase_C	3.1
452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fi	SS	3.1
447629	AF034790	Hs.19105	translocase of inner mitochond	Tim17,SS,TM,pkinase,OTU	3.1
401097			C12000858*:gi|7363437|ref|NP_0	SS,TM,7tm_1,SS	3.1
452736	C01164	Hs.4232	Homo sapiens PAC clone RP1-130	SS,SS,TM,TBC,Surp,ubiquit	3.1
435507	AI143579	Hs.26510	vacuolar protein sorting 33B (	SS,Sec1,Sec1	3.1
424934	U75370	Hs.153880	polymerase (RNA) mitochondrial	PPR,SS,TM,cNMP_binding,RN	3.1
413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6	SS,TM,kazal,Ribosomal_S8,	3.1
409858	NM_006586	Hs.56828	trinucleotide repeat containin	SS,SS,TM,B56	3.1
424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	AAA,SS,PI-PLC-X,PH,PI-PLC	3.1
431677	AK000496	Hs.306989	hypothetical protein FLJ20489	SS	3.1
417947	AA323563	Hs.325309	hypothetical protein FLJ14596	SS,TM,PTPA	3.1
409283	NM_004860	Hs.52788	fragile X mental retardation,	KH-domain,SS,TM,HMG_box	3.1
412813	AF086947	Hs.74617	dynactin 1 (p150, Glued (Droso	CAP_GLY,SS	3.1
456535	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B,SS,p450,actin	3.1
432482	L19267	Hs.275924	dystrophia myotonica-containin	WD40,SS,pkinase,pkinase	3.1
437256	AL137404	Hs.97871	Homo sapiens, clone IMAGE:3845	TM,SS	3.1
440191	AI990417		tubulin, beta 5	SS,formiminotr,prenyltran	3.0
407972	AA827639	Hs.18587	KIAA1588 protein	SS,TM	3.0
420890	AA434058	Hs.100071	6-phosphogluconolactonase	Glucosamine_iso,SS	3.0
440060	AI696387	Hs.126451	ESTs, Weakly similar to A46302	SS	3.0
452222	AW806287	Hs.21432	SEX gene	SS,TM,Sema,TIG,PSI,GDI	3.0
401772			NM_014520:Homo sapiens MYB bin	SS	3.0
453754	AW972580	Hs.172753	ESTs	SS,TM,ras,Ribosomal_S19,T	3.0
423865	H05202	Hs.133968	FGF receptor activating protei	SS,TM	3.0
450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma	SS,TM	3.0
441954	AI744935	Hs.8047	Fanconi anemia, complementatio	TPR,SS,TM,AAA,cdc48_N,Ban	3.0
412787	D87452	Hs.74579	KIAA0263 gene product	zf-CCCH,SS,TM,NTP_transfe	3.0
422034	AC006486	Hs.333069	Ets2 repressor factor	Ets,SS,pkinase,PAF-AH_Ib	3.0
450788	AI738410		ESTs	SS,TM	3.0
452511	BE408178	Hs.285165	Homo sapiens cDNA FLJ20845 fis	SS,thiored,P5CR	3.0
414380	BE391815	Hs.75981	ubiquitin specific protease 14	UCH-2,UCH-1,ubiquitin,SS	3.0
407597	AA043925	Hs.339352	Homo sapiens brother of CDO (B	SS,TM,SS,TM	3.0
434955	BE276128	Hs.284286	mitochondrial ribosomal protei	SS	3.0
435632	AF220049	Hs.43549	uncharacterized hematopoietic	SS,UQ_con	3.0
432465	D56165	Hs.275163	non-metastatic cells 2, protei	NDK,SS,NDK	3.0
430526	AF181862	Hs.242407	G protein-coupled receptor, fa	7tm_3,homeobox,SS,TM	3.0
453412	AJ003290		gb:AJ003290 Selected chromosom	pkinase	3.0
446456	BE613933	Hs.15106	chromosome 14 open reading fra	UPF0143,SS	3.0
433180	AB038651	Hs.31854	K562 cell-derived leucine-zipp	TM,Acetyltransf,TM,Acetyl	3.0
447322	BE617649	Hs.77690	RAB5B, member RAS oncogene fam	SS,oxidored_molyb,heme_1,	3.0
422268	N25485	Hs.330310	maternal G10 transcript	G10,SS,WD40	3.0
419578	AF064853	Hs.91299	guanine nucleotide binding pro	WD40,SS,EPO_TPO	3.0
446929	AA076132	Hs.9460	Homo sapiens mRNA; cDNA DKFZp5	SS,TM,WD40	3.0

TABLE 21B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408215	10478_1	BE614290 AA307674 N35629 AA338538 AI193603 AA781096 AI680061 AI613258 AW276647 BE221263 AI348910 AI985031 AI090078 AI359617 AA666391 AI160210 AI446461 AI355345 AI343638 AI343640 AI275091 M78746 AW262795 AW250002 AA503756 AI934519 AW272086 N26520 AA626639
409938	116091_1	AW974648 AA652153 AA649671 AA078582
411674	1253746_1	AW861123 AW861125 AW856717 AW861116 AW856706 AW856788 AW856774 AW856787 AW856780 AW856782 AW856789 AW856772 AW856784 AW856786 AW856776 AW856635 AW856767
413052	1347214_1	BE249841 BE062657 BE062771 BE062636 BE062813 BE062699 BE062895 BE062747 BE062719 BE293541
413837	139363_1	AW163525 AW163255 AW163385 AI929359 BE279279 AA132590 AW157329 AA584408 AW157252 AI692198 AW003514 T24436 AI765658 AW157459 AI810740 AI659582 AI969924 AI929284 AI340993 AI349083 AW299522 AW664650 AW299513 AA132529 AI340991 AI912836 AI341293 AI650609 AA279
413891	139759_1	BE271020 AI763358 AI925430 AI806151 AW003726 T15590 AA649945 AW129911 AI570748 T57492 AA828002 AW237602 AW003539 AI139045 AI950958 BE042625 AW778973 AI287859 AI983931 AW515101 AW150029 AI358496 AI621173 AA846016 AI470921 AW169748 AI991000 AW513748 AI04058
414023	1410860_1	BE243628 BE246081 BE247016 BE241984 BE241534 BE246091 BE245679 BE243620 BE245998 BE242329 BE241417 BE241457 BE242522 BE241989 BE241464
416535	1599332_1	H61851 H74099 T67099
417998	171375_1	AW967420 AA210915 AA236991 AA210916
418984	181094_1	AA421401 T49326 AA330666 AA328941 W63573 AA758023 AA976306 H52254 AA877107 BE207784 AW664584 AI924890 AA458586 AI422142 AI891097 AI811174 R69866 T49327 AA233722 AA631138 AA910314 AI379416 AI129321 AA861574 AA635649 AI339443 AW009533 AA677036 AA948287 AA62
419069	181650_3	AA233801 BE383487 AA913939 AI632681 AI813277 AI373652 AW134802 AI863574 AW305364 AI858557 AI670746 AI015036 AI935384 AI935317 AW138668 AW204971 AI765223 AA884146 AA973341 AA234062
419250	183289_2	AW770185 AW296271 H11254 AW403510 AI032786 AA767046 AI376115 AI582209 AA460965 AI868663 AI016900 R05715 AI127382 AI660953 AI023644 H00465 AW959578 AA815039 AW292253 R05714 AA815462 AA235654 AA461274 W24933 AA300091 H00515
420160	191054_1	AI492840 AI287657 AA255989 AI698206 AI468558
421572	204022_1	AA531607 AI565370 AI376907 AI811618 AW138145 AW139465 AA421658 AA293069 AW118141 AI214980 AW663502 AI343486 AI553789 AA650416 AI498947

423696	23112_1	Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
425080	246559_1	AI393498 R42314 AI088818 AI696468 AI418641 AA573152 F08817 AI910796 AW338984 R39024 AA729145 BE245956 AI093722 AA541730 F09835 AI242755 AA350447 AA865667 T93903 AW081029 AA493711 AA650030 N35995 N21491 T57002 Z25379 AI906851
427239	27647_1	BE270447 AW409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719 BE268715 BE513876 BE295291 BE297066 AA210923 BE407519 H51344 BE622905 AW248281 AW250313 T19021 AA355115 AA316879 BE269633 BE621936 AA290724
427391	27815_1	W60675 AK001212 AA155752 AA878366 AA090872 AB033013 AW249107 AA031890 AA112820 AW366388 N55156 AA326756 AW952294 AA180820 C03570 C04358 W60676 AW248674 AA034989 AA044781 AA074274 H26212 AI800572 AI127583 AI951785 AA856557 AI571746 H23835 AI589543 AI215670
428092	286920_1	AW879141 AA421182 AI734104 AI733923 AA430600
429545	305902_1	AI824164 AI676005 AW129612 AI825903 AA773987 AI823645 AI823860 AA456229 AI824295 AA454622 AI264049 AI090237 AI669787 AI804012 AI306153 W96164 AI298273 AW884073 AW883986
430168	313927_1	AW968343 AA468507 AI478223 AW513008 AI762122 AI554512 AA862642 AA468976
433519	368801_2	BE263901 AA596086 AI190276 AI094806 AI831250 AI572668 AW204652 AI660600 AI922941 R49621
438707	46360_1	L08239 BE618914 AW385394 AW385398 AW385401 AI922683 AA907337 AA160504 AA928142 AA601969 AA010594 BE618528 AA160591
440191	48804_3	AI990417 AI304400 AI193071 AI742483 AW003408 AW131566 AI400201 AI656740 AI309186 AW665173 AW204722 AI215122 AI200785 BE467373 AI147599 AI215120 AI076110 AI803429 AI262491 AI808243 AI281007 AW135212 AW205103 AI754349 AI004801 AI051273 AW768918 AW103289 AI4
443402	5681_1	U77846 AA479373 AA346348 AA348194 M26867 AA728901 AA715367 AA377787 R64236 AI752721 R77311 AA339685 BE074254 AW938712 AW068444 AA330624 AA347098 AA327507 AW391973 AA495763 AA479278 AW605018 T19644 AI204484 AW834745 AW081309 AW090002 AI095659 AI131556 AI56
444590	6116_1	AA457456 AA907921 AI567715 AA579472 T64216 AA373128 F35533 AA722113 T64403 AA653738 F28806 AA595689 AA047537 AA022499 AW440532 F36782 AI554180 AI183767 AI806052 AA160379 AA481678 AI185031 AI148988 AI174482 AA868833 AI674395 AA481440 AI914985 AI698771 AA44
445625	64558_1	BE246743 AA436942 AW024744 AW242177 AA975476 AW385185 R07536 R73462 AV654529 T57442 AI399986 R50073 R48743 AI769689 AI863005 AA317806 AI678000 AW189963 AI986207 AW471273 R73463 AI335104 AI590161 AI469257 AI954604 H21954 T25141 AA856793 R50074 AI708253 AI2
448606	77159_1	BE613362 AA447862 H72036 AA393664 AI681334 AW139128 AA932579 AI302241 AI936800 AW960628 AI492148 C06192 AA336107 AA808008 AW615212 BE297403 BE298978 AI187207 AA928695 AI620631 AA938128 AI346527 AI040261 AA808401 AW130326 AI440313 AA868693 AI653329 AI33246
448677	775217_1	AI560769 AI857497 AW151454
450788	846840_1	AI738410 AW016905 AI971725
452160	901991_1	BE378541 AI863051
453412	966264_1	AJ003290 AJ003288 AW276947
455857	1376021_1	T70192 BE147696
455928	1383899_1	BE170313 BE158339 BE158290
457022	274445_1	AW377258 BE067468 BE067511 BE067515 BE067467 BE067514 AA397442

TABLE 21C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400460	8389428	Plus	35559-36295
400563	9844011	Plus	81941-82434
400747	7329330	Minus	71249-71441
400846	9188605	Plus	39310-39474
401097	9965518	Minus	60356-61096
401128	8699792	Plus	37349-37885
401655	9099093	Plus	79556-80132
401727	8134856	Plus	54342-54482
401751	9828651	Plus	139165-139322
401772	9966243	Plus	183917-184042
402365	9454515	Minus	70928-71185
402463	9796896	Minus	8818-8952
402665	8077033	Minus	11824-12090,14290-14544
402793	6136940	Minus	69012-69165
402916	7406502	Minus	361-474,541-687
403028	7670577	Minus	114150-114272
403325	8440025	Minus	109763-109926
404256	9367203	Plus	146931-147796
405189	7229907	Minus	168236-168795
405325	6094661	Minus	25818-26380
405356	2155224	Plus	36116-36276
405496	8468968	Plus	147706-148062
406101	9124019	Plus	125325-125831
406307	8576099	Plus	95473-95585,98900-99180
406535	7711477	Plus	83135-83362

Table 22A lists about 811 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 96th percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 75th percentile value amongst various non-malignant tissues, the "average" ovarian cancer value was greater than or equal to 80 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of transducing an intracellular signal, or of being modulatable by small molecules (e.g., pkinase, peptidase, phosphatase, or ion_transporter). Predicted protein domains are noted.

TABLE 22A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number
Unigene Title: Unigene gene title
Protein Dom.: Predicted protein domain
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UniGene ID	Unigene Title	Protein Dom.	R1
407223	H96850		gb:yw03b12.s1 Soares melanocyt		58.9
430281	AI878842	Hs.237924	CGI-69 protein	mito_carr	46.7
410418	D31382	Hs.63325	transmembrane protease, serine	ldl_recept_a,trypsin	41.0
431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH	37.1
438424	AI912498	Hs.25895	hypothetical protein FLJ14996		35.3
418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3	35.2
453028	AB006532	Hs.31442	RecQ protein-like 4	DEAD,helicase_C	28.2
407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB	28.2
451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocyt	spectrin,PH,CH	27.9
416819	U77735	Hs.80205	pim-2 oncogene	pkinase	27.9
430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp	27.7
450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2	26.7
418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	lipoxygenase,PLAT	25.3
424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG	25.1
412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand	24.4
430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	FKBP	24.3
444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,laminin_G,EGF	24.0
413726	AJ278465	Hs.75510	annexin A11	annexin	23.1
438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	oxidored_nitro	23.0
429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase	23.0
431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2	22.4
422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase	22.4
413436	AF238083	Hs.68061	sphingosine kinase 1	DAGKc	22.3
422639	AI929377	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt	21.5
429869	AI907018	Hs.15977	Target CAT		21.3
418891	NM_002419	Hs.89449	mitogen-activated protein kina	SH3,pkinase,pyridoxal_deC	21.1
419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal	RYDR_ITPR,RyR,SPRY,ion_tr	21.0
432866	BE395875	Hs.279609	mitochondrial carrier homolog	mito_carr	20.9
452875	BE275760	Hs.30928	DNA segment on chromosome 19 (	Euk_porin	20.8
426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cy	pro_isomerase	20.8
402916			ENSP00000202587*:Bicarbonate t	HCO3_cotransp	20.8
425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase	20.7
400419	AF084545		Target	EGF,Ig,lectin_c,sushi,Xll	20.0
419444	NM_002496	Hs.90443	Target CAT	fer4	19.5
459133	U40343	Hs.29656	cyclin-dependent kinase inhibi	ank	19.2
447595	AW379130	Hs.18953	phosphodiesterase 9A	PDEase	19.2
422708	AB017430	Hs.119324	kinesin-like 4	kinesin,homeobox	19.0
414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	18.8
429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidored_q6	18.5
425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	GST_C,GST_N,Tropomyosin	18.4
451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	18.1
447859	AK002194	Hs.19851	peroxisomal biogenesis factor		17.5
426457	AW894667	Hs.169965	chimerin (chimaerin) 1	DAG_PE-bind,RhoGAP	17.3
421612	AF161254	Hs.106196	8D6 antigen	ldl_recept_a	17.1
421363	NM_001381	Hs.103854	docking protein 1, 62kD (downs	PH,IRS	16.9
442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thio	Acyl-CoA_hydro	16.8
420568	F09247	Hs.247735	protocadherin alpha 10	cadherin	16.8
421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054	asp	16.8
425424	NM_004954	Hs.157199	ELKL motif kinase	pkinase,KA1,UBA	16.7
446329	NM_013272	Hs.14805	solute carrier family 21 (orga	kazal,OATP_N,OATP_C	16.5
406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,I	16.4
429109	AL008637	Hs.196352	neutrophil cytosolic factor 4	PX,SH3,OPR	16.3
429183	AB014604	Hs.197955	KIAA0704 protein	PH,Oxysterol_BP	16.2
444664	N26362	Hs.11615	map kinase phosphatase-like pr	DSPc,Rhodanese	16.2
427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF,late_protein_L2	16.2
425123	AW205274	Hs.154695	phosphomannomutase 2	PMM	16.0
416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	15.8
412942	AL120344	Hs.75074	mitogen-activated protein kina	pkinase	15.8
423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	15.7
426391	AW161050	Hs.169611	second mitochondria-derived ac		15.7
424568	AF005418	Hs.150595	cytochrome P450, subfamily XXV	p450	15.5
420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red	15.5
433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	7tm_2,EGF,cadherin,lamini	15.4
407619	AL050341	Hs.37165	collagen, type IX, alpha 2	Collagen	15.3
427326	AI287878		gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	7tm_1	15.2
442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668		15.1
458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	15.0
449936	AA938293	Hs.60088	hypothetical protein MGC11314		15.0
409230	AA852431	Hs.51299	NM_021074:Homo sapiens NADH de	complex1_24kD	14.7
423801	NM_015071	Hs.132942	GTPase regulator associated wi	RhoGAP,SH3,PH	14.0
419639	AK001502	Hs.91753	hypothetical protein		13.6
419298	AA853479	Hs.89890	pyruvate carboxylase	CPSase_L_chain,PYC_OADA,H	13.6
426108	AA622037	Hs.166468	programmed cell death 5	DUF122	13.5
448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec	13.5
418736	T18979	Hs.87908	Snf2-related CBP activator pro	helicase_C,AT_hook	13.5
436543	NM_002212	Hs.5215	integrin beta 4 binding protei	eIF6	13.3
431515	NM_012152	Hs.258583	endothelial differentiation, l	7tm_1	13.3
429469	M64590	Hs.27	glycine dehydrogenase (decarbo	GDC-P	13.2

431462	AW583672	Hs.256311	granin-like neuroendocrine pep		13.2
444855	BE409261	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	13.2
423464	NM_016240	Hs.128856	CSR1 protein	Collagen	13.1
450787	AB006190	Hs.25475	aquaporin 7	MIP	13.0
428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr	13.0
436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C	12.9
416866	AA297356	Hs.80324	serine/threonine protein phosp	Metallophos	12.9
433867	AK000596	Hs.3618	hippocalcin-like 1	efhand	12.9
411408	U76666	Hs.69949	calcium channel, voltage-depen	ion_trans	12.8
432329	NM_002962	Hs.2960	S100 calcium-binding protein A	S_100,efhand	12.7
447887	AA114050	Hs.19949	caspase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	12.7
427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2	12.7
428820	AA436187	Hs.172631	integrin, alpha M (complement	FG-GAP	12.7
446603	NM_014835	Hs.15519	oxysterol-binding protein-rela	Oxysterol_BP	12.6
422633	X56832	Hs.118804	enolase 3, (beta, muscle)	enolase	12.6
446839	BE091926	Hs.16244	mitotic spindle coiled-coil re	Troponin	12.6
414757	U46922	Hs.77252	fragile histidine triad gene	HIT	12.5
428593	AW207440	Hs.185973	degenerative spermatocyte (hom		12.5
432370	AA308334	Hs.274424	N-acetylneuraminic acid phosph	Antifreeze,NeuB	12.5
401542			C15001413*:gi|10645199|ref|NP_		12.4
428782	X12830	Hs.193400	interleukin 6 receptor	fn3,ig	12.3
425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022	FAD_binding_2	12.3
422301	AI752163	Hs.114599	collagen, type VIII, alpha 1	C1q,Collagen	12.2
410720	AF035154	Hs.65756	regulator of G-protein signall	RGS,G-gamma,DEP	12.2
407143	C14076	Hs.332329	EST		12.1
421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2	12.1
425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	PWWP,PHD	12.0
420421	AF281133	Hs.343589	exosome component Rrp41	RNase_PH,RNase_PH_C	12.0
416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-	ig,ITAM,Zn_clus	12.0
427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH	12.0
409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	11.9
436319	H90727	Hs.5123	inorganic pyrophosphatase	Pyrophosphatase	11.9
400748			NM_022122:Homo sapiens matrix		11.9
428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIP5K	11.8
401215			C12000457*:gi|7512178|pir||T30	trypsin	11.7
401281			DKFZP586N2124 protein		11.7
427397	AI929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RmaAD	11.7
453496	AA442103	Hs.33084	solute carrier family 2 (facil	sugar_tr	11.7
409608	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G	7tm_2,cadherin,GPS,lamini	11.7
424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase	11.7
447495	AW401864	Hs.18720	programmed cell death 8 (apopt	pyr_redox	11.6
426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-ci	adh_short	11.6
405371			NM_005569*:Homo sapiens LIM do	pkinase,LIM,PDZ	11.5
416282	R86664	Hs.167257	brain link protein-1	Xlink	11.4
452295	BE379936	Hs.28866	programmed cell death 10		11.4
430390	AB023186	Hs.241161	KIAA0969 protein	PH	11.4
430594	AK000790	Hs.246885	hypothetical protein FLJ20783	PH	11.2
443814	BE281240	Hs.9857	carbonyl reductase		11.2
440242	AW295871		glucose transporter protein 10		11.1
447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SH3,PH,RhoGEF	11.1
400843			NM_003105*:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	11.1
422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	11.0
400232			NM_001895*:Homo sapiens casein	pkinase	10.9
426828	NM_000020	Hs.172670	activin A receptor type II-lik	pkinase,Activin_recp	10.9
431157	AI823969	Hs.132678	ESTs	MAPEG	10.8
422616	BE300330	Hs.118725	selenophosphate synthetase 2	AIRS,AIRS_C	10.8
406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg		10.8
400389	AL135841		olfactory receptor, family 2,	7tm_1	10.8
402207			Target Exon	A2M_N,A2M	10.8
435615	Y15065	Hs.4975	potassium voltage-gated channe	ion_trans,KCNQ1_channel	10.8
452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c	10.7
402053			C11001722*:gi|11436283|ref|XP_		10.7
418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	10.6
431512	BE270734	Hs.2795	lactate dehydrogenase A	ldh,ldh_C	10.6
403213			NM_019595:Homo sapiens interse	SH3,efhand,C2,PH,RhoGEF	10.6
412158	BE241740	Hs.785	integrin, alpha 2b (platelet g	FG-GAP,integrin_A	10.6
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (m	Peptidase_M10,hemopexin	10.6
403949			C10000813*:gi|5453992|ref|NP_0		10.6
457670	AF119666	Hs.23449	insulin receptor tyrosine kina	SH3	10.5
418416	U11700	Hs.84999	ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hydrolas	10.4
419594	AA013051	Hs.91417	topoisomerase (DNA) II binding	BRCT	10.4
422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIR,TK	10.4
453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI	10.4
425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2	10.4
438800	AB037108	Hs.6418	seven transmembrane domain orp		10.3
402478			Target Exon	Carn_acyltransf	10.3
444202	AL031685	Hs.12785	KIAA0939 protein	Na_H_Exchanger,ABC2_membr	10.3
425597	U28694	Hs.158324	chemokine (C-C motif) receptor	7tm_1	10.3
413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E	UQ_con	10.2
415200	AL040328	Hs.78202	SWI/SNF related, matrix associ	SNF2_N,helicase_C,bromodo	10.2
414874	D26351	Hs.77515	inositol 1,4,5-triphosphate re	RYDR_ITPR,ion_trans,MIR	10.2
423524	AF055989	Hs.129738	potassium voltage-gated channe	ion_trans,K_tetra,thaumat	10.2
457558	AF083955	Hs.279852	G protein-coupled receptor	7tm_1,globin	10.2

445629	AI245701	Hs.193326	fibroblast growth factor recep		10.1
434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf	10.1
402497			C1001261*:gi|2695979|emb|CAA70		10.1
449853	AF006823	Hs.24040	potassium channel, subfamily K	ion_trans	10.0
427672	AA356615	Hs.336916	death-associated protein 6		10.0
412048	AW866863	Hs.73090	nuclear factor of kappa light	RHD,TIG,ank,death	10.0
410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8	10.0
420319	AW406289	Hs.96593	hypothetical protein	ras,arf	10.0
420332	NM_001756	Hs.1305	serine (or cysteine) proteinas	serpin	9.9
405474			NM_001093*:Homo sapiens acetyl	CPSase_L_chain,biotin_lip	9.9
401507			C15000810*:gi|11131272|sp|P793		9.9
431434	BE267696	Hs.254105	enolase 1, (alpha)	enolase	9.9
447232	AW499834	Hs.327	interleukin 10 receptor, alpha		9.8
432343	NM_002960	Hs.2961	S100 calcium-binding protein A	S_100	9.8
408931	AA251995	Hs.334648	poly(A) polymerase alpha	NTP_transf_2	9.8
421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11		9.8
430323	U40714	Hs.239307	tyrosyl-tRNA synthetase	DUF101	9.8
412270	AC005262	Hs.73797	guanine nucleotide binding pro	G-alpha,arf	9.7
424649	BE242035	Hs.151461	embryonic ectoderm development	WD40	9.7
400772			NM_003105*:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	9.7
450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	9.7
401510			NM_017434:Homo sapiens dual ox	efhand,Ferric_reduct	9.7
404596			Target Exon		9.7
451367	AA923729	Hs.26322	cell cycle related kinase	pkinase	9.7
417810	D28419	Hs.82609	*hydroxymethylbilane synthase*	*Porphobil_deam*	9.6
432855	AF017988	Hs.279565	secreted frizzled-related prot	Fz,NTR	9.6
424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK	9.6
430398	AF105202	Hs.241376	potassium voltage-gated channe	ion_trans,KCNQ1_channel	9.6
424339	BE257148		endoglycan	MCM	9.6
429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	PGAM	9.6
407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF	9.6
433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta		9.6
409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc	9.6
404968			C4001170:gi|6863176|gb|AAF3040		9.5
400833			C11000890:gi|3746443|gb|AAC639	7tm_1	9.5
410191	AI609645		NM_021075*:Homo sapiens NADH d		9.5
444633	AF111713	Hs.286218	junctional adhesion molecule 1	ig	9.4
427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase	9.4
415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F	9.4
432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD	9.4
422328	X60459	Hs.1513	interferon (alpha, beta and om		9.4
445143	U29171	Hs.75852	*casein kinase 1, delta*	*pkinase*	9.4
450883	NM_001348	Hs.25619	death-associated protein kinas	pkinase	9.4
414625	AA335738	Hs.76686	glutathione peroxidase 1	GSHPx	9.3
401935			Target Exon	PH	9.3
418329	AW247430	Hs.84152	cystathionine-beta-synthase	PALP,CBS	9.3
425242	D13635	Hs.155287	KIAA0010 gene product	HECT,IQ	9.3
400404	AF161221		kallikrein 14	trypsin	9.2
442332	AI693251	Hs.8248	Target CAT	fer2,molybdopterin,bac_dn	9.2
431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4		9.2
402823			C1002456*:gi|9930918|emb|CAC05		9.1
404527			peptide YY, 2 (seminalplasmin)	GDA1_CD39	9.1
439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_Ib,Lipase_GDSL	9.1
412970	AB026436	Hs.177534	dual specificity phosphatase 1	Rhodanese,DSPc	9.1
443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran	9.1
400933			NM_004347:Homo sapiens caspase	ICE_p20,ICE_p10,CARD	9.0
403268			NM_002210*:Homo sapiens integr	FG-GAP	9.0
446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid	acid_phosphat	9.0
422531	AW967280	Hs.293894	ESTs, Weakly similar to HERC2	pkinase	9.0
421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	9.0
401885			Target Exon	kinesin	9.0
402651			NM_000721*:Homo sapiens calciu	ion_trans	9.0
457432	NM_005136	Hs.268538	potassium voltage-gated channe	ISK_Channel	9.0
433146	AB033002	Hs.21413	*solute carrier family 12, (pot*		9.0
420090	AA220238	Hs.94986	ribonuclease P (38kD)	Ribosomal_L7Ae	9.0
425281	AA444390	Hs.155482	hydroxyacyl glutathione hydrol	lactamase_B	9.0
410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	SNF2_N,helicase_C	9.0
407986	U32659	Hs.41724	interleukin 17 (cytotoxic T-ly		9.0
431131	N84730	Hs.250616	isocitrate dehydrogenase 3 (NA	isodh	9.0
422802	NM_004278	Hs.27008	phosphatidylinositol glycan, c	DUF158	9.0
447958	AW796524	Hs.68644	Homo sapiens microsomal signal		9.0
438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_H		9.0
418843	AJ251016	Hs.89230	potassium intermediate/small c	CaMBD,SK_channel	9.0
419244	AI436567	Hs.89761	ATP synthase, H transporting,	ATP-synt_DE	8.9
404676			Target Exon		8.9
428744	BE267033	Hs.192853	ubiquitin-conjugating enzyme E	UQ_con	8.9
421474	U76362	Hs.104637	solute carrier family 1 (gluta	SDF	8.9
419056	M89957	Hs.89575	CD79B antigen (immunoglobulin-	ig,ITAM	8.9
424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutа	2OG-FeII_Oxy,Glycos_trans	8.9
444628	U01120	Hs.242	glucose-6-phosphatase, catalyt	PAP2	8.9
404199			ENSP00000211797*:Helicase SKI2	RasGAP,PH	8.9
428826	AL048842	Hs.194019	attractin	lectin_c,CUB,Kelch,PSI,EG	8.9
410681	AW246890	Hs.65425	calbindin 1, (28kD)	efhand	8.8
415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1	8.8

400471			Target Exon		8.8
406591			NM_003888*:Homo sapiens retina	aldedh	8.8
425427	AI652662	Hs.157205	branched chain aminotransferas	aminotran_4	8.8
410839	NM_006849	Hs.66581	protein disulfide isomerase	thiored,Rho_GDI,gntR	8.7
430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	8.7
450848	AI677994	Hs.428	fms-related tyrosine kinase 3	flt3_lig	8.7
414534	BE257293	Hs.76366	BCL2-antagonist of cell death		8.7
401454			NM_014226*:Homo sapiens renal	pkinase	8.7
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (mus	PGAM	8.7
433333	AI016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina	8.7
430432	AB037758	Hs.241419	KIAA1337 protein	Patched	8.7
406128			NM_002920*:Homo sapiens regula	Oest_recep,zf-C4,hormone_	8.7
419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI	8.7
439569	AW602166	Hs.222399	CEGP1 protein	CUB,EGF	8.6
401134			C12001198:gi|3183183|sp|Q92142	biopterin_H	8.6
442286	W31847	Hs.50335	cytochrome P450 monooxygenase		8.6
428376	AF119665	Hs.184011	pyrophosphatase (inorganic)	Pyrophosphatase	8.6
433494	AB029396		beta-1,3-glucuronyltransferase	Glyco_tranf_43	8.6
427001	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-	pkinase	8.6
437278	AA748017	Hs.290145	ESTs	cNMP_binding	8.6
414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin	lipocalin,Kunitz_BPTI	8.6
421871	AK001416	Hs.306122	glycoprotein, synaptic 2	Steroid_dh	8.6
447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM	8.6
403379			Target Exon	DNA_pol_A	8.6
446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G	7tm_1	8.6
432857	NM_016103	Hs.279582	GTP-binding protein Sara	arf,ras	8.5
420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	8.5
427221	L15409	Hs.174007	von Hippel-Lindau syndrome	VHL	8.5
402209			Target Exon	A2M_N,A2M	8.5
400518			C10002057*:gi|3211705|gb|AAC21		8.5
425606	U52112	Hs.158331	renin-binding protein		8.5
437965	AA843222	Hs.193534	ESTs, Moderately similar to AL	RasGEF	8.5
433392	AF038535	Hs.127588	synaptotagmin VII	C2	8.5
402191			NM_021733*:Homo sapiens testis		8.5
458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat hom	ras	8.5
431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p	PARP,PARP_reg	8.5
457579	AB030816	Hs.36761	HRAS-like suppressor		8.5
409656	NM_005133	Hs.288626	RCE1, prenyl protein protease	Abi	8.5
456373	BE247706	Hs.89751	membrane-spanning 4-domains, s		8.4
432499	BE276633		RAB6B, member RAS oncogene fam	ras,arf	8.4
400565			Target Exon		8.4
401960			Target Exon	Branch	8.3
432545	X52486	Hs.3041	uracil-DNA glycosylase 2	cyclin	8.3
445303	AW362198	Hs.12503	interleukin 15 receptor, alpha	sushi	8.3
404528			peptide YY, 2 (seminalplasmin)	GDA1_CD39	8.3
428542	D79989		KIAA0167 gene product	ank,PH,ArfGap,ras	8.3
406868	AA505445	Hs.300697	immunoglobulin heavy constant		8.3
405473			NM_001093*:Homo sapiens acetyl	CPSase_L_chain,biotin_lip	8.3
408601	U47928	Hs.86122	protein A	7tm_1	8.3
415008	NM_002777	Hs.928	proteinase 3 (serine proteinas	trypsin	8.3
430258	AU076644	Hs.236963	protein phosphatase 2A, regula		8.3
436483	AJ272063	Hs.283010	vanilloid receptor subtype 1	ank,ion_trans	8.3
459302	NM_002314	Hs.36566	LIM domain kinase 1		8.3
437644	AA748575	Hs.136748	lectin-like NK cell receptor	lectin_c	8.3
421707	NM_014921	Hs.107054	lectomedin-2	Latrophilin,OLF,7tm_2,Gal	8.2
414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/m	COesterase	8.2
453898	AW003512	Hs.232770	arachidonate lipoxygenase 3		8.2
424053	AF057036	Hs.138520	collagen-like tail subunit (si	Collagen	8.2
457398	BE258532	Hs.251871	CTP synthase	GATase	8.2
421504	AW402997	Hs.105052	adaptor protein with pleckstri	SH2,PH	8.1
406495			Target Exon	SRCR	8.1
453610	AW368882	Hs.33818	RecQ protein-like 5	DEAD,helicase_C	8.1
424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase re	RCC1	8.1
423847	U16997	Hs.133314	RAR-related orphan receptor C	hormone_rec,zf-C4	8.1
409829	M33552	Hs.56729	lymphocyte-specific protein 1	Caldesmon	8.1
401180			eukaryotic translation elongat	ion_trans,IQ	8.1
452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf	8.1
426484	AA379658	Hs.272759	KIAA1457 protein	IP_trans	8.1
402453			C1002496:gi|7363439|ref|NP_039	7tm_1	8.1
457310	W28363	Hs.239752	nuclear receptor subfamily 2,		8.1
422069	AJ010063	Hs.343603	titin-cap (telethonin)	globin,cNMP_binding,pkina	8.1
400275			NM_006513*:Homo sapiens seryl-	NA	8.0
434357	AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases	8.0
430299	W28673	Hs.106747	serine carboxypeptidase 1 prec		8.0
413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR	8.0
402393			ENSP00000085284*:CDNA FLJ20404	RhoGEF,PH	8.0
429252	NM_004658	Hs.198312	RAS protein activator like 1 (	C2,PH,RasGAP,BTK	8.0
456181	L36463	Hs.1030	ras inhibitor	RA,SH2,VPS9	7.9
431493	AI791493	Hs.129873	ESTs, novel cytochrome P450	p450	7.9
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-fami	ABC_tran,SRP54	7.8
415758	BE270465	Hs.78793	protein kinase C, zeta	pkinase,DAG_PE-bind,pkina	7.8
419270	NM_005232	Hs.89839	EphA1	EPH_lbd,pkinase,SAM,fn3	7.8
422837	U25441	Hs.121478	dopamine receptor D3	7tm_1	7.8
401118			Target Exon	pkinase	7.8

426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr	7.8
418635	L11329	Hs.1183	dual specificity phosphatase 2	DSPc,Rhodanese,Y_phosphat	7.8
432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin	7.8
403672			C4001244:gi|539933|pir||A61275	tubulin	7.8
437806	AI424921	Hs.122487	ESTs, Weakly similar to A54854	RasGAP	7.7
456890	U48213	Hs.155402	D site of albumin promoter (al	DAGKc,bZIP	7.7
424107	AB014606	Hs.139648	kinesin family member 1C	kinesin,FHA	7.7
452695	AW780199	Hs.30327	mitogen-activated protein kina		7.7
433262	AI571225	Hs.284171	KIAA1535 protein	cNMP_binding,ion_trans	7.7
424198	AB029010	Hs.143026	KIAA1087 protein	Na_Ca_Ex,Calx-beta	7.6
406496			Target Exon	SRCR	7.6
425423	NM_005897	Hs.157180	intracisternal A particle-prom	BTB,Kelch	7.6
402211			KIAA0430 gene product	ion_trans,K_tetra	7.6
408710	Y10256	Hs.47007	mitogen-activated protein kina	pkinase,SAM_decarbox	7.5
457615	W56321	Hs.111460	calcium/calmodulin-dependent p	pkinase	7.5
402760			NM_021797*:Homo sapiens eosino	Glyco_hydro_18,CBM_14	7.5
425428	AL110261	Hs.157211	DKFZP586B0621 protein	C1q,Collagen	7.4
423579	NM_004121	Hs.1675	gamma-glutamyltransferase-like	G_glu_transpept	7.4
413104	L42374	Hs.75199	protein phosphatase 2, regulat	B56	7.4
419660	BE280337	Hs.194693	solute carrier family 7 (catio	aa_permeases	7.4
424774	BE244179	Hs.153022	TATA box binding protein (TBP)		7.4
402632			Target Exon	Fz,kringle,ig	7.4
444159	AF116846	Hs.10431	dead ringer (Drosophila)-like	ARID,SNF	7.4
405714			ENSP00000221137:Olfactory rece	7tm_1	7.3
442732	AA257161	Hs.8658	*hypothetical protein DKFZp434E*	EGF,*laminin*_EGF,Xlink,S_m	7.3
421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	7.3
415995	NM_004573		phospholipase C, beta 2	PI-PLC-X,PI-PLC-Y,C2	7.3
405137			Target Exon		7.3
402460			C1001261*:gi|2695979|emb|CAA70		7.3
431398	BE616547	Hs.2785	keratin 17	filament	7.3
429592	AB029041	Hs.209646	KIAA1118 protein	Troponin	7.3
429225	BE250337	Hs.198273	Target CAT		7.2
423015	U18548	Hs.123034	G protein-coupled receptor 12		7.2
454373	NM_005133	Hs.288626	RCE1, prenyl protein protease	Abi	7.2
440188	AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK	7.2
432920	U37689	Hs.3128	polymerase (RNA) II (DNA direc		7.2
446143	BE245342	Hs.306079	sec61 homolog	secY	7.2
422201	NM_001505	Hs.113207	G protein-coupled receptor 30	7tm_1	7.2
440869	NM_014297	Hs.7486	protein expressed in thyroid	lactamase_B	7.1
435099	AC004770	Hs.4756	flap structure-specific endonu	XPG_N,XPG_I,5_3_exonuclea	7.1
437161	AA054477	Hs.25391	ESTs		7.1
429683	AF148213	Hs.211604	a disintegrin-like and metallo	tsp_1,Reprolysin,Pep_M12B	7.1
426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	pkinase	7.1
445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	7.1
416377	AA179930	Hs.293867	caspase recruitment domain pro		7.1
421748	NM_014718	Hs.107809	KIAA0726 gene product	cadherin	7.1
426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	pkinase	7.0
428599	AB033078	Hs.186613	sphingosine-1-phosphate lyase	pyridoxal_deC	7.0
411898	BE409714	Hs.44856	hypothetical protein FLJ12116		7.0
427010	AW138332		muscle RAS oncogene homolog	ras	7.0
457305	BE268048	Hs.236494	RAB10, member RAS oncogene fam	ras,arf	7.0
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	7.0
457764	AW028284	Hs.4815	nudix (nucleoside diphosphate	NUDIX	6.9
435575	AF213457	Hs.44234	triggering receptor expressed	ig	6.9
456488	AW015098	Hs.301946	ESTs, Weakly similar to T30867		6.9
428761	AF236119	Hs.193076	GRB2-related adaptor protein 2	SH2,SH3	6.9
430396	D49742	Hs.241363	hyaluronan-binding protein 2	trypsin,kringle,EGF	6.9
422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	ldh,ldh_C,adh_short,Semia	6.9
445937	AI452943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2	6.9
457499	AA953015	Hs.274370	hypothetical protein FLJ20260	PH	6.8
400845			NM_003105*:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	6.8
416931	D45371	Hs.80485	adipose most abundant gene tra	C1q,Collagen	6.8
414915	NM_002462	Hs.76391	myxovirus (influenza) resistan	dynamin_2,dynamin,GED	6.8
432990	AL036071	Hs.279899	*tumor necrosis factor receptor*	TNFR_c6	6.8
458128	W32474	Hs.301746	RAP2A, member of RAS oncogene	ras,arf,ldh	6.8
429542	AF038660	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2,ig	6.8
401488			Target Exon	Glyco_hydro_1	6.7
456243	AI345001	Hs.82380	menage a trois 1 (CAK assembly	zf-C3HC4	6.7
424321	W74048	Hs.1765	lymphocyte-specific protein ty	SH2,SH3,pkinase	6.7
405187			NM_014272:Homo sapiens a disin	Reprolysin,tsp_1,Pep_M12B	6.7
413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450	6.7
448496	BE379077	Hs.130849	ESTs, Weakly similar to I38022	NADHdh_2	6.7
419667	AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	6.7
417103	Z33905	Hs.81218	hypothetical protein MGC3597	TPR,zf-C3HC4,PHD	6.7
407687	AK002011	Hs.37558	hypothetical protein FLJ11149	FAD_Synth	6.7
456469	NM_005109	Hs.95220	*oxidative-stress responsive 1*	*zf-C2H2,pkinase*	6.7
449546	W86248	Hs.58819	ESTs	hexokinase	6.6
428926	NM_001702	Hs.194654	brain-specific angiogenesis in	7tm_2,tsp_1,GPS,HRM	6.6
404953			C1002000*:gi|12735712|ref|XP_0		6.6
449401	AL135401	Hs.23557	serologically defined colon ca	pro_isomerase	6.6
429962	M69113	Hs.226795	glutathione S-transferase pi	GST_C,GST_N	6.6
421547	AA489908	Hs.1390	proteasome (prosome, macropain	Clathrin_lg_ch,proteasome	6.6
430035	NM_003463	Hs.227777	protein tyrosine phosphatase t	Y_phosphatase,DSPc	6.6
406867	AA157857	Hs.182265	keratin 19	filament,bZIP	6.6

404946			Target Exon	3Beta_HSD	6.5
435213	AA092510	Hs.5985	non-kinase Cdc42 effector prot		6.5
411201	T74588	Hs.8509	ESTs, Weakly similar to C3HU c	A2M_N,A2M	6.5
419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bi	6.5
426194	T50872	Hs.2001	thromboxane A synthase 1 (plat	p450	6.5
424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK	6.5
417903	NM_002342	Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6	6.5
408905	AV655783	Hs.661	Target CAT		6.5
438646	AI973076	Hs.231958	matrix metalloproteinase 28		6.5
431530	X61615	Hs.2798	leukemia inhibitory factor rec	fn3	6.5
428883	AA436959	Hs.258802	ATPase, (Na)/K transporting, b	Na_K-ATPase	6.5
404757			Target Exon		6.4
406370			interleukin 11	trypsin	6.4
443611	NM_014397	Hs.9625	NIMA (never in mitosis gene a)	pkinase	6.4
424008	R02740	Hs.137555	putative chemokine receptor; G	7tm_1	6.4
444912	AW247380	Hs.12124	putative prostate cancer susce	lactamase_B	6.4
454460	X66945	Hs.748	fibroblast growth factor recep	ig,pkinase	6.4
432269	NM_002447	Hs.2942	macrophage stimulating 1 recep	pkinase,Sema,PSI,TIG,A4_E	6.4
458718	AI359476	Hs.157699	ESTs		6.4
405282			Target Exon	Cache	6.4
447245	AK001713	Hs.17860	hypothetical protein FLJ10851	E1_dehydrog	6.3
442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-spe	PDEase	6.3
400894			C11000129:gi|9938014|ref|NP_06	7tm_1	6.3
440446	NM_013385	Hs.7189	pleckstrin homology, Sec7 and	PH,Sec7	6.3
430886	L36149	Hs.248116	chemokine (C motif) XC recepto	7tm_1	6.3
451394	NM_003595	Hs.26350	tyrosylprotein sulfotransferas	Sulfotransfer	6.3
436523	BE612990	Hs.5212	single-strand selective monofu		6.3
422714	AB018335	Hs.119387	KIAA0792 gene product	DUF221	6.3
408924	AW295606	Hs.236131	homeodomain-interacting protei		6.3
414551	AI815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH,Peptidase_U7	6.3
413254	U40272	Hs.75253	isocitrate dehydrogenase 3 (NA	isodh	6.3
415010	NM_004203	Hs.77783	membrane-associated tyrosine-	pkinase	6.3
449761	AB009698	Hs.23965	solute carrier family 22 (orga	sugar_tr	6.3
432221	M21191	Hs.273415	aldolase A, fructose-bisphosph	glycolytic_enzy,Adeno_E3_	6.3
414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C	6.2
458516	BE010749	Hs.255097	ESTs		6.2
417985	AA187545	Hs.83114	crystallin, zeta (quinone redu	adh_zinc	6.2
447507	H59696	Hs.18747	POP7 (processing of precursor,		6.2
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibi	Y_phosphatase,DSPc	6.2
428443	BE618106	Hs.184326	CDC10 (cell division cycle 10,	GTP_CDC,M	6.2
423229	AC003965	Hs.125532	protease, serine, 26	trypsin	6.2
408903	BE244377	Hs.48876	farnesyl-diphosphate farnesylt	SQS_PSY,dsrm,z-alpha	6.2
426176	AB000462	Hs.167679	SH3-domain binding protein 2	PH,SH2	6.1
421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoam	E1_dehydrog	6.1
430517	S80071	Hs.241597	solute carrier family 6 (neuro	SNF	6.1
435906	AI686379	Hs.110796	SAR1 protein	arf,ras	6.1
402758			C1001899*:gi|12722636|ref|XP_0	Glyco_hydro_18	6.1
434202	BE382411	Hs.3764	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
402115			NM_021624:Homo sapiens histami	7tm_1	6.1
407601	AC002300	Hs.37129	sodium channel, nonvoltage-gat	ASC	6.1
404679			Target Exon		6.0
450739	AI732707		ESTs, Weakly similar to ALU7_H	V1R	6.0
439888	AB040949	Hs.6733	pancreas-enriched phospholipas	C2,PI-PLC-Y,PI-PLC-X,RasG	6.0
415742	BE410243	Hs.78769	thimet oligopeptidase 1	Peptidase_M3	6.0
453190	AB002354	Hs.32312	KIAA0356 gene product	PH,PHD,RUN	6.0
439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Ham1p_like	6.0
412800	AW950852	Hs.74598	polymerase (DNA directed), del	homeobox	6.0
432805	X94630	Hs.3107	CD97 antigen	7tm_2,GPS,EGF	6.0
418964	T74640		gb:yc57c12.r1 Stratagene liver	A2M_N,A2M	6.0
417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0
419755	H18444	Hs.134846	BAI1-associated protein 3	C2	6.0
457276	AF235097	Hs.227583	Homo sapiens chromosome X map		6.0
423908	AJ006422	Hs.135183	centaurin-alpha	PH,ArfGap	6.0
432118	N98718		gb:yy65g02.r1 Soares_multiple_		5.9
427334	R44789	Hs.33191	Homo sapiens, Similar to trans		5.9
424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	pkinase,SH3	5.9
453082	H18835	Hs.31608	hypothetical protein FLJ20041	ion_trans	5.9
421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB	p450	5.9
422287	F16365	Hs.114346	cytochrome c oxidase subunit V	COX7a,Phage_G	5.9
401736			C16000492*:gi|3127193|gb|AAD05	AMP-binding	5.9
434755	AA648502		ESTs		5.9
414962	AF273304	Hs.235376	XPMC2 protein	Exonuclease	5.8
407338	AA773213		gb:ab66f10.s1 Stratagene lung	ig	5.8
448426	BE018315	Hs.280776	tankyrase, TRF1-interacting an		5.8
409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp4	ABC_tran	5.8
450778	U81375	Hs.25450	solute carrier family 29 (nucl	Nucleoside_tran	5.8
423612	NM_002067	Hs.1686	guanine nucleotide binding pro	G-alpha,arf	5.8
430845	AF024690	Hs.248056	G protein-coupled receptor 43	7tm_1	5.8
424741	AF051941	Hs.343824	nucleoside diphosphate kinase	NDK	5.8
412958	BE391579	Hs.75087	Fas-activated serine/threonine		5.8
415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conj	GATase	5.8
423158	H97991	Hs.193313	Target CAT	MoaA_NifB_PqqE	5.8
414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	5.8
412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH de		5.7

420904	AL035964	Hs.100221	nuclear receptor subfamily 1,	hormone_rec,zf-C4	5.7
415503	U36601	Hs.78473	N-deacetylase/N-sulfotransfera	Sulfotransfer	5.7
433074	AL045019	Hs.323462	Homo sapiens cDNA FLJ11214 fis	DEAD,helicase_C,dsrm,Vira	5.7
409124	AW292809	Hs.50727	N-acetylglucosaminidase, alpha		5.7
428270	BE501549	Hs.107040	ESTs		5.7
435114	AA775483	Hs.288936	mitochondrial ribosomal protei	ODC_AZ	5.7
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	asp	5.7
453054	AI878908	Hs.31547	Target CAT		5.7
420730	NM_002691	Hs.99890	polymerase (DNA directed), del	ICL	5.7
415117	AF120499	Hs.78016	polynucleotide kinase 3'-phosp	Viral_helicase1	5.7
400985			Target Exon		5.7
413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3,ig,Y_phosphatase	5.7
413858	NM_001610	Hs.75589	acid phosphatase 2, lysosomal	acid_phosphat	5.7
457308	AI416988	Hs.238272	inositol 1,4,5-triphosphate re	ion_trans,RYDR_ITPR,MIR	5.7
400551			C10001991*:gi|6624920|emb|CAB6	SRCR	5.7
433472	AI541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	5.7
409531	BE384319	Hs.54702	xylosylprotein beta1,4-galacto	Galactosyl_T_2	5.7
449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-	neur	5.7
450207	T87615	Hs.14716	ESTs		5.7
400266			NM_002858*:Homo sapiens ATP-bi	ABC_tran	5.6
430713	AA351647	Hs.2642	eukaryotic translation elongat	GTP_EFTU,GTP_EFTU_D3,GTP_	5.6
420911	U77413	Hs.100293	O-linked N-acetylglucosamine (	TPR	5.6
405683			Target Exon		5.6
449181	X96783	Hs.23179	synaptotagmin V	C2	5.6
414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	ATP-synt_C	5.6
415193	AL048891	Hs.12185	hypothetical protein MGC14333		5.6
434883	AW381538	Hs.19807	hypothetical protein MGC12959		5.6
433135	AA443873	Hs.110477	dolichyl-phosphate mannosyltra		5.6
413049	NM_002151	Hs.823	hepsin (transmembrane protease	trypsin	5.6
420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-ac	MAPEG	5.6
423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor	7tm_1	5.5
443759	BE390832	Hs.134729	FXYD domain-containing ion tra		5.5
454112	NM_000885	Hs.40034	integrin, alpha 4 (antigen CD4	integrin_A,FG-GAP	5.5
405594			NM_021949:Homo sapiens ATPase,	E1-E2_ATPase,Hydrolase	5.5
416322	BE019494	Hs.79217	pyrroline-5-carboxylate reduct	P5CR,Octopine_DH_N	5.5
446755	AW451473	Hs.16134	serine/threonine kinase 10	pkinase,TYA	5.5
411030	BE387193	Hs.67896	7-60 protein		5.5
431498	AK001777	Hs.258551	aspartyl aminopeptidase	Peptidase_M18	5.5
433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, y	HMA	5.5
414907	X90725	Hs.77597	polo (Drosophia)-like kinase	pkinase,POLO_box	5.5
424572	M19650	Hs.92909	2',3'-cyclic nucleotide 3' pho		5.5
406617			Target Exon	efhand,Ferric_reduct	5.5
421883	X55079	Hs.1437	glucosidase, alpha; acid (Pomp	trefoil,Glyco_hydro_31	5.4
419525	T79257	Hs.1259	asialoglycoprotein receptor 2	lectin_c	5.4
448093	AW977382	Hs.15898	2,4-dienoyl CoA reductase 2, p	adh_short	5.4
411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF	5.4
406432			CD1E antigen, e polypeptide	Sulfotransfer	5.4
428921	Z43809	Hs.194638	polymerase (RNA) II (DNA direc		5.4
430337	M36707	Hs.239600	calmodulin-like 3	efhand	5.4
427162	AB011133	Hs.173864	KIAA0561 protein	pkinase,PDZ	5.4
414216	D86970	Hs.75822	TGFB1-induced anti-apoptotic f	oxidored_q4,myosin_head,b	5.4
422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase,	lipoxygenase,PLAT	5.4
424373	AJ133798	Hs.146219	copine VII	C2	5.4
449405	AA001350		gb:zh83h05.r1 Soares_fetal_liv	mito_carr	5.4
409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch	5.4
455818	AI733747	Hs.71174	interleukin 21 receptor		5.4
424357	AW961058	Hs.44856	hypothetical protein FLJ12116		5.4
423606	AB011094	Hs.129892	KIAA0522 protein	PH,bZIP,IQ,Sec7	5.3
432311	BE083080	Hs.274323	similar to sialyltransferase 7	Glyco_transf_29	5.3
450080	AB037831	Hs.24372	ESTs, Weakly similar to dJ207H	DEAD,GSPII_E	5.3
423778	Y09267	Hs.132821	flavin containing monooxygenas	FMO-like,pyr_redox	5.3
402338			Target Exon	p450	5.3
412276	BE262621	Hs.73798	macrophage migration inhibitor	MIF	5.3
437967	BE277414	Hs.5947	mel transforming oncogene (der	ras,arf	5.3
424766	BE388855	Hs.152978	proteaseome (prosome, macropai	PA28_alpha,PA28_beta	5.3
447766	NM_016011	Hs.19513	CGI-63 protein	adh_zinc	5.3
453660	X98507	Hs.286226	myosin IC	myosin_head,IQ	5.2
435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	HLH,Myc_N_term,Myc-LZ	5.2
432336	NM_002759	Hs.274382	protein kinase, interferon-ind	dsrm,pkinase	5.2
445139	AB037848	Hs.12365	synaptotagmin XIII	C2	5.2
429214	AB012722	Hs.198256	kinesin-like 3	kinesin	5.2
432462	AK000013	Hs.274701	thymidine kinase 2, mitochondr	dNK	5.2
424387	AI739312	Hs.284163	ANKHZN protein		5.2
405697			gb:Human homeobox-like mRNA		5.2
450321	Y16521	Hs.24812	CDP-diacylglycerol synthase (p	Cytidylyltrans,Adeno_VII	5.1
412939	AW411491	Hs.75069	eukaryotic translation elongat	SHMT	5.1
445109	AF039916	Hs.12330	ectonucleoside triphosphate di	GDA1_CD39	5.1
419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis	ig,tsp_1,ZU5	5.1
409958	NM_001523	Hs.57697	hyaluronan synthase 1	Glycos_transf_2	5.1
442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank	5.1
424305	BE386095	Hs.112272	histone deacetylase 8	Hist_deacetyl	5.1
427247	AW504221	Hs.174103	integrin, alpha L (antigen CD1	vwa,integrin_A,FG-GAP	5.1
429061	Y14039	Hs.195175	CASP8 and FADD-like apoptosis	DED,ICE_p20	5.1
420849	X52221	Hs.99987	excision repair cross-compleme		5.1

453337	R73417	Hs.25391	gb:yj92g12.r1 Soares breast 2N	GSPII_III	5.1
418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH	5.1
425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyro	SH2,SH3,pkinase,PH,BTK	5.1
405202			NM_021734*:Homo sapiens deoxyn	mito_carr	5.1
451452	BE560065	Hs.26433	dolichyl-phosphate (UDP-N-acet	Glycos_transf_4	5.0
418231	AA326895	Hs.83848	triosephosphate isomerase 1	TIM	5.0
425165	NM_014434	Hs.154899	Target CAT		5.0
407876	NM_004519	Hs.40866	potassium voltage-gated channe	ion_trans,KCNQ1_channel	5.0
417831	H16423	Hs.82685	CD47 antigen (Rh-related antig	ig	5.0
404716			NM_007313*:Homo sapiens v-abl	SH2,SH3,pkinase	5.0
405020			Target Exon	7tm_1	5.0
426236	NM_004798	Hs.168212	kinesin family member 3B	kinesin	5.0
433178	AB038269	Hs.253706	cysteinyl leukotriene CysLT2 r	7tm_1	5.0
422340	AW296219	Hs.115325	RAB7, member RAS oncogene faml	arf,ras	5.0
439414	NM_001183	Hs.6551	ATPase, H transporting, lysoso		5.0
425846	AA102174	Hs.159629	myosin IXB	myosin_head,DAG_PE-bind,I	5.0
413599	AJ006239	Hs.75438	quinoid dihydropteridine reduc	adh_short	5.0
424168	L29277	Hs.321677	signal transducer and activato	SH2,STAT,STAT_bind,STAT_p	5.0
436042	AF284422	Hs.119178	cation-chloride cotransporter-	aa_permeases	5.0
410775	AB014460	Hs.66196	nth (E.coli endonuclease III)-	HhH-GPD	5.0
428734	BE303044	Hs.192023	eukaryotic translation initiat	WD40	5.0
420340	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide	ITAM	4.9
433075	NM_002959		sortilin 1	BNR	4.9
400300	X03363		HER2 receptor tyrosine kinase	pkinase	4.9
426811	BE259228	Hs.172609	*nucleobindin 1*	*efhand*	4.9
401577			NM_000761:Homo sapiens cytochr	p450	4.9
409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp4	Collagen	4.9
426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase	4.9
430904	U65402	Hs.248124	G protein-coupled receptor 31	7tm_1	4.9
423552	AF107028	Hs.129783	sodium channel, voltage-gated,	ig,Adeno_E3_CR2	4.9
421487	AF027406	Hs.104865	serine/threonine kinase 23	pkinase	4.9
402183			NM_004491*:Homo sapiens glucoc	FF	4.9
456748	AW137749	Hs.125902	ubiquitin specific protease 2	UCH-1,UCH-2	4.9
424771	BE397151	Hs.153003	serine/threonine kinase 16	pkinase	4.9
406441			Target Exon	Aa_trans	4.9
437053	AU077018	Hs.3235	keratin 4	filament,bZIP,Tropomyosin	4.9
443044	N28522	Hs.8935	*quinolinate phosphoribosyltran*	*QRPTase,QRPTase_N*	4.9
431204	F28841	Hs.250760	cytochrome c oxidase subunit V	dUTPase,COX6A,ras,ATP-syn	4.9
456417	L36531	Hs.91296	integrin, alpha 8	integrin_A,FG-GAP	4.8
436735	L48489		mannosyl (beta-1,4-)-glycoprot		4.8
441455	AJ271671	Hs.7854	zinc/iron regulated transporte	Zip	4.8
446948	BE409053	Hs.299629	peroxisomal long-chain acyl-co		4.8
451564	AU076698	Hs.132760	hypothetical protein MGC15729	sugar_tr,Condensation	4.8
403771			NM_003061:Homo sapiens slit (D	EGF,laminin_G,LRR,LRRNT,L	4.8
403248			ESTs, Weakly similar to I78885	SLT	4.8
410214	L29555	Hs.301698	sialyltransferase 4A (beta-gal	Glyco_transf_29	4.8
407047	X65965		gb:H.sapiens SOD-2 gene for ma	sodfe	4.8
422668	AF199364	Hs.119120	E3 ubiquitin ligase SMURF1	C2,WW,HECT	4.8
436057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding	4.8
431262	NM_006672	Hs.251395	solute carrier family 22 (orga	sugar_tr	4.8
406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delta	FA_desaturase	4.8
428659	U66579	Hs.188859	G protein-coupled receptor 20		4.8
432716	AI762964	Hs.205180	ESTs		4.8
414460	L00727	Hs.898	dystrophia myotonica-protein k	pkinase	4.8
400287	S39329	Hs.181350	kallikrein 2, prostatic	trypsin	4.8
428946	D42046	Hs.194665	DNA2 (DNA replication helicase	UvrD-helicase,Viral_helic	4.7
420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosam	Sulfotransfer	4.7
402912			Target Exon	pkinase	4.7
443329	BE262943	Hs.9234	hypothetical protein MGC1936		4.7
426120	AA325243	Hs.166887	copine I	C2	4.7
430609	AA302921	Hs.247362	dimethylarginine dimethylamino		4.7
451320	AW118072		diacylglycerol kinase, zeta (1	zf-C2H2,BAR,SH3	4.7
447131	NM_004585	Hs.17466	retinoic acid receptor respond		4.7
431222	X56777	Hs.273790	zona pellucida glycoprotein 3A	zona_pellucida	4.7
406458			C14000133*:gi|1082739|pir||C44	proteasome	4.7
427804	AL049654	Hs.180871	protein kinase C, alpha bindin	PDZ	4.7
450748	AI733093	Hs.247686	ESTs	7tm_1	4.7
422937	U03270	Hs.122511	centrin, EF-hand protein, 1	efhand	4.7
407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodul	PDEase	4.7
428773	BE256238	Hs.193163	bridging integrator 1	SH3,BAR	4.7
456444	AA884517	Hs.31856	ESTs, Weakly similar to KIAA14		4.7
405574			Target Exon	pkinase	4.7
442414	BE408758	Hs.8297	ribonuclease 6 precursor	ribonuclease_T2	4.7
418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome		4.6
421601	AI660190	Hs.106070	cyclin-dependent kinase inhibi	CDI	4.6
422795	AB033109	Hs.120866	KIAA1283 protein	kazal,A2M,A2M_N	4.6
433019	AI208513	Hs.279915	translocase of inner mitochond	zf-Tim10_DDP	4.6
431522	AI625859	Hs.258609	protein tyrosine phosphatase,	fn3,Y_phosphatase	4.6
400846			sortilin-related receptor, L(D	ldl_recept_a,fn3,ldl_rece	4.6
456881	AW028302	Hs.155079	protein phosphatase 2, regulat	B56	4.6
418172	X61157	Hs.83636	adrenergic, beta, receptor kin	pkinase,PH,RGS	4.6
408433	AW162931	Hs.45002	ras-related C3 botulinum toxin	ras	4.6
439921	AL110209	Hs.6770	LCAT-like lysophospholipase	LACT	4.6
427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase	pkinase,Furin-like,Recep_	4.6

427945	AW137156	Hs.181202	hypothetical protein FLJ10038	Collagen	4.6
451777	U09210	Hs.459	solute carrier family 18 (vesi	sugar_tr	4.6
429938	BE296804	Hs.226377	phosphate cytidylyltransferase	Cytidylyltransf,COX6C	4.6
412974	R18978	Hs.75105	emopamil-binding protein (ster		4.6
414702	L22005	Hs.76932	cell division cycle 34	UQ_con	4.6
425795	AJ000479	Hs.159543	endothelial differentiation, G	7tm_1	4.6
422454	U49070	Hs.161362	protein (peptidyl-prolyl cis/t	Rotamase,WW	4.6
408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4	4.6
457388	AF035300	Hs.264157	cadherin-like 22	cadherin,Cadherin_C_term	4.6
421140	AA298741	Hs.102135	signal sequence receptor, delt	Herpes_UL3	4.6
434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-a	Acyltransferase	4.6
413407	AI356293	Hs.75339	inositol polyphosphate phospha	SH2,SAM	4.6
402463			NM_014624:Homo sapiens S100 ca	efhand,S_100	4.5
417891	W79410	Hs.82887	protein phosphatase 1, regulat		4.5
421681	AA384922	Hs.195175	CASP8 and FADD-like apoptosis	ICE_p20,DED	4.5
426516	BE262660	Hs.170197	glutamic-oxaloacetic transamin	aminotran_1_2	4.5
418963	BE304571	Hs.89529	aldo-keto reductase family 1,	aldo_ket_red	4.5
423664	NM_004714	Hs.130988	dual-specificity tyrosine-(Y)-	pkinase	4.5
427681	AB018263	Hs.180338	tumor necrosis factor receptor	TNFR_c6,death,PH,Xlink,Rh	4.5
432893	NM_016154	Hs.279771	Homo sapiens clone PP1596 unkn	ras,arf	4.5
413815	AL046341	Hs.75562	discoidin domain receptor fami	F5_F8_type_C,pkinase	4.5
405546			NM_018833*:Homo sapiens transp	ABC_membrane,ABC_tran	4.5
416297	AA157634	Hs.79172	solute carrier family 25 (mito	mito_carr	4.5
421962	D82061	Hs.288354	FabG (beta-ketoacyl-[acyl-carr	adh_short	4.5
415341	R00602		gb:ye74c04.r1 Soares fetal liv	pkinase	4.5
456668	W81526	Hs.118329	ESTs, Moderately similar to GA	Neur_chan_LBD,Neur_chan_m	4.5
456652	AW327546	Hs.111024	solute carrier family 25 (mito	mito_carr	4.5
407863	AA317089	Hs.597	glutamic-oxaloacetic transamin	aminotran_1_2	4.5
435891	AW249394	Hs.5002	copper chaperone for superoxid	sodcu,HMA	4.5
453997	AW247615	Hs.37003	v-Ha-ras Harvey rat sarcoma vi	ras	4.5
449029	N28989	Hs.22891	solute carrier family 7 (catio	aa_permeases	4.5
424829	NM_002507	Hs.1827	nerve growth factor receptor (	death,TNFR_c6	4.5
429362	T25833	Hs.200478	ubiquitin-conjugating enzyme E	UQ_con	4.5
429133	N31854	Hs.197116	solute carrier family 7 (catio	aa_permeases	4.5
426079	D31220	Hs.166168	peter pan (Drosophila) homolog	7tm_1	4.4
414814	D14697	Hs.77393	famesyl diphosphate synthase	polyprenyl_synt	4.4
433261	AB040967	Hs.112034	KIAA1534 protein	PH,Oxysterol_BP	4.4
402915			ENSP00000202587*:Bicarbonate t	HCO3_cotransp	4.4
418267	BE389537	Hs.83919	glucosidase I	Glyco_hydro_63	4.4
430716	BE387257	Hs.247831	Homo sapiens, Similar to myosi	efhand	4.4
420874	X66357	Hs.336478	cyclin-dependent kinase 3	pkinase	4.4
439902	AF174499	Hs.6764	histone deacetylase 6	Hist_deacetyl,zf-UBP	4.4
400223			Eos Control	Skp1	4.4
450611	NM_004405	Hs.419	distal-less homeo box 2	homeobox	4.4
412965	L06419	Hs.75093	procollagen-lysine, 2-oxogluta	2OG-FeII_Oxy	4.4
435564	AF210652	Hs.16614	5(3)-deoxyribonucleotidase (dN		4.4
416121	X92762	Hs.79021	tafazzin (cardiomyopathy, dila	Acyltransferase	4.4
423323	AI951628	Hs.127007	potassium channel, subfamily K	Ion_trans	4.4
448191	NM_005881	Hs.20644	branched chain alpha-ketoacid	HATPase_c	4.4
456217	BE253181	Hs.81687	non-metastatic cells 3, protei	NDK,Arteri_glycop	4.4
436415	BE265254	Hs.343258	proliferation-associated 2G4,	Peptidase_M24	4.4
429218	AA225065	Hs.198269	Target CAT		4.4
407433	AF209923		gb:Homo sapiens orphan G-prote	7tm_3	4.4
425955	T96509	Hs.248549	ESTs, Moderately similar to S6		4.4
407230	AA157857	Hs.182265	keratin 19	filament,bZIP	4.3
410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coe	HMG_CoA_synt	4.3
416409	R61573	Hs.79300	ubiquitin-conjugating enzyme E	UQ_con	4.3
447957	NM_014821	Hs.20126	KIAA0317 gene product	Filamin,HECT	4.3
421771	NM_001224	Hs.108131	caspase 2, apoptosis-related c	ICE_p20,CARD,ICE_p10	4.3
448886	AL137291	Hs.22451	hypothetical protein FLJ10357	PH,RhoGEF	4.3
414821	M63835	Hs.77424	Fc fragment of IgG, high affin	ig	4.3
431096	AA324358	Hs.249227	Homo sapiens DNA, cosmid clone		4.3
429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	ig,fn3	4.3
450126	BE018138	Hs.24447	sigma receptor (SR31747 bindin		4.3
413781	J05272	Hs.850	IMP (inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD	4.3
406530			NM_005546*:Homo sapiens IL2-in	SH2,SH3,pkinase,PH,BTK	4.3
428363	AK000284	Hs.183860	hypothetical protein FLJ20277	GNT-I	4.3
413954	AL037111	Hs.75641	galactose-1-phosphate uridylyl	GalP_UDP_transf,GalP_UDP_	4.3
432179	X75208	Hs.2913	EphB3	EPH_lbd,fn3,pkinase,SAM	4.3
456529	AF014643	Hs.100072	connexin46.6	connexin	4.3
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
426626	AI124572	Hs.323879	inhibitor of kappa light polyp	zf-C2H2	4.3
432956	AL037895	Hs.279861	CGI-31 protein	thiored	4.3
428970	BE276891	Hs.194691	retinoic acid induced 3	7tm_3	4.3
428953	AA306610	Hs.348183	tumor necrosis factor receptor	TNFR_c6	4.2
423922	AK001663	Hs.135458	muscle-specific beta 1 integri		4.2
426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydro	adh_short	4.2
426566	AF131836	Hs.170453	tropomodulin	Tropomodulin,pkinase	4.2
425179	AJ224442	Hs.155020	putative methyltransferase		4.2
412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)		4.2
459298	R86701		gb:ym86d09.r1 Soares adult bra		4.2
404879			NM_030807:Homo sapiens glucose		4.2
400836			Target Exon	Apolipoprotein	4.2
430940	Z25470	Hs.248145	melanocortin 5 receptor		4.2

400563			Target Exon	Pep_M12B_propep	4.2
430237	AI272144	Hs.236522	DKFZP434P106 protein	abhydrolase	4.2
425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	DAG_PE-bind,C2	4.2
409067	BE260459	Hs.50267	putative GTP-binding protein s	ras	4.2
419982	AA252544	Hs.55610	solute carrier family 30 (zinc		4.2
428394	AU076472	Hs.184141	glutaryl-Coenzyme A dehydrogen	Acyl-CoA_dh,Acyl-CoA_dh_M	4.2
437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	Hydrolase	4.2
454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 famil	aldedh	4.2
410237	AI750589	Hs.61258	argininosuccinate lyase	lyase_1	4.1
451478	NM_012331	Hs.26458	methionine sulfoxide reductase	PMSR	4.1
415410	AF037332	Hs.278569	sorting nexin 17	PX,fn3,pkinase,SAM,EPH_lb	4.1
406538			Target Exon	trypsin	4.1
424349	AF141289	Hs.145550	solute carrier family 7 (catio	aa_permeases	4.1
441164	AB023180	Hs.7724	KIAA0963 protein	helicase_C	4.1
421318	U63973	Hs.103501	rhodopsin kinase	pkinase,pkinase_C,RGS	4.1
439340	AB032436	Hs.6535	brain-specific Na-dependent in	sugar_tr,BT1	4.1
417447	N73703	Hs.293267	ESTs	Glyco_hydro_31	4.1
409693	AA010233	Hs.55921	glutamyl-prolyl-tRNA synthetas	WHEP-TRS,GST_C,HGTP_antic	4.1
403655			NM_003071:Homo sapiens SWI/SNF	SNF2_N,helicase_C,zf-C3HC	4.1
411142	NM_014256	Hs.69009	transmembrane protein 3	Galactosyl_T	4.1
437016	AU076916	Hs.5398	guanine monphosphate synthetas	GMP_synt_C,GATase	4.1
422699	BE410590	Hs.119257	ems1 sequence (mammary tumor a	SH3,HS1_rep	4.1
427202	BE272922	Hs.173936	interleukin 10 receptor, beta	Tissue_fac	4.1
421380	D31833	Hs.1372	arginine vasopressin receptor	7tm_1	4.1
434142	U47927	Hs.3759	ubiquitin specific protease 5	zf-UBP,UCH-2,UBA,UCH-1	4.1
427407	BE268649	Hs.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,PARP_re	4.1
413749	AI929320	Hs.75516	tyrosine kinase 2	pkinase	4.1
411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1	4.1
419726	U50330	Hs.1274	bone morphogenetic protein 1	EGF,CUB,Astacin	4.1
423814	AF105020	Hs.132989	putative protein O-mannosyltra	PMT,MIR	4.1
451355	NM_004197	Hs.444	serine/threonine kinase 19		4.1
422556	NM_006245	Hs.118244	protein phosphatase 2, regulat	B56	4.1
428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH de		4.1
431968	AF117222	Hs.272261	UDP-Gal:betaGlcNAc beta 1,3-ga	Galactosyl_T	4.0
443639	BE269042	Hs.9661	proteasome (prosome, macropain	proteasome	4.0
410039	AF207989	Hs.58014	Homo sapiens, Similar to G pro	7tm_3	4.0
431066	AF026273	Hs.249175	interleukin-1 receptor-associa	pkinase,death	4.0
452715	Z21093	Hs.30352	ribosomal protein S6 kinase, 5	pkinase	4.0
403692			NM_007037*:Homo sapiens a disi	Reprolysin,tsp_1,Pep_M12B	4.0
442549	AI751601	Hs.8375	TNF receptor-associated factor	zf-C3HC4,MATH,zf-TRAF	4.0
427239	BE270447		ubiquitin carrier protein	UQ_con	4.0
451125	AA015779	Hs.226923	ESTs	Y_phosphatase	4.0
425081	X74794	Hs.154443	minichromosome maintenance def	MCM	4.0
402171			Target Exon	C2	4.0
402665			Target Exon		4.0
420148	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B	myosin_head,IQ,MyTH4,SH3,	4.0
412187	U68487	Hs.73739	5-hydroxytryptamine (serotonin	7tm_1	4.0
412656	AF006011	Hs.74375	dishevelled 1 (homologous to D	PDZ,DEP,DIX,Dishevelled	4.0
425786	U35234	Hs.159534	protein tyrosine phosphatase,	fn3,ig,Y_phosphatase,DSPc	4.0
424288	AW137198	Hs.278682	Phosphatidylglycerophosphate S		4.0
452230	AW135360	Hs.224170	ESTs	pkinase	4.0
408449	NM_004408	Hs.166161	dynamin 1	PH,GED,dynamin,dynamin_2	4.0
423883	AF250238	Hs.134514	ATP-binding cassette, sub-fami	ABC_tran,photoRC,SRP54,Ca	4.0
422676	D28481	Hs.1570	histamine receptor H1	7tm_1	4.0
458639	BE247683	Hs.14611	dual specificity phosphatase 1	DSPc	4.0
400726			C13000717*:gi|129376|sp|P26196	DEAD,helicase_C	4.0
405370			NM_005569*:Homo sapiens LIM do	pkinase,LIM,PDZ	4.0
413654	AA331881	Hs.75454	peroxiredoxin 3	AhpC-TSA	4.0
432917	NM_014125	Hs.241517	PRO0327 protein		4.0
448362	AA641767	Hs.21015	hypothetical protein DKFZp564L	sugar_tr	4.0
424512	X53002	Hs.149846	integrin, beta 5	integrin_B,EGF	4.0

TABLE 22B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410191	11824_1	AI609645 AI818201 AA948024 AI278970 AA688086 AA858279 F21973 W95840 AW969644 X99726 AA431579 AA970887 AI885085 AI767835 BE566516 AA725824 AI000871 AW242322 AW007204 W68289 AA431450 AW466973 BE222544 AA483454 AI968050 W95975 AI381017 AA776726 AI040976 AA89
415341	1534442_1	R00602 Z42921 F06132
415995	1564_1	NM_004573 M95678 BE242666 AW504110 AW408049 AW402206 AA774879 AW630959 AI439623 AI933994 AW751282 AW374413 AA578823 H18054 AA310466 F12578 T74300 AA353176 AW950138 AW950600 AA912021 AI524064 AW183098 AI416986 AW769231 AI767111 AA293723 AI422290 AA465038 A
418964	1809680_1	T74640 T74649
424339	23827_1	BE257148 BE312111 AF219137 NM_015720 BE313658 BE382652 BE252205 BE251553 F12128 T66208 BE255806 BE254484 AA324163 H07952 AL134164 AI867802 AI204971 AI282924 AW192547 AI652760 AI266471 AI083778
427010	27436_1	AW138332 AW207450 AW138931 AW136963 NM_012219 AF043938 AA931386 AI084600 AA975999 BE551105 AA450260 AI080368 AA324154 AF022080 BE009901 AL118847 W44458 AI765270 AA453121 AI148638 AI373696 AA324153 BE174809 AA350765
427239	27647_1	BE270447 AW409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719 BE268715 BE513876 BE295291 BE297066 AA210923 BE407519 H51344 BE622905 AW248281 AW250313 T19021 AA355115 AA316879 BE269633 BE621936 AA290724
427326	277229_1	AI287878 AI804160 AA400787

428542	29266_1	D79989 NM_014770 U81031 AA352392 AA984512 H38328 AL120358 AL134787 AL134589 AI637763 AI671506 AA526909 AI651627 AW243560 AA939069
428948	29737_1	BE514362 AI879343 BE272870 BE616390 AW163444 AW161588 AW378754 AW238803 BE267205 BE047746 BE207213 BE312782 BE266301 BE266413 BE278348 BE280885 BE278833 BE281417 BE407786 BE378176 BE392818 AW377597 BE395951 BE393978 AW327483 BE394175 BE385795 BE275663 BE3
432118	341702_-1	N98718
432499	34857_1	BE276633 NM_016577 AF166492 BE276152 AF091031 AA908607 U66623 AI570393 AA682567 AW593957 AI148105 AW002431 AI637463 AI767195 AA339439 R13005 R23431 AW961068 AA233819 AA224118 R19618 AI890314 Z46184
433075	35820_1	NM_002959 X98248 AA233278 AA846376 AI470560 AI470533 BE327147 AW291971 AA017125 AI198417 AI365213 AI168442 AI337018 AI475049 H85459 AA969895 AA888000 AA418326 AA418378 N71981 AL043634 AA426361 AA418275 AA232975 AL036861 BE277220 BE387505 N99710 AW375004 A
433494	3679_1	AB029396 T04934 R21715 R19005 H11563 H14256 R46605 Z40857 BE218899 AI457785 BE550988 AI693847 AA961017 H40944 M78617 H38447 N80090 BE549719 BE550952 AW005546 AI332686 AI928848 N49234 R44075 AI694943 AI858538 AI290722 BE550759 R43116 H40212 H40089 AA018091
434755	392764_1	AA648502 AA814365 AW976711 AA746117
436735	425_1	L48489 AL022312 D13789 AI761974 AW173260 AW271715 AA837437 AI075278 AI367012 AI953032 AI571173 H44868 AA743691 H47026 AA837368 AA829826 AA713585 AW502618 AW500856 AW501353 AW499765 AA339125 H19141 H29645 R18883 AW450375 AA326081 AW406015 BE263659 N52684 A
440242	489536_1	AW295871 AI005144 AA909877 T52634 AI239684 AA875959 BE171353 AI767633 AW510907 AI742007
449405	80651_1	AA001350 AA203114 H83070 R00660
450739	844917_1	AI732707 AI742120
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623
459298	983107_1	R86701 R84600 AL157655.,

TABLE 22C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400471	9931670	Minus	105629-105760
400518	9796703	Plus	37240-37774
400551	9801071	Minus	40629-40934
400563	9844011	Plus	81941-82434
400565	9863505	Minus	93178-93429
400726	8118950	Plus	51524-51786
400748	8119063	Plus	84237-84398
400772	8131629	Minus	34896-35021,41078-41197
400833	8705148	Minus	187599-188138
400836	8954179	Plus	677-1188
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400845	9188605	Plus	34428-34612
400846	9188605	Plus	39310-39474
400894	9958307	Minus	84607-85554
400933	7651935	Minus	105330-105503
400985	8085497	Minus	5856-6006,6236-6402
401118	9966714	Minus	111939-112126
401134	7210005	Plus	51210-51406
401180	9438648	Minus	150981-152128
401215	9858408	Plus	103739-103919
401281	9800073	Minus	13622-15130
401454	9186923	Minus	114659-114832
401488	7341775	Plus	54523-54686,55364-55451,55737-55846,58047-58175,58261-58356
401507	7534110	Plus	71055-71259
401510	7622346	Minus	46835-47126
401542	8072607	Minus	87695-87840
401577	9280797	Minus	139377-139674,141195-141281,142217-142340
401736	3219338	Plus	1771-1894
401885	8140731	Plus	148234-148321,150365-150559
401935	3808091	Plus	46329-46473
401960	3249127	Minus	87589-88081
402053	8083229	Plus	62703-63179
402115	8547592	Minus	101750-102018
402171	8575908	Minus	79357-79514,83258-83476
402183	7658390	Minus	100618-104298
402191	8576073	Minus	69410-69583
402207	8576119	Plus	41683-41851
402209	8576119	Minus	53315-53472
402211	7689783	Minus	67414-68229
402338	6957691	Minus	36915-37250
402393	9929688	Plus	19813-20084,20163-20263
402453	7534025	Plus	41-631
402460	9796884	Minus	108901-109254,110246-110581,113613-113960
402463	9796896	Minus	8818-8952
402478	9797301	Minus	106204-106535
402497	9797775	Plus	98984-99452
402632	9931268	Plus	101166-101419
402651	7960391	Plus	174215-174380
402665	8077033	Minus	11824-12090,14290-14544
402758	9213869	Plus	87638-87924

402760	9213869	Plus	136829-136952,137336-137521
402823	8217451	Plus	57916-58170,58475-58759,59580-59867
402912	7263904	Plus	145965-146257,150876-151368
402915	7406502	Minus	140-276
402916	7406502	Minus	361-474,541-687
403213	7630897	Minus	162572-162739,164442-164540
403248	7656833	Minus	167439-167606
403268	7230852	Minus	73832-73962
403379	9438244	Minus	117348-117560
403655	8736093	Plus	65668-65859
403672	7283286	Minus	96600-96881,96951-97280,97393-97594
403692	7387384	Minus	93803-93938
403771	7770492	Plus	112901-113045
403949	7711972	Minus	1731-1941
404199	6010176	Minus	1669-2740
404527	8152087	Plus	127737-127796,128080-128210,129888-130054,132545-132869
404528	8152087	Plus	135325-135486
404596	9958262	Minus	104807-105043
404676	9797204	Minus	56167-56342,58066-58189,58891-59048,60452-60628
404679	9797204	Plus	125964-126092,126691-127011,127774-127893
404716	9838068	Minus	123145-123417
404757	7706327	Plus	100933-101083,101580-101782
404879	5103013	Plus	78346-78473,78693-78893
404946	7382189	Plus	134445-134750
404953	7387324	Plus	16588-17031
404968	6899755	Plus	39287-39606
405020	7137674	Plus	106606-107309
405137	8570507	Plus	158969-159423
405187	7229826	Plus	117025-117170,118567-118736
405202	7230116	Plus	40209-40429
405282	3810573	Minus	10482-10689
405370	2078469	Minus	38980-39111
405371	2078469	Minus	47657-47766,48461-48596
405473	8439781	Plus	153074-153343,154501-154598,156879-156999,158863-159051,159910-160053,161109-161229,163035-163131,165163-165259,165868-166003,167375-167552,169252-169364,171127-171281
405474	8439781	Plus	172005-172175
405546	1054740	Plus	124010-124183
405574	3820491	Minus	33200-33646
405594	6960456	Plus	161628-161734,162823-163014,164439-164652
405683	4508157	Minus	21701-21844
405697	4309923	Minus	56765-57010,57696-58016
405714	4156179	Minus	42789-43553
406128	9159110	Plus	50425-50876
406370	9256130	Plus	125320-125482
406432	9256504	Plus	3804-3930,4026-4120,4929-5109
406441	9280715	Plus	26200-26458
406458	9756020	Plus	145874-146911
406495	7711328	Minus	174661-174978
406496	7711328	Minus	178947-179264,181779-182087
406530	7711474	Minus	11703-11860,14711-14829,14920-14984,16232-16448,16916-17087
406538	7711478	Plus	35196-35367,38229-38476,40080-40216,43522-43840
406591	8224230	Minus	2117-2257,2436-2540
406617	8439858	Plus	36430-36552

Table 23A lists about 779 genes up-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal ovaries was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 93rd percentile value amongst various non-malignant adult ovaries, the "average" ovarian cancer value was greater than or equal to 200 units.

TABLE 23A:
Pkey: Unique Eos probeset identifier number
Ex. Accn: Exemplar Accession number, Genbank accession number
UG ID: UniGene number
Title: UniGene gene title
Protein Dom.: Predicted protein domain
R1: Ratio of tumor to normal ovaries

Pkey	Ex. Accn	UG ID	Title	Protein Dom.	R1
421296	NM_002666	Hs.103253	perilipin	perilipin,SS	37.8
437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,zf-DHHC	29.2
453028	AB006532	Hs.31442	RecQ protein-like 4	DEAD,helicase_C,Fork_head	27.6
441021	AW578716	Hs.7644	H1 histone family, member 2		27.2
422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS,TM,pkinase,fn3,ig	26.5
454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	25.9
438424	AI912498	Hs.25895	hypothetical protein FLJ14996	SS,TM	25.8
435017	AA336522	Hs.12854	angiotensin II, type I recepto		25.0
409518	BE384836	Hs.3454	KIAA1821 protein	SS	23.3
410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ldl_recept_a,trypsi	22.8
439924	AI985897	Hs.125293	ESTs	SS	22.7
446374	AA329256	Hs.24756	ESTs, Moderately similar to al		22.6
431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH,SS,LIM,Troponin	21.4
420839	AI792682	Hs.282960	hypothetical protein MGC10870	SS,DS,UPF0139,Glyco_hydro	21.4
413436	AF238083	Hs.68061	sphingosine kinase 1	DAGKc	21.2

424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG,SS,TM,MAPEG	20.7
422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase,SS,Ets	20.7
436725	BE045223	Hs.136912	hypothetical protein MGC10796		20.4
422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.2
429556	AW139399	Hs.98988	ESTs	SS,pkinase,PMP22_Claudin	20.1
434068	AA977935	Hs.127274	ESTs	SS	20.0
423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	19.9
423652	AF052122	Hs.130712	Homo sapiens clone 23929 mRNA	ABC1,SS,PID,PID	19.8
422179	AF091619	Hs.112667	dynein, axonemal, intermediate	WD40,SS	19.3
441356	BE384361	Hs.182885	ESTs, Weakly similar to JC5024	SS,TM,ank	18.5
418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	17.2
432631	H08379	Hs.165563	hypothetical protein DKFZp434N	TM,DnaJ,UBA,ArfGap,homeob	17.2
439108	AW163034	Hs.6467	synaptogyrin 3	Synaptogyrin,SS,TM,PDZ,WD	17.2
451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	17.2
434518	H56995	Hs.37372	Homo sapiens DNA binding pepti	SS	16.9
413244	AW955951	Hs.159265	kruppel-related zinc finger pr	SS,TM,BTB,Pep_M12B_propep	16.3
456642	AW451623	Hs.109752	putative c-Myc-responsive		16.2
421612	AF161254	Hs.106196	8D6 antigen	ldl_recept_a,SS,TM	16.0
456177	NM_012391	Hs.79414	prostate epithelium-specific E	Ets,SAM_PNT	15.7
409261	BE315042	Hs.19210	hypothetical protein MGC11308		15.6
414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	15.6
401278			Target Exon	Band_41	15.4
444804	AI084452	Hs.22158	hypothetical protein FLJ21988	SS	15.4
406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,I	15.1
421495	AI583067	Hs.149152	ESTs, Weakly similar to RHOP M		15.0
416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rrm,SS	15.0
442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668	SS,RNA_pol_K	14.9
406901	M14624		gb:Human 4-beta-galactosyltran		14.6
416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	14.6
455557	AW995839		gb:QV4-BN0044-110200-108-h07 B	Metallophos	14.4
416819	U77735	Hs.80205	pim-2 oncogene	pkinase,SS,TM,OTU,K_tetra	14.3
444441	AW613841	Hs.301394	hypothetical protein MGC3101		14.0
406918	M88357		gb:Homo sapiens DNA-binding pr	zf-C2H2,SS	14.0
407605	W03512	Hs.6479	hypothetical protein MGC13272	SS,Sema,pkinase,TIG,PSI,e	13.6
447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS,Peptidase_C2	13.6
402365			Target Exon	SS,SS,TM,Ig	13.4
407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	13.3
432931	AF174487	Hs.293753	Bcl-2-related ovarian killer p		12.7
439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
423801	NM_015071	Hs.132942	GTPase regulator associated wi	RhoGAP,SH3,PH	12.6
430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.6
411570	BE144584	Hs.314341	ESTs		12.5
400206			Eos Control	SS,SS,Glyco_tranf_43,COLF	12.3
457941	AI004525	Hs.14587	ESTs, Weakly similar to AF1518	SS,TM,SS,TM	12.2
412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand,SS,CAP_GLY	12.0
400460			C11002253*:gi|129091|sp|P23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	11.6
428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	11.5
424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema	11.5
444359	AI697160	Hs.143594	ESTs, Weakly similar to HS4L_H		11.5
435158	AW663317	Hs.65588	DAZ associated protein 1	rrm,SS,rrm	11.3
407688	W25317	Hs.37616	Human D9 splice variant B mRNA		11.3
450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	11.2
427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2
406230			Target Exon		11.2
432143	AL040183	Hs.123484	Homo sapiens, clone IMAGE:4178	SS,TM,cys_rich_FGFR	11.2
433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cadherin,	11.1
413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	11.1
431974	AW972689	Hs.200934	ESTs	bZIP	11.0
428167	AA770021	Hs.16332	ESTs	SS,ig,fn3	11.0
450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS	10.9
412738	N34731	Hs.74562	siah binding protein 1; FBP in	homeobox	10.9
445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,lipoc	10.9
444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_H	SS,SS,SAC3_GANP	10.7
444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	10.6
444607	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PH,PI-PLC-Y,C	10.6
404333			C7001735*:gi|7768636|dbj|BAA95	vwd	10.5
401210			C12000519:gi|7710046|ref|NP_05		10.5
434743	AI363410		ribosomal protein S18	SS,TM	10.4
434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	10.4
450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	10.4
439632	AW410714	Hs.334437	hypothetical protein MGC4248	SS,TM,transmembrane4	10.3
438185	Y19188	Hs.320461	ESTs	SS	10.2
432031	AF039196	Hs.272367	hairless protein (putative sin	jmjC	10.2
405371			NM_005569*:Homo sapiens LIM do	pkinase,LIM,PDZ	10.1
456741	W37608	Hs.184492	ESTs	SS,pkinase	10.1
458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	10.0
456977	AK000252	Hs.169758	hypothetical protein FLJ20245		10.0
420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	10.0
445625	BE246743		hypothetical protein FLJ22635	SS,TM	9.9
423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	9.8
458216	AW024282	Hs.104938	hypothetical protein MGC15906		9.8
451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocyt	spectrin,PH,CH,SS,Peptida	9.7
421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054	asp,SS,TM,Ion_trans,K_tet	9.7

431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	SS,PWWP,PHD	9.7
443780	NM_012068	Hs.9754	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	9.7
448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.7
444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	9.7
427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF,late_protein_L2,SS,GS	9.6
419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS	9.6
424618	L29472	Hs.1802	major histocompatibility compl	TM,ig,MHC_II_beta,SS,TM,A	9.6
427497	AW139476	Hs.31240	ESTs		9.6
420423	AA827718	Hs.88218	ESTs	SS	9.6
414756	AW451101	Hs.159489	ESTs, Moderately similar to JC	hexokinase2,hexokinase	9.6
407893	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	9.5
408294	BE141732		gb:QV0-HT0101-061099-032-e07 H	Ammonium_transp	9.5
442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	9.4
416866	AA297356	Hs.80324	serine/threonine protein phosp	Metallophos,Metallophos	9.4
419823	AW271708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS,TM	9.4
422625	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin	9.3
401264			C18000090*:gi|6678656|ref|NP_0	SS,laminin_Nterm,laminin_	9.3
407507	U73799		gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.2
400833			C11000890:gi|3746443|gb|AAC639	SS,TM,7tm_1	9.2
422064	AW452589	Hs.335742	ESTs	TM	9.2
452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	9.2
421363	NM_001381	Hs.103854	docking protein 1, 62kD (downs	PH,IRS,TM,PH,IRS,trypsin,	9.1
427397	AI929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RrnaAD,SS,efhand	9.1
431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	9.0
434796	AA812046		ESTs	SS,myb_DNA-binding,myb_DN	9.0
422639	AI929377	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt	9.0
447867	AI525268	Hs.164303	ESTs	TM	9.0
442472	AW806859		gb:MR0-ST0020-081199-004-c03 S	SS,TM,Inos-1-P_synth,Occl	8.9
455588	AI129903	Hs.74669	vesicle-associated membrane pr	synaptobrevin,SS,TM	8.9
454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	8.9
429527	AA454184	Hs.289014	ESTs		8.9
432603	AA554920	Hs.105794	UDP-glucose:glycoprotein gluco	SS,TM	8.9
410338	W03445	Hs.38205	gb:za05g11.r1 Soares melanocyt	pkinase	8.9
452833	BE559681	Hs.30736	KIAA0124 protein	WD40	8.9
407363	AF035032	Hs.181125	gb:Homo sapiens clone MCA1L my	SS,ig,SS,G_glu_transpept	8.8
414413	BE294877		gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2,SS,TM	8.8
421694	BE387430	Hs.106880	bystin-like		8.8
453683	AL079854	Hs.118598	Homo sapiens mRNA for KIAA1878	SS	8.8
418736	T18979	Hs.87908	Snf2-related CBP activator pro	SS,helicase_C,AT_hook,SS,	8.7
450958	AL137669	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4		8.7
419725	U66048	Hs.92683	Homo sapiens clone 161455 brea		8.7
415126	D60945		gb:HUM141D04B Clontech human f	SS,TM	8.7
406301			Target Exon	TM	8.6
418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	8.6
433396	AI742071	Hs.133205	ESTs	SS,TM	8.6
434333	AA186733	Hs.292154	stromal cell protein		8.6
407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	8.6
452851	AW173191	Hs.213117	ESTs	SS,Sema	8.6
422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	8.6
447859	AK002194	Hs.19851	peroxisomal biogenesis factor		8.6
420836	AW958453	Hs.204959	hypothetical protein FLJ14886	SS,ras	8.6
429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	8.6
419639	AK001502	Hs.91753	hypothetical protein		8.6
429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidored_q6,SS,TM,rrm	8.5
452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	8.5
441076	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343		8.5
428860	U38291	Hs.194301	microtubule-associated protein	M	8.5
421901	AB014554	Hs.109299	protein tyrosine phosphatase,	SAM,SS,TM,rrm,PDZ	8.4
441363	AW450211	Hs.126825	ESTs, Weakly similar to A46302	SS,TM,HSP20,7tm_1	8.4
443801	AW206942	Hs.253594	intron of: trichorhinophalang	GATA	8.4
432862	AW004958	Hs.236720	amnionless protein	SS,MATH,zf-TRAF,zf-C3HC4	8.4
431849	AI670823	Hs.85573	hypothetical protein MGC10911	SS,TM	8.4
423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	8.3
404365			Target Exon	SS	8.3
425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2,he	8.3
423098	AA321980	Hs.204682	ESTs		8.3
434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	8.2
418361	AW505368	Hs.12460	gb:UI-HF-BN0-alu-d-03-0-UI.r1		8.2
427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,pkinase	8.2
420138	BE268854	Hs.177729	ESTs	SS	8.2
426391	AW161050	Hs.169611	second mitochondria-derived ac	SS	8.1
457613	AA598869	Hs.173770	ESTs		8.1
427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	8.1
437215	AL117488		Human clone 23564 mRNA sequenc	SS	8.1
423384	AL133632	Hs.127808	Homo sapiens mRNA; cDNA DKFZp4		8.1
447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	8.0
431898	AK000020	Hs.272018	hypothetical protein FLJ20013		8.0
454291	AW384847	Hs.213534	ESTs, Weakly similar to MUC2_H	SS,XRCC1_N,BRCT,lactamase	8.0
430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,ig	8.0
459302	NM_002314	Hs.36566	LIM domain kinase 1		8.0
422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIR,TK,SS,TM	8.0
425944	AK000664	Hs.164256	hypothetical protein FLJ20657		7.9
450873	BE464016	Hs.238956	ESTs	SS,zf-C2H2,rrm	7.9

454246	AW245185	Hs.6996	ESTs		7.9
450635	AW403954	Hs.25237	mesenchymal stem cell protein	4HBT	7.9
422305	AI928242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.9
425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase,SS,TM	7.9
413534	BE146961		gb:QV4-HT0222-011199-019-b12 H	SS,TM	7.8
446931	AI348856	Hs.21627	gb:tb05a05.x2 NCI_CGAP_Lu26 Ho		7.8
421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	7.8
427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	7.8
448993	AI471630		KIAA0144 gene product		7.8
443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosin,SS,TM	7.8
427725	U66839	Hs.180533	mitogen-activated protein kina	pkinase	7.8
400923			Target Exon	SS,TM,DUF289	7.8
419757	AA773820	Hs.63970	ESTs	SS,TM	7.8
458834	AI566883	Hs.196446	ESTs		7.8
427899	AA829286	Hs.332053	serum amyloid A1	SS,SAA_proteins,SS,SAA_pr	7.7
452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin	7.7
436543	NM_002212	Hs.5215	integrin beta 4 binding protei	eIF6	7.7
431811	AB040972	Hs.301696	hypothetical protein FLJ11560	SS,TM,Band_7,AAA,cdc48_N,	7.7
414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	7.7
455885	BE153524		gb:PM0-HT0339-241199-002-C03 H	SS,pkinase	7.7
427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	7.6
430432	AB037758	Hs.241419	KIAA1337 protein	TM,Patched,TM	7.6
427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	7.6
450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2,SS	7.6
413564	BE260120		gb:601146990F1 NIH_MGC_19 Homo		7.6
410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23	7.6
439539	BE348395	Hs.121589	ESTs	SS,Fork_head	7.5
400286			C16000922:gi|7499103|pir||T209	TM,ABC_tran,ABC_membrane	7.5
416472	AA180756	Hs.340316	ESTs, Moderately similar to AL	zf-C2H2	7.5
418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	7.5
419492	AA243547	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb,Metalloph	7.5
420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	7.5
406495			Target Exon	SRCR,TM,Acetyltransf	7.5
448043	AI458653	Hs.201881	ESTs	PHD	7.4
401724			C16001374:gi|6755086|ref|NP_03	TM,PLAT,SS	7.4
424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK,SS,TM,fn3,ig,R	7.4
428092	AW879141		ESTs	SS,TM	7.3
453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	7.3
400137			Eos Control		7.3
436127	W94824	Hs.11565	RIKEN cDNA 2010100O12 gene	Corona_7,SS,TM	7.3
412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.3
448859	BE272446	Hs.265317	hypothetical protein MGC2562	SS,TPR	7.3
407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.3
429299	AI620463	Hs.347408	hypothetical protein MGC13102	SS,TM,gla	7.3
401674			C16001417*:gi|7500345|pir||T21	FAD-oxidase_C,FAD_binding	7.2
412289	AW935967	Hs.170162	KIAA1357 protein	SS	7.2
424198	AB029010	Hs.143026	KIAA1087 protein	SS,TM,Na_Ca_Ex,Calx-beta,	7.2
412173	T71071		gb:yc50b05.r1 Stratagene liver	CPSase_L_chain	7.2
438113	AI467908	Hs.8882	ESTs	SS,TM,7tm_1	7.2
429869	AI907018	Hs.15977	Target CAT	rrm	7.2
439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_Ib,Lipase_GDSL,SS,	7.2
425041	AI377150	Hs.150914	ESTs	SS	7.2
448340	AI492910	Hs.32362	ESTs		7.1
406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	7.1
431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	WD40	7.1
421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,tRNA-synt_1,GST_C,G	7.1
409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	7.0
430281	AI878842	Hs.237924	CGI-69 protein	mito_carr,SS,TM	7.0
444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,laminin_G,EGF	7.0
405928			Target Exon	SS,cystatin,Coprogen_oxid	7.0
421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2,SS,TM,LRR	6.9
439905	AW799755	Hs.110953	retinoic acid induced 1	HLH	6.9
451937	AF119664	Hs.27299	transcriptional regulator prot	SS,integrin_B,fn3,Calx-be	6.9
426675	AW084791	Hs.133122	hypothetical protein FLJ14524	SS,TM,aminotran_1_2	6.9
438627	AI087335	Hs.123473	ESTs	TM,Reticulon	6.9
438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	6.8
421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	6.8
423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	6.8
405346			Rag C protein	RCC1	6.8
432746	AA564512	Hs.24301	polymerase (RNA) II (DNA direc	SS,TM,EF1BD	6.8
452798	AI918771	Hs.257170	ESTs	SS,TM,TNFR_c6	6.7
426315	AA854219	Hs.348137	Homo sapiens, clone IMAGE:3542	SS,crystall	6.7
440317	BE561888		gb:601346093F1 NIH_MGC_8 Homo		6.7
438857	AI627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	6.7
452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf,SS,PDEase	6.7
433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta	TM	6.7
423106	N52572	Hs.13702	ESTs, Moderately similar to AL		6.7
453101	AW952776	Hs.94943	ESTs	TM	6.7
420307	AW502869	Hs.66219	ESTs	SS,TM	6.7
415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1,SS,TM	6.7
454262	AW612232	Hs.254835	ESTs	SS,TM,voltage_CLC,CBS	6.7
409227	AA806165	Hs.130323	Homo sapiens, clone IMAGE:3960		6.6
413908	BE409966	Hs.323813	Homo sapiens, clone MGC:2867,	SS,zf-C2H2	6.6

457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	6.6
419157	AA234540	Hs.23871	ESTs	pkinase	6.6
431424	AI222969		ESTs	SS	6.6
412464	T78141	Hs.22826	ESTs, Weakly similar to I55214	SS,cadherin,crystall	6.6
430168	AW968343		DKFZP434I1735 protein	SS,TM,efhand,efhand	6.6
455035	AW851734		gb:MR2-CT0222-011199-007-e10 C		6.6
422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	6.6
453367	AW732847	Hs.70573	PKCI-1-related HIT protein	SS,TM	6.6
450593	AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,lactam	6.6
420319	AW406289	Hs.96593	hypothetical protein	ras,arf	6.6
431131	N84730	Hs.250616	isocitrate dehydrogenase 3 (NA	isodh,isodh	6.6
431297	AA651771	Hs.3076	ESTs		6.6
410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	SS,HECT,phoslip	6.5
441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	6.5
454682	AW816029		gb:MR3-ST0220-151299-027-b10 S	filament	6.5
407299	AA460205	Hs.289770	ESTs, Weakly similar to I38022		6.5
422837	U25441	Hs.121478	dopamine receptor D3	7tm_1,SS,TM,7tm_1	6.5
407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB,SS	6.4
417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	6.4
445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
402197			Target Exon	SS,TM,ATP1G1_PLM_MAT8,ig,	6.3
419390	AI701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	6.3
447754	AW073310	Hs.163533	intron of HER4		6.3
444664	N26362	Hs.11615	map kinase phosphatase-like pr	DSPc,Rhodanese,SS,TM	6.3
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobro	Cys_knot,vwc	6.3
432872	AI908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	6.3
430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	6.3
413343	BE392026	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	6.2
417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.2
403128			KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_t	6.2
413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450	6.2
427812	AA770424	Hs.98162	ESTs	SS	6.2
457761	AW401809	Hs.4779	KIAA1150 protein	SS,LIM,SS	6.2
453099	H62087	Hs.31659	thyroid hormone receptor-assoc	SS	6.2
426048	AI768853	Hs.134478	ESTs	TM	6.2
407223	H96850		gb:yw03b12.s1 Soares melanocyt	SS,TM,SS,TM,DDOST_48kD	6.2
445634	AI624849	Hs.344612	ESTs, Weakly similar to NEL1_H	vwd	6.2
441197	BE244638	Hs.166	sterol regulatory element bind	HLH	6.1
421707	NM_014921	Hs.107054	lectomedin-2	Latrophilin,OLF,7tm_2,Gal	6.1
435750	AB029012	Hs.4990	KIAA1089 protein	SS,TM	6.1
432353	NM_016558	Hs.274411	SCAN domain-containing 1	SCAN	6.1
427326	AI287878		gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	SS,TM,7tm_1,SS,TM	6.1
447128	AI271898		cyclin K		6.1
419444	NM_002496	Hs.90443	Target CAT	fer4,SS,TM,V_ATPase_sub_a	6.1
457978	AA776638		gb:ae78g04.s1 Stratagene schiz	SS,PH,IQ,RasGEF,RasGEFN,R	6.1
410445	AA199830		gb:zq75h01.r1 Stratagene hNT n		6.1
431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p	PARP,PARP_reg,SS,TM,Pepti	6.1
407143	C14076	Hs.332329	EST	SS,TM	6.0
408724	AI685842	Hs.294143	ESTs, Weakly similar to T22914	SS,pkinase,tubulin	6.0
436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,pkinase,Activin_rec	6.0
441583	AI791499	Hs.205742	ESTs, Weakly similar to ALUA_H		6.0
418802	AB028989	Hs.88500	mitogen-activated protein kina	WD40,Pico_P2A,M,SS	6.0
414927	T83587	Hs.186476	ESTs	SS,Sulfatase	6.0
434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf,SS	6.0
414157	BE297801	Hs.103845	ESTs, Moderately similar to I5	SS	6.0
424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase,SS,Atrophin-1,Atr	6.0
406487			Target Exon	SS,TM	6.0
447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SH3,PH,RhoGEF	6.0
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,Ig	6.0
442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-spe	PDEase	5.9
426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr	5.9
418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	5.9
431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	5.9
430344	AA476827	Hs.171012	hypothetical protein FLJ22349	HLH	5.9
428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	5.9
403938			Target Exon	Ephrin	5.9
456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	5.9
451481	AA300228	Hs.295866	hypothetical protein DKFZp434N		5.9
434357	AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases,SS,TM	5.9
443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran,SS	5.9
433333	AI016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina	5.9
430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	5.9
409034	AI684149	Hs.172035	hypothetical protein similar t	SS	5.9
421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11	SS,SS	5.9
431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,ras	5.9
409608	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,cadherin,GPS,	5.9
423464	NM_016240	Hs.128856	CSR1 protein	Collagen,SS	5.9
422379	AA932860	Hs.133864	ESTs		5.8
443887	NM_004729	Hs.9933	Ac-like transposable element	zf-BED	5.8
450122	BE313765	Hs.343443	ESTs, Weakly similar to I38022	SS,TM,Y_phosphatase,LON,A	5.8
404807			Target Exon	UPF0027	5.8
445303	AW362198	Hs.12503	interleukin 15 receptor, alpha	SS,sushi,SS	5.8
445631	AK001822		Homo sapiens cDNA FLJ10960 fis		5.8
412091	R06185		gb:ye94d03.r1 Soares fetal liv	SS,TM,IBR,IBR	5.8

446536	W74413	Hs.15251	hypothetical protein	SS	5.8
432866	BE395875	Hs.279609	mitochondrial carrier homolog	mito_carr	5.8
402393			ENSP00000085284*:CDNA FLJ20404	RhoGEF,PH,SS,zf-CCCH,vwd	5.8
413041	BE061580	Hs.61622	gb:MR0-BT0249-091299-201-c07 B	SS	5.8
414356	AW505085	Hs.335147	gb:UI-HF-BN0-als-a-10-0-UI.r1	SS,TM	5.8
402916			ENSP00000202587*:Bicarbonate t	HCO3_cotransp,SS	5.7
459133	U40343	Hs.29656	cyclin-dependent kinase inhibi	ank,SS,Adap_comp_sub	5.7
404757			Target Exon	TM,zf-C2H2	5.7
409879	BE083422	Hs.56851	hypothetical protein MGC2668	SS,TM	5.7
411219	AW832917		gb:QV2-TT0003-161199-013-h06 T		5.7
421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	5.7
434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis		5.7
416759	AK000978	Hs.79741	hypothetical protein FLJ10116		5.7
446562	BE272686	Hs.15356	hypothetical protein FLJ20254	hormone,SS,pfkB	5.7
407117	AA146625		gb:zo71c07.s1 Stratagene pancr	SS	5.7
444855	BE409261	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	5.7
421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	5.7
407757	BE048414	Hs.165215	hypothetical protein MGC5395	SS,EF1G_domain,GST_C,GST_	5.7
419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	5.7
437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	5.7
408905	AV655783	Hs.661	Target CAT		5.7
450787	AB006190	Hs.25475	aquaporin 7	MIP,SS,TM	5.7
432496	D45576	Hs.187959	ESTs		5.7
429367	AB007867	Hs.278311	plexin B1	Sema,PSI,TIG,SS,TM,TIG,Se	5.7
422708	AB017430	Hs.119324	kinesin-like 4	kinesin,homeobox,SS,TM,zf	5.7
417442	AA199940	Hs.124039	ESTs		5.7
432751	AF152099	Hs.278911	interleukin 17C	SS	5.7
432004	BE018302	Hs.2894	placental growth factor, vascu	PDGF,SS	5.7
454151	AA047169	Hs.154088	hypothetical protein FLJ22756	SS,TM,Glycos_transf_4	5.7
456145	BE299427	Hs.21446	KIAA1716 protein	SS,DIX,PDZ,DEP,Dishevelle	5.6
417677	NM_016055	Hs.82389	CGI-118 protein		5.6
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-fami	ABC_tran,SRP54,SS,TM,ECH	5.6
408795	AW749126	Hs.170345	hypothetical protein FLJ13710	hormone_rec,zf-C4	5.6
407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	5.6
452849	AF044924	Hs.30792	hook2 protein	bZIP,SS,AhpC-TSA	5.6
439343	AF086161	Hs.114611	hypothetical protein FLJ11808		5.6
459271	AL045934		gb:DKFZp434M116_r1 434 (synony	SS,PI3_PI4_kinase,PI3Ka	5.6
401609			C16001614:gi|7801278|emb|CAB91		5.6
447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	5.6
409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	5.6
450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	5.6
415514	F11301	Hs.138329	ESTs	SS,TM	5.6
437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	5.6
406663	U24683		immunoglobulin heavy constant	SS	5.6
421678	AA419008	Hs.106730	chromosome 22 open reading fra	SS,TM,UBA,Rhomboid,SS,TM	5.6
422472	R59096	Hs.279939	mitochondrial carrier homolog	mito_carr	5.6
414918	AI219207	Hs.72222	hypothetical protein FLJ13459	SS,TM,efhand	5.6
434906	BE410573	Hs.283636	Homo sapiens, clone IMAGE:4053	SS,TM,Exo_endo_phos,BNR,A	5.6
414757	U46922	Hs.77252	fragile histidine triad gene	HIT	5.6
436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	5.6
421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA		5.6
408015	AW136771	Hs.244349	epidermal differentiation comp		5.6
445871	AI702901	Hs.145582	ESTs, Weakly similar to FOR4 M	SS,TM,efhand,efhand	5.5
411813	NM_014931	Hs.72172	KIAA1115 protein	SS,TM,Y_phosphatase	5.5
425098	AW295349	Hs.8038	ESTs	SS,TM	5.5
429720	M79091		gb:EST01239 Subtracted Hippoca		5.5
453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	SS,TM,lipoxygenase,PLAT,s	5.5
449225	R39108	Hs.6777	ESTs	SS,TM,Na_sulph_symp	5.5
423233	BE048021	Hs.11067	ESTs, Highly similar to T46395		5.5
432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5
408215	BE614290		syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	5.5
406244			Target Exon		5.5
436041	AI803516	Hs.272891	hippocalcin-like protein 4	SS,efhand,TGF-beta,TGFb_p	5.5
422013	N92696	Hs.293354	ESTs	SS,TM	5.5
442451	AI498080	Hs.129616	ESTs	SS	5.5
427859	AA416856	Hs.98170	ESTs	SS,TM,DUF60,trypsin,CUB,u	5.5
436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM	5.5
427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase,SS,TM,synaptobrev	5.4
441456	AI458911	Hs.127765	ESTs		5.4
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	5.4
415976	R43144	Hs.21919	ESTs	TM	5.4
447374	AF263462	Hs.18376	KIAA1319 protein	SS,Myosin_tail,M	5.4
431275	T56571	Hs.10041	ESTs	SS,HLH	5.4
404343			C7002191*:gi|5053028|gb|AAD388	SS,ABC_tran	5.4
431461	BE299671	Hs.256310	likely ortholog of mouse ZFP28		5.4
421779	AI879159	Hs.108219	wingless-type MMTV integration	SS,wnt,SS	5.4
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	5.4
457310	W28363	Hs.239752	nuclear receptor subfamily 2,		5.3
417193	AI922189	Hs.288390	hypothetical protein FLJ22795	SS	5.3
432545	X52486	Hs.3041	uracil-DNA glycosylase 2	cyclin,SS,cyclin	5.3
456573	AI279811		Homo sapiens, clone IMAGE:3953		5.3
409164	AA706639		gb:ag90e09.r1 Stratagene hNT n	SS,TM,Hint,HH_signal,tubu	5.3
442296	NM_007275	Hs.8186	lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	5.3
438670	AI275803	Hs.123428	ESTs		5.3

400257			ENSP00000000452:BAD protein (B	SS,hormone_rec,zf-C4	5.3
449514	AW970440	Hs.23642	protein predicted by clone 236	SS,PX,arf,lipocalin,PHD,z	5.3
427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	5.3
414551	AI815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH,Peptidase_U7,SS,TM	5.3
447960	AW954377	Hs.26412	ring finger protein 26	SS,TM,Cbl_N,Cbl_N2,Cbl_N3	5.3
430605	AJ245433	Hs.247323	G4 protein	SS,TM,G-patch,ubiquitin,a	5.3
456849	AA622394	Hs.153177	ribosomal protein S28	SS,TM	5.2
430513	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	5.2
424437	BE244700	Hs.147049	cut (Drosophila)-like 1 (CCAAT	CUT,homeobox,beta-lactama	5.2
427815	BE072019	Hs.12851	phosphatidylserine synthase 2	SS,TM,7tm_1	5.2
417903	NM_002342	Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6,SS	5.2
420476	AW575863	Hs.136232	ESTs	SS,HLH	5.2
409960	BE261944		hexokinase 1	SS,TM	5.2
436325	AL390088	Hs.7393	hypothetical protein from EURO	SS,Synapsin_C,SS	5.2
444439	AI458883	Hs.143545	hypothetical protein MGC11303	SS,TM,PAF-AH_p_II	5.2
412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH de		5.2
418891	NM_002419	Hs.89449	mitogen-activated protein kina	SH3,pkinase,pyridoxal_deC	5.2
430323	U40714	Hs.239307	tyrosyl-tRNA synthetase	DUF101,SS,tRNA-synt_1b,tR	5.2
432396	AW295956	Hs.11900	hypothetical protein FLJ14972	SS	5.2
457843	AW138211	Hs.128746	ESTs		5.2
429252	NM_004658	Hs.198312	RAS protein activator like 1 (	C2,PH,RasGAP,BTK,SS,C2,PH	5.1
429225	BE250337	Hs.198273	Target CAT	WD40	5.1
412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN	SS,TM	5.1
449750	H28586	Hs.32325	ESTs	SS,ras	5.1
442725	AI935786	Hs.131035	ESTs, Weakly similar to CA24_H	SS,SS,TM,PX,PH,PLDc,arres	5.1
430390	AB023186	Hs.241161	KIAA0969 protein	PH,SS,TM	5.1
421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	5.1
426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-ci	adh_short,SS,adh_short,TG	5.1
428924	AI016405	Hs.98959	ESTs, Weakly similar to JC5314	SS,TM,lectin_c	5.1
458876	AI650896	Hs.195347	ESTs		5.1
402632			Target Exon	Fz,kringle,ig	5.1
413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR,SS	5.1
419451	AI907117	Hs.90535	syntaxin binding protein 2	Sec1,SS,TM	5.1
456155	R85182	Hs.7175	ESTs, Weakly similar to AF1568	SS	5.1
422396	W21872	Hs.7907	ESTs, Weakly similar to T19486		5.1
413983	BE348384	Hs.279194	ESTs		5.0
447598	AI799968	Hs.199630	ESTs	SS,TM	5.0
425858	AA364923		gb:EST75602 Pineal gland II Ho	SS,TM,Peptidase_M10,fn2,h	5.0
440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE,Ribosomal_S17,	5.0
452661	AW449413	Hs.257152	ESTs		5.0
412800	AW950852	Hs.74598	polymerase (DNA directed), del	homeobox,SS,efhand,hexoki	5.0
446603	NM_014835	Hs.15519	oxysterol-binding protein-rela	Oxysterol_BP,SS	5.0
402884			ENSP00000164597:PRO0566.	laminin_Nterm,laminin_Nte	5.0
448680	AW245890	Hs.21753	JM5 protein	WD40,SS,TM,KOW,HLH	5.0
431515	NM_012152	Hs.258583	endothelial differentiation, l	7tm_1	5.0
427204	AA405404	Hs.215725	ESTs	SS,SS	5.0
425169	AW292500	Hs.128514	ESTs	SS	5.0
412940	BE295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	5.0
440839	AI142078	Hs.135562	ESTs	SS	5.0
443814	BE281240	Hs.9857	carbonyl reductase		5.0
434243	AA628062	Hs.200358	ESTs, Moderately similar to AL	SS,TM	5.0
435605	AF151815	Hs.4973	hypothetical protein	SS,TM,SS,TM,ABC_tran,ABC_	5.0
417116	Z43916	Hs.7634	hypothetical protein FLJ12287	SS,TM,filament,IF_tail	5.0
403055			C2002219*:gi|12737280|ref|XP_0		5.0
420856	BE513294	Hs.205736	HLA class II region expressed	kazal,SS,TM,ig,pkinase	4.9
405594			NM_021949:Homo sapiens ATPase,	E1-E2_ATPase,Hydrolase,SS	4.9
405334			Target Exon	SS,TM,MIP	4.9
419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI,SS,CDK5_activator	4.9
413764	BE162704		gb:PM1-HT0454-301299-001-d08 H	SS	4.9
409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light		4.9
446933	AL137659	Hs.297214	HSPC141 protein	SS,TM,ank,EGF,notch,MATH,	4.9
409139	AI681917	Hs.3321	ESTs, Highly similar to IRX1_H	SS,homeobox	4.9
456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327,	SS,PK,PK_C,myosin_head,Rh	4.9
420842	AI083668	Hs.50601	hypothetical protein MGC10986	SS	4.9
421909	NM_013375	Hs.109428	TATA-binding protein-binding p		4.9
419667	AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	4.9
443496	AJ006973	Hs.9482	target of myb1 (chicken) homol	VHS,GAT,TM,Heme_oxygenase	4.9
400933			NM_004347:Homo sapiens caspase	ICE_p20,ICE_p10,CARD,SS,I	4.9
456143	H11097	Hs.61960	hypothetical protein	SS,pkinase	4.9
427527	AI809057	Hs.153261	immunoglobulin heavy constant	SS,TM,ig	4.9
414265	BE410411	Hs.75864	endoplasmic reticulum glycopro		4.9
433933	AI754389		Homo sapiens clone TCCCIA00164	SS,TM,SS,TM,SH2,Y_phospha	4.9
452302	AF173867	Hs.28906	glucocorticoid modulatory elem	SAND,SS	4.9
409938	AW974648		gb:EST386752 MAGE resequences,	SS,Adap_comp_sub,GYF	4.8
400845			NM_003105*:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	4.8
425976	C75094	Hs.334514	NG22 protein	SS,TM,pkinase,SH2,SH3,BNR	4.8
452969	W92792	Hs.77575	hypothetical protein MGC3136		4.8
413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3,ig,Y_phosphatase,SS,T	4.8
434962	AK001574	Hs.4291	golgi perepheral membrane prot		4.8
418572	AI751740	Hs.86172	paired related homeobox protei	homeobox	4.8
440869	NM_014297	Hs.7486	protein expressed in thyroid	lactamase_B,SS,XRCC1_N,BR	4.8
453446	BE299996		gb:600944574F1 NIH_MGC_17 Homo		4.8
412159	AF286598	Hs.9271	KIAA1071 protein	bZIP	4.8
438999	AW276811		gb:xp66c02.x1 NCI_CGAP_Ov39 Ho		4.8

420233	AA256714	Hs.194864	hypothetical protein FLJ22578	SS	4.8
414576	AK000405	Hs.76480	ubiquitin-like 4	ubiquitin,SS,TM,G6PD,G6PD	4.8
433669	AL047879	Hs.80475	ESTs, Weakly similar to ALU2_H	SS,TM,RNA_pol_L,RasGAP,C2	4.8
448984	AW751955	Hs.22753	hypothetical protein FLJ22318	SS	4.8
426912	AL043054	Hs.256657	ESTs, Weakly similar to A46302	SS	4.8
418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	lipoxygenase,PLAT,SS	4.8
440333	AI378424	Hs.288761	hypothetical protein FLJ21749	SS,TM,IP_trans,pkinase,pk	4.8
425615	AF023614	Hs.158341	transmembrane activator and CA	TM	4.8
458040	BE280562	Hs.287711	hypothetical protein FLJ22692		4.8
458367	AA088470	Hs.83135	Homo sapiens, Similar to RIKEN	SS,tRNA-synt_2d	4.8
433294	AA582082	Hs.199410	ESTs		4.8
437671	AA536047	Hs.9850	hypothetical protein MGC1842		4.8
425338	H16716	Hs.182648	Homo sapiens cDNA FLJ14444 fis		4.8
447946	AI566164	Hs.165827	ESTs	SS,PTN_MK,7tm_1,DAGKc,DAG	4.7
447205	BE617015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRRCT,Sema	4.7
416880	H99640	Hs.53687	EST		4.7
440150	AW975738	Hs.7001	Homo sapiens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	4.7
426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	pkinase,pkinase	4.7
429253	Y11739	Hs.198313	winged-helix nude	Fork_head,SS,TM,glycolytl	4.7
450261	AA788727	Hs.34068	ESTs, Weakly similar to A43932	SS	4.7
439246	AI498072		membrane-associated tyrosine-	SS,SS,TM	4.7
419120	BE271922		ESTs, Weakly similar to zinc f	SS,TM,DENN,Cytidylyltrans	4.7
416487	AW190458	Hs.79347	KIAA0211 gene product	SS,zf-C2H2	4.7
413837	AW163525		titin-cap (telethonin)	SS,Methyltransf_3	4.7
419887	AW292562	Hs.187628	ESTs	TM	4.7
410277	R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	4.7
415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,SS,TM,CH,Filam	4.7
410892	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis		4.7
407754	AA527348	Hs.288967	Homo sapiens cDNA FLJ14105 fis	SS,TM,SS,TM,TSPN,tsp_3,SE	4.7
409877	AW502498	Hs.15220	zinc finger protein 106		4.7
431629	AU077025	Hs.265827	interferon, alpha-inducible pr	pkinase,SH2,SH3	4.7
438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	4.7
420823	R96881	Hs.63609	HpaII tiny fragments locus 9C	TM	4.7
418900	BE207357	Hs.3454	KIAA1821 protein	SS	4.7
402400			Target Exon	SS,TM,RNase_HII,bZIP,DUF2	4.7
419625	U91616	Hs.91640	nuclear factor of kappa light	ank,SS,TM	4.7
433319	AA583232		ESTs	SS	4.7
424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	pkinase,SH3	4.7
432750	NM_014440	Hs.278910	interleukin 1, epsilon	IL1	4.7
425954	AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	4.7
447245	AK001713	Hs.17860	hypothetical protein FLJ10851	E1_dehydrog	4.7
427101	R87591	Hs.172884	ESTs	SS,TM	4.6
447544	AA401573	Hs.288284	hypothetical protein FLJ22378	SS,TM	4.6
400266			NM_002858*:Homo sapiens ATP-bi	ABC_tran	4.6
412841	AI751157	Hs.101395	hypothetical protein MGC11352	SS,TM	4.6
422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	ldh,ldh_C,adh_short,Semia	4.6
414874	D26351	Hs.77515	inositol 1,4,5-triphosphate re	TM,RYDR_ITPR,Ion_trans,MI	4.6
418373	AW750770	Hs.84344	CGI-135 protein	SS,TM,PMP22_Claudin,2OG-F	4.6
424487	T08754	Hs.6259	KIAA1698 protein	SS,SS,TM,Glyco_hydro_31,G	4.6
426571	AA381642		gb:EST94816 Activated T-cells		4.6
433941	AA620612		ESTs	SS,TM,TNFR_c6	4.6
421717	AF230924	Hs.107187	divalent cation tolerant prote		4.6
450883	NM_001348	Hs.25619	death-associated protein kinas	pkinase,GTP_EFTU,EFG_C,GT	4.6
427361	AW732480	Hs.7678	cellular retinoic acid-binding	SS,TM,aminotran_1_2,LRR	4.6
420421	AF281133	Hs.343589	exosome component Rrp41	RNase_PH,RNase_PH_C	4.6
414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C,SS,	4.6
431498	AK001777	Hs.258551	aspartyl aminopeptidase	SS,Peptidase_M18,SS,TM,Y_	4.6
432593	AW301003	Hs.51483	ESTs, Weakly similar to hypoth	SS,TM,adh_short	4.6
404661			C9000306*:gi|12737280|ref|XP_0		4.6
412790	NM_014767	Hs.74583	KIAA0275 gene product	kazal,thyroglobulin_1,zf-	4.6
456243	AI345001	Hs.82380	menage a trois 1 (CAK assembly	zf-C3HC4	4.6
426222	BE391706	Hs.168073	DKFZP727M231 protein	GSH_synthase	4.6
439594	AI245026	Hs.111099	hypothetical protein MGC10974	CLP_protease	4.6
409114	AA070021		gb:zm67h03.r1 Stratagene neuro		4.6
429049	AW452125	Hs.119273	KIAA0296 gene product	SS,TM,trypsin	4.6
424271	AI991887	Hs.305882	5-oxoprolinase (ATP-hydrolysin		4.6
418741	H83265	Hs.8881	ESTs, Weakly similar to S41044	SS,TM,pkinase,Activin_rec	4.6
450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	4.6
433074	AL045019	Hs.323462	Homo sapiens cDNA FLJ11214 fis	DEAD,helicase_C,dsrm,Vira	4.6
444893	AW249312	Hs.12109	WD40 protein Ciao1	WD40	4.6
420508	AJ270993	Hs.98428	homeo box B6	homeobox,SS,homeobox,home	4.6
409591	AA532963	Hs.9100	Homo sapiens cDNA FLJ13100 fis	SS,TM,LIM,homeobox	4.6
456181	L36463	Hs.1030	ras inhibitor	RA,SH2,VPS9,SS,TM,Nucleos	4.6
439270	BE268278	Hs.28393	hypothetical protein MGC2592	SS,TM,HCO3_cotransp	4.6
440104	AA132838	Hs.239894	hypothetical protein MGC2803	SS,DS	4.5
423279	AW959861	Hs.290943	ESTs	SS	4.5
445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	4.5
404036			Target Exon	SS,TM,cadherin,cadherin	4.5
431832	AW276866	Hs.192715	ESTs	Ets,SAM_PNT	4.5
433886	AA613596	Hs.28412	ESTs	SS	4.5
426735	T78716	Hs.120446	ESTs	Oxysterol_BP,PH	4.5
417825	AW838994	Hs.6363	heparan sulfate 6-O-sulfotrans	SS,TM	4.5
455600	BE061053		gb:QV0-BT0041-271099-037-d09 B	C4	4.5
423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	4.5

421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,rrm,zf-RanBP,rrm,GA	4.5
408157	AA047685	Hs.62946	ESTs	pkinase	4.5
434303	AW204058		transforming growth factor bet	SS,TM,SSF,FG-GAP,vwa,inte	4.5
440745	AW303627	Hs.143301	ESTs		4.5
419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bi	4.5
447208	BE315291	Hs.237971	hypothetical protein MGC5627		4.5
436163	R84938		gb:yt65f04.r1 Soares retina N2		4.5
456856	AK001528	Hs.347285	Homo sapiens, Similar to DiGeo		4.5
410817	AI262789	Hs.93659	protein disulfide isomerase re	SS,thiored	4.5
434558	AW264102	Hs.39168	ESTs	SS,TM,LRRCT,LRR	4.5
440548	AL117408	Hs.7274	DKFZP434P1750 protein		4.5
450200	AW975625	Hs.173088	ESTs	zf-UBP,zf-C3HC4	4.5
432434	AL161977	Hs.2994	PCTAIRE protein kinase 3	SS,pkinase	4.5
440042	AI073387	Hs.133898	ESTs	SS	4.5
454328	AW372097	Hs.278429	hepatocellular carcinoma-assoc		4.5
458196	AI802408		ubiquitin A-52 residue ribosom	SS,TM,fn3,FKBP,TPR	4.5
433472	AI541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	4.5
408928	AW295827	Hs.255479	hypothetical protein MGC5566	A_deaminase,A_deaminase	4.5
448093	AW977382	Hs.15898	2,4-dienoyl CoA reductase 2, p	adh_short,NDK	4.5
426272	AW450671	Hs.189284	ESTs		4.5
453610	AW368882	Hs.33818	RecQ protein-like 5	SS,DEAD,helicase_C,SS,DEA	4.5
441327	AK001706	Hs.7778	hypothetical protein FLJ10751	SS,TM,7tm_1	4.5
424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK,SS,TM,7tm_	4.5
443443	AI344042	Hs.9347	regulator of G-protein signall	TM,Na_Pi_cotrans	4.5
426677	AW949856	Hs.97165	ESTs	SS	4.5
412482	AI499930	Hs.334885	mitochondrial GTP binding prot	SS	4.4
425236	AW067800	Hs.155223	stanniocalcin 2	Stanniocalcin,SS	4.4
423229	AC003965	Hs.125532	protease, serine, 26	trypsin,SS	4.4
412338	AA151527	Hs.69485	hypothetical protein FLJ12436	SS,TM,TIG,Sema,PSI	4.4
419395	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide	AICARFT_IMPCHas,MGS,AICAR	4.4
442462	AF031405		gb:AF031405 Soares fetal liver		4.4
439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Ham1p_like,SS	4.4
423876	BE502835	Hs.15463	Homo sapiens, clone IMAGE:2959	SS,efhand	4.4
423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_recp,pkin	4.4
411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF,SS,TM	4.4
448947	BE615408	Hs.337228	ESTs, Weakly similar to AXHU a	SS,TM,ig,pkinase	4.4
407755	AI151353	Hs.29742	Homo sapiens serine palmitoyl	SS,TM,aminotran_1_2	4.4
414849	AW372721	Hs.291623	ESTs, Weakly similar to unname	TM,pkinase	4.4
458171	AI420016	Hs.192090	ESTs	SS,TM	4.4
424443	AI751281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	4.4
427002	AA524093	Hs.23158	ESTs	SS,zf-C2H2	4.4
404344			C7002191*:gi|5053028|gb|AAD388	SS,ABC_tran	4.4
427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU p	SS,F5_F8_type_C,EGF,TGT	4.4
419764	BE262524	Hs.93183	vasodilator-stimulated phospho	WH1	4.4
446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G	7tm_1,SS,TM	4.4
435615	Y15065	Hs.4975	potassium voltage-gated channe	ion_trans,KCNQ1_channel	4.4
403945			Target Exon		4.3
435593	R88872	Hs.4964	DKFZP586J1624 protein	Herpes_HEPA,SS	4.3
421899	AJ011895	Hs.109281	Nef-associated factor 1	Virus_HS,bZIP,G-gamma,Myo	4.3
425245	AI751768	Hs.155314	KIAA0095 gene product	SS,TM	4.3
423348	AA324687		gb:EST27558 Cerebellum II Homo	SS,TM	4.3
452105	AA022838	Hs.6570	ESTs, Weakly similar to S10889	SS,TM,TBC,rrm	4.3
431934	AB031481	Hs.272214	STG protein	SS	4.3
429499	AA453809	Hs.99350	ESTs		4.3
453485	BE620712	Hs.33026	hypothetical protein PP2447	SS,TM	4.3
459393	BE409283	Hs.193264	hypothetical protein MGC3234		4.3
405364			ENSP00000239138*:Guanine nucle		4.3
428345	AI242431	Hs.118282	PAP-1 binding protein	SS,TM	4.3
435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	SS,HLH,Myc_N_term,Myc-LZ,	4.3
413053	AW963263	Hs.65377	ESTs, Moderately similar to KI	TM,SS,TM,EF_TS,UBA,transm	4.3
409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch,SS,TM	4.3
409936	AK001691	Hs.57655	hypothetical protein FLJ10829	SS,TM	4.3
421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila)	homeobox,SS	4.3
424251	AA677466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,helicase_C,brom	4.3
414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	4.3
432805	X94630	Hs.3107	CD97 antigen	SS,TM,7tm_2,GPS,EGF,SS,TM	4.3
424927	AW973666	Hs.153850	hypothetical protein C321D2.4	SS,TM	4.3
456863	T16837	Hs.4241	ESTs	fusion_gly,homeobox,TM	4.3
417823	R88869	Hs.102447	TSC-22-like	PWWP	4.3
406621	X57809	Hs.181125	immunoglobulin lambda locus	SS	4.3
431493	AI791493	Hs.129873	ESTs, novel cytochrome P450	SS,p450,SS	4.3
412958	BE391579	Hs.75087	Fas-activated serine/threonine	SS,pkinase	4.3
431658	BE409917	Hs.266935	tRNA selenocysteine associated	rrm,SS,RCC1	4.3
419579	W49529	Hs.296200	hypothetical protein AF053356_	MSP_domain,SS,TM,CUB,NTR,	4.3
410076	T05387	Hs.7991	ESTs	SS	4.2
406773	AA812424	Hs.76067	heat shock 27kD protein 1	HSP20,SS	4.2
424709	AL137589	Hs.152149	hypothetical protein DKFZp434K		4.2
418419	X55039	Hs.85004	centromere protein B (80kD)	CENP-B,HTH_5	4.2
447377	X77343	Hs.334334	transcription factor AP-2 alph	TF_AP-2,TF_AP-2	4.2
416931	D45371	Hs.80485	adipose most abundant gene tra	C1q,Collagen,SS	4.2
411674	AW861123		gb:RC3-CT0297-120200-014-a05 C	SS	4.2
419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis	SS,ig,tsp_1,ZU5,SS,TM,Nuc	4.2
406887	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	4.2
432183	AW151952	Hs.46679	hypothetical protein FLJ20739	SS	4.2

418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH,SS,TM,aminotran_3,ABC	4.2
437300	AL040504	Hs.25063	PRO0461 protein	SS,TM,pkinase,cyclin,F-bo	4.2
426615	AA400678	Hs.6473	gb:zu70a11.r1 Soares_testis_NH		4.2
421453	AA234652	Hs.104555	neuropeptide FF-amide peptide	SS,bZIP,zf-C2H2,bZIP,zf-C	4.2
409616	AA076248		gb:zm18c10.r1 Stratagene pancr		4.2
444744	BE394732	Hs.147562	ESTs	SS	4.2
412575	AA113177		gb:zm29e05.s1 Stratagene pancr	TM,ER_lumen_recept	4.2
429542	AF038660	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2,ig,SS,TM,A	4.2
435995	BE260415	Hs.348198	hypothetical protein FLJ20262		4.2
451585	AK001171	Hs.326422	hypothetical protein MGC4549	SS,Metallophos	4.2
456153	AW972270	Hs.144054	ESTs	SS,TM	4.2
455340	AW901435		gb:RC0-NN1012-270300-031-a10 N		4.2
457268	AW272279		ESTs, Moderately similar to AL		4.2
432311	BE083080	Hs.274323	similar to sialyltransferase 7	Glyco_transf_29	4.2
409656	NM_005133	Hs.288626	RCE1, prenyl protein protease	Abl,SS,CPSase_L_chain,HMG	4.2
424919	BE314461	Hs.153768	U3 snoRNP-associated 55-kDa pr	WD40,SS,KH-domain	4.2
416528	H65052	Hs.337621	ESTs		4.2
415137	AI634834	Hs.72451	Homo sapiens PAC clone RP5-108		4.2
417334	AA337572	Hs.157240	hypothetical protein MGC4737	SS,TM,ion_trans	4.2
451920	AA224483	Hs.27239	DKFZP586K0524 protein	SS,TM,SS,TM	4.2
413049	NM_002151	Hs.823	hepsin (transmembrane protease	trypsin,SS,TM,ATP1G1_PLM_	4.2
458988	AW410431	Hs.283670	CGI-119 protein		4.2
406964	M21305		FGENES predicted novel secrete		4.2
451595	AW965569	Hs.20996	ESTs	SS,WD40	4.2
449728	AI820751	Hs.107635	ESTs	SS	4.1
453245	T99801	Hs.339751	ESTs	TM,ABC_tran	4.1
432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp4	WD40,LRR	4.1
430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	4.1
442196	AI902646	Hs.31844	hypothetical protein FLJ12586	SS,SCAN	4.1
425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	4.1
415014	AW954064	Hs.24951	ESTs		4.1
440088	BE559877	Hs.183232	hypothetical protein FLJ22638	SS,zf-C3HC4,SPRY,zf-B_box	4.1
418837	U48263	Hs.89040	prepronociceptin	Opiods_neuropep,SS	4.1
410239	AI568350	Hs.61273	hypothetical protein MGC2650	SS,ART,TM	4.1
446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1	ThiF,UBACT	4.1
453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	4.1
448241	AW811064		gb:MR2-ST0131-211099-008-c06 S	SS	4.1
441455	AJ271671	Hs.7854	zinc/iron regulated transporte	Zip,SS,TM,Cytidylyltransf	4.1
450848	AI677994	Hs.428	fms-related tyrosine kinase 3	flt3_lig,SS,Ribosomal_L13	4.1
429218	AA225065	Hs.198269	Target CAT	SS,Nop	4.1
425437	AK000482	Hs.181780	hypothetical protein FLJ20241		4.1
406613			Target Exon	SS,pkinase,LRR,LRRCT,Ribo	4.1
431239	AL039971	Hs.251216	hypothetical protein DKFZp434A	ank,WH2	4.1
436057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding,SS,TM,cNMP_b	4.1
415193	AL048891	Hs.12185	hypothetical protein MGC14333	SS,TM,aminotran_1_2,LRR	4.1
424619	BE387282	Hs.207443	hypothetical protein MGC10848		4.1
432968	BE614192	Hs.279869	melanoma-associated antigen re	SS,TM,RGS,DIX	4.1
428156	BE269388	Hs.182698	mitochondrial ribosomal protei	SS	4.1
414084	AW168771	Hs.71574	hypothetical protein FLJ14926	SS,P5CR,EF1BD	4.1
424964	AW161271	Hs.153961	ARP1 (actin-related protein 1,	actin,SS	4.1
431410	AW299534	Hs.105739	ESTs		4.1
435968	AW161481	Hs.111577	integral membrane protein 3	TM	4.1
432351	AI270313	Hs.127762	hypothetical protein MGC12982		4.1
426120	AA325243	Hs.166887	copine I	C2,SS,aminotran_5	4.1
416877	BE386266	Hs.85658	hypothetical protein FLJ23436		4.1
425970	AK001500	Hs.165186	hypothetical protein FLJ13852	SS,P5CR,Epimerase,zf-C2H2	4.1
434848	BE256304	Hs.32148	AD-015 protein	SS,TM,SS,TM,LRR,P,Peptida	4.1
458715	AK000973	Hs.16725	hypothetical protein FLJ10111	IBR,zf-C3HC4,SS,TM,IRF,CK	4.1
435851	AA700946		ESTs		4.1
425538	BE270918	Hs.164026	Homo sapiens, clone IMAGE:3534	SS,SNF2_N,helicase_C,brom	4.1
444416	AW288085	Hs.11156	hypothetical protein	zf-C3HC4,SpoA,PHD,TM,syna	4.0
426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase,SS	4.0
444596	BE560662	Hs.11417	Rab acceptor 1 (prenylated)	SS,TM,lig_chan,ANF_recept	4.0
439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_H	SS,PWWP,TSC22	4.0
447402	H54520	Hs.18490	hypothetical protein FLJ20452	SS,TM	4.0
450184	W31096	Hs.237617	Homo sapiens, clone IMAGE:3447	SS	4.0
426068	AF029778	Hs.166154	jagged 2	DSL,EGF,vwc,granulin,SS,T	4.0
459255	AI493244	Hs.239500	hypothetical protein MGC13114	SS	4.0
403182			Target Exon	SS	4.0
432078	BE314877	Hs.24553	hypothetical protein FLJ12541	SS,TM	4.0
459167	BE504370		ESTs, Weakly similar to CA13_H	SS	4.0
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	SS,TM,ig,HLH	4.0
444633	AF111713	Hs.286218	junctional adhesion molecule 1	ig,SS,TM,HLH	4.0
434171	BE247688	Hs.347349	KIAA0948 protein		4.0
422155	AW249152		sirtuin (silent mating type in	SIR2,HLH,Myc_N_term,Myc-L	4.0
433262	AI571225	Hs.284171	KIAA1535 protein	SS,TM,cNMP_binding,ion_tr	4.0
442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank,SS,TM,HHH,ig	4.0
452500	AW373011	Hs.54558	hypothetical protein FLJ22222		4.0
437563	AI217204	Hs.144968	ESTs		4.0
432234	AA531128	Hs.115803	ESTs	SS	4.0
433135	AA443873	Hs.110477	dolichyl-phosphate mannosyltra		4.0
447495	AW401864	Hs.18720	programmed cell death 8 (apopt	pyr_redox,SS,Ets	4.0
452857	BE072814	Hs.258519	ESTs, Moderately similar to S6	SS	4.0
427834	AA506101	Hs.285813	hypothetical protein FLJ11807	SS,TM	4.0

418963	BE304571	Hs.89529	aldo-keto reductase family 1,	aldo_ket_red	4.0
437340	AL353935	Hs.135917	hypothetical protein DKFZp761D	TBC,bZIP,WD40,WD40	4.0
455928	BE170313		gb:QV4-HT0536-040500-193-g02 H	SS	4.0
400607			Target Exon	SS,homeobox	4.0
424825	AF207069	Hs.153357	procollagen-lysine, 2-oxogluta	2OG-FeII_Oxy,Glycos_trans	4.0
438143	BE500981	Hs.269652	ESTs		4.0
433173	Z35093	Hs.3196	surfeit 1	SURF1,SS,TM,SURF1,SURF4	4.0
412550	R52452	Hs.26370	gb:yg80g07.r1 Soares infant br		4.0

TABLE 23B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408215	10478_1	BE614290 AA307674 N35629 AA338538 AI193603 AA781096 AI680061 AI613258 AW276647 BE221263 AI348910 AI985031 AI090078 AI359617 AA666391 AI160210 AI446461 AI355345 AI343638 AI343640 AI275091 M78746 AW262795 AW250002 AA503756 AI934519 AW272086 N26520 AA626639
408294	1050553_1	BE141732 U75823 BE141331 AW178416 AW178430 BE141343 BE141298 BE141702 BE141285
409114	110088_1	AA070021 AA126205 AA082771 AA102169 AA083530 AA082183 AA115915 AA085147 AA125905 AA063336 AA079206
409164	110421_1	AA706639 AA064707 AL036920 AI651598
409616	114348_1	AA076248 AA120958 AA122152 AA076249
409938	116091_1	AW974648 AA652153 AA649671 AA078582
409960	116270_1	BE261944 AA715461 AA318136 AA134972 AA319849 W04622 AI291655 AW879092 AA130778 BE314003 AA908246 AW960808 AA385346 AA205977 C02043 AA135057 AA078870 AA377395 AA318795 AA318785 AA319160 BE000960 AW370250 AW370244 T85930 AA759250 AI567682 AA932839 AI056920
410445	120374_2	AA199830 AI143895 AW961629 AA322482
411219	1236055_1	AW832917 AW832913 AW832906 AW832788 AW832915 AW832776
411674	1253746_1	AW861123 AW861125 AW856717 AW861116 AW856706 AW856788 AW856774 AW856787 AW856780 AW856782 AW856789 AW856772 AW856784 AW856786 AW856776 AW856635 AW856767
412091	1276564_1	R06185 AW891805 AW901892 AW901895
412173	1280870_1	T71071 AW902279 AW897608
412575	130769_1	AA113177 AW894515 AA113847
413534	1375357_1	BE146961 BE146780 BE146788 BE146967 BE146774 BE146963 BE146907
413564	1376722_1	BE260120 BE148538
413764	1387163_1	BE162704 BE162705 BE162732 BE162702 BE162694
413837	139363_1	AW163525 AW163255 AW163385 AI929359 BE279279 AA132590 AW157329 AA584408 AW157252 AI692198 AW003514 T24436 AI765658 AW157459 AI810740 AI659582 AI969924 AI929284 AI340993 AI349083 AW299522 AW664650 AW299513 AA132529 AI340991 AI912836 AI341293 AI650609 AA279
414413	1443696_1	BE294877 BE294759
415126	1523506_1	D60945 D61346 D81568 D80539
419120	182026_1	BE271922 N54771 AA234233 AA471354 BE171081 AA253482 AA470113 AA824327 H24470 AW504757 N51688 AI400700 AA578548 AA714130 AA609917 AW780349 AW664465 AW467553 AW571643 AA469943 AW474826 AA767165 AA326817 AA593859 AW952245 AW341739 AA805093 AA779455 AW016655
422155	21235_1	AW249152 AW249153 BE298958 AW192872 AF095714 R05553 AF083107 AF160214 NM_012237 BE258447 BE253088 AA297721 H68948 W39153 AA070372 H14246 AL079367 R24561 AW403997 AA297034 AA297092 F11858 AI372597 AA297787 Z42780 AA297072 T81280 T83544 AA297053 H26063 AA26
423348	227276_1	AA324687 AA325155 AW962038
425858	257265_1	AA364923 AW963483 BE182774 C21461
426571	269283_1	AA381642 AA381664 AW963560 AW949848 AA381728 AA381608
427326	277229_1	AI287878 AI804160 AA400787
428092	286920_1	AW879141 AA421182 AI734104 AI733923 AA430600
429720	308153_1	M79091 AA773950 AA586573 AA457225
430168	313927_1	AW968343 AA468507 AI478223 AW513008 AI762122 AI554512 AA862642 AA468976
431424	333110_1	AI222969 AA806560 AA504839 AA805261
433319	363095_1	AA583232 AA601715
433933	377703_1	AI754389 AW295190 AI056058 AI056059 AI863364 AI863355 AW131720 AI674922 AI949042 AI990060 AI623178 AW469497 AA620354
433941	377883_1	AA620612 AA994983 AA994990
434303	383224_1	AW204058 AI424379 AI669663 AA629077 AW613033
434743	3925_1	AI363410 AI356019 H00141 T78748 AL049365 AL079911 AI750972 Z42602 AW452523 AI223826 AA215407 AI633829 AA292122 N42783 AW505595 AF086096 N90340 N63271 AA131836 AW607273 AA527132 T32315 AA421961 T34951 AW966080 M78807 N31947 AA521151 AA278866 AA044784 AA700
434796	393400_1	AA812046 AW974514 AA764999 AA649302
435851	411522_1	AA700946 AA702712 AA947620
436163	41515_6	R84938 AL047151 AA310309 AW063200 AI569528 AI307823 N49975
437215	43473_1	AL117488 AL044479
438999	467686_1	AW276811 AA829050 AA829190
439246	47021_3	AI498072 AW251083 AA985226 AA852987 AI392809 AA206609 AW190187 AA555262 AF086057 F35814 AW516382 AA377885 N50847 F27148 AA731186 AA417728 AI003145
440317	49187_1	BE561888 BE560615 BE562102
442462	543232_1	AF031405 H73415
442472	543371_1	AW806859 AW806852 AF049582
445625	64558_1	BE246743 AA436942 AW024744 AW242177 AA975476 AW385185 R07536 R73462 AV654529 T57442 AI399986 R50073 R48743 AI769689 AI863005 AA317806 AI678000 AW189963 AI986207 AW471273 R73463 AI335104 AI590161 AI469257 AI954604 H21954 T25141 AA856793 R50074 AI708253 AI2
445631	6457_1	AK001822 AW860325 AA335296 AW965531 AW130957 AW193951 AI347975 AW081323 AW662527 AI343924 AI380749 AA938153 T66966 AI655000 AW418837 AI380485 AA410698 AI520726 BE501355 AI637925 AW779200 AI524755 AW593995 AI336927 AI336928 AI357036 R60592 H19058 R11124 T1
447128	70934_1	AI271898 BE048502 AI452509 AI244810 X84721 AI858001 AI553937 AA149853 H00719 AI765259 AW973696 F25787 F35749 AI568815 AW015380 AA554539 C00201 AA961610 AW059537 R77127
448241	756181_1	AW811064 AW811160 AI478413
448993	79225_1	AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265 AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245 AA730380 AA394063 AA454

453446	967533_1	BE299996 BE297115 BE270415 BE295214 BE296526
454682	1228976_1	AW816029 AW813292 AW816156 AW813333 AW816159 AW813302 AW813344 AW813172
455035	1249762_1	AW851734 AW851676 AW851693 AW851713 AW851722 AW851616 AW851731 AW851618 AW851648 AW852215
455340	1283604_1	AW901435 BE094527
455557	1325974_1	AW995839 AW995907
455600	1335877_1	BE061053 BE008959 BE008957 BE091618
455885	1380385_1	BE153524 BE153576 BE153583
455928	1383899_1	BE170313 BE158339 BE158290
456573	201205_1	AI279811 AI301071 AI214696 AI279813 AA588460 AA287256 BE171665
457268	310453_1	AW272279 AA461542 AA460615
457978	448900_1	AA776638 BE439540
458196	503719_1	AI802408 AA907424 AI279233 AI302762 N33153 BE045678 AI863332 AW173558 AI302328 Z20793 D25594 BE326823
459167	92053_1	BE504370 AI243453 AI809556 AI702878 AI702163 AI300626 AW072219 AI369492 AI349587 AW779061 W78149 AA055693 AA974162 AI394380 AI830098 AW054857 AI870008 AW207658 AW665508 AW300595 AI192992 AW628019 AI274365 AA906922 N92547 AW054727 AW206667 AW136707 AW13761
459271	969257_1	AL045934 AL039532 H55631

TABLE 23C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400460	8389428	Plus	35559-36295
400607	9887666	Plus	3112-4159
400833	8705148	Minus	187599-188138
400845	9188605	Plus	34428-34612
400923	7637836	Minus	94518-94659
400933	7651935	Minus	105330-105503
401210	7712287	Plus	166969-167133,169760-169877,171563-171733
401264	9797154	Plus	130810-130927,133367-133504
401278	9799936	Plus	98428-98573
401609	7705041	Minus	9877-11997
401674	7689903	Plus	138786-138927,139157-139298,139440-139599,139960-140159
401724	7656694	Plus	150063-150241
402197	8576113	Plus	199466-199585
402365	9454515	Minus	70928-71185
402393	9929688	Plus	19813-20084,20163-20263
402400	9945145	Minus	80123-80322
402632	9931268	Plus	101166-101419
402884	9926562	Plus	47980-48191
402916	7406502	Minus	361-474,541-687
403055	8748904	Minus	109532-110225
403128	7331426	Plus	122884-123018,123134-123283,123372-123695,123779-123940,124059-124256
403182	9838273	Plus	102163-102345,102545-102725
403938	7711795	Plus	48636-48822
403945	7711869	Minus	32141-32263
404036	8567760	Minus	65247-67529,112537-114863
404333	9802821	Minus	137948-138024,138111-138300
404343	9838093	Plus	122664-122931
404344	9838093	Plus	127865-128384
404365	9964977	Plus	50151-50319,50859-51098
404661	9797073	Plus	33374-33675,33769-34008
404757	7706327	Plus	100933-101083,101580-101782
404807	4165210	Minus	124246-124422
405334	3135285	Plus	139386-139856
405346	2981263	Plus	101982-102171
405364	2281075	Minus	48325-48491,49136-49252
405371	2078469	Minus	47657-47766,48461-48596
405594	6960456	Plus	161628-161734,162823-163014,164439-164652
405928	7717155	Minus	2923-3209
406230	4760409	Plus	71716-72515
406244	7417725	Plus	39422-39595
406301	8575868	Plus	57291-57494
406487	7711306	Plus	82039-82902
406495	7711328	Minus	174661-174978
406613	2957168	Plus	5029-5147

Table 24A lists about 117 genes down-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 23A, except that the numerator was set to the 75th percentile amongst various non-malignant ovary specimens, the denominator was set to the 96th percentile value amongst various ovarian cancers, the numerator was greater than or equal to 75 units, and the ratio was greater than or equal to 2.0 (i.e., 2-fold downregulation in tumor vs. normal ovaries).

TABLE 24A:
Pkey: Unique Eos probeset identifier number
Ex. Accn: Exemplar Accession number, Genbank accession number
UG ID: UniGene number
Title: UniGene gene title
Protein Dom.: Predicted protein domain
R1: Ratio of normal ovaries to tumor

Pkey	Ex. Accn	UG ID	Title	Protein Dom.	R1
428232	BE272452	Hs.183109	monoamine oxidase A	Amino_oxidase,pyr_redox,F	16.9
433563	AI732637	Hs.277901	ESTs	SS	10.8
444931	AV652066		general transcription factor I	SS,Glypican	8.7
451573	AW130351		ESTs	SS	8.3
429570	BE242256	Hs.2441	KIAA0022 gene product	lectin_c,SS,TM	7.9
453510	AI699482	Hs.42151	ESTs	SS	7.5
410295	AA741357		nidogen (enactin)	SS,EGF,ldl_recept_b,thyro	6.9
438549	BE386801	Hs.21858	trinucleotide repeat containin	SS,serpin,SS,WD40,FYVE	6.5
407969	AA046217	Hs.105370	ESTs	SS,Pep_M12B_propep,Reprol	6.2
414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 famil	aldedh	6.0
448438	BE613081	Hs.24654	Homo sapiens cDNA FLJ11640 fis		5.7
441422	R43777	Hs.21364	ESTs	SS,TM	5.1
413391	AI223328	Hs.75335	glycine amidinotransferase (L-	Amidinotransf	3.9
428022	Z39686	Hs.27865	ESTs	SS	3.6
423044	AA320829	Hs.97266	protocadherin 18		3.6
416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class	adh_zinc,HCV_NS4a,TM,adh_	3.5
452854	AA437061	Hs.14060	prokineticin 1 precursor	SS	3.4
436772	AW975688		metallothionein 1E (functional	SS,TM,7tm_2,HRM	3.2
415162	AF035718	Hs.78061	transcription factor 21	HLH	3.2
427794	AA709186	Hs.99070	ESTs	SS	3.1
433072	AI928037	Hs.158832	ESTs	SS	3.1
418318	U47732	Hs.84072	transmembrane 4 superfamily me	transmembrane4	2.9
410059	NM_007038	Hs.58324	a disintegrin-like and metallo	Reprolysin,tsp_1,Pep_M12B	2.9
431933	AI187057	Hs.132554	ESTs	TM,SS,TM	2.9
420303	AA258282	Hs.278436	KIAA1474 protein		2.8
438780	M64936		gb:Homo sapiens retinoic acid-		2.8
427661	AA410292	Hs.104761	ESTs	SS,wnt	2.8
437342	AW903297	Hs.236438	hypothetical protein DKFZp761K	Sec7,PH	2.8
453828	AW970960	Hs.293821	ESTs	SS,Pep_M12B_propep,Reprol	2.7
418444	AI902899	Hs.85155	butyrate response factor 1 (EG	zf-CCCH,SS	2.7
453767	AB011792	Hs.35094	extracellular matrix protein 2	vwc,LRR,SS,LRR	2.7
413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hevin)	kazal,SS,kazal	2.7
413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fi	laminin_B,laminin_EGF,lam	2.7
414504	AW069181	Hs.115175	sterile-alpha motif and leucin	SS,pkinase,SAM	2.7
439897	NM_015310	Hs.6763	KIAA0942 protein	Sec7,PH	2.7
421639	NM_012082	Hs.106309	Friend of GATA2	SS	2.7
442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrog	HATPase_c,HATPase_c	2.6
410494	M36564	Hs.64016	protein S (alpha)	EGF,laminin_G,gla	2.6
452958	AA883929	Hs.40527	ESTs	SS	2.6
449648	AW205607	Hs.253499	ESTs	SS	2.5
435519	AI218950	Hs.125461	hypothetical protein FLJ11539	SS	2.5
433690	AI373949	Hs.279610	hypothetical protein FLJ10493	SS	2.5
424319	AW961026	Hs.96752	ESTs, Weakly similar to ALU8_H		2.5
420174	AI824144	Hs.199749	ESTs		2.5
421709	AA159394	Hs.107056	CED-6 protein	PID,Herpes_UL6	2.4
417622	AW298163	Hs.82318	WAS protein family, member 3	WH2	2.4
453655	AW960427	Hs.342874	transforming growth factor, be	SS,TM,zona_pellucida	2.4
408468	AI909712		phosphatidylinositol transfer	SS,PX,PH,PLDc,PH,PLDc,PX	2.4
400829			C11000244:gi|11056030|ref|NP_0	SS,TM,SS,TFIID_30kD	2.3
453125	AW779544	Hs.115497	hypothetical protein FLJ22655	ras	2.3
437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp5	HLH	2.3
425462	AI491852	Hs.46783	Homo sapiens cDNA: FLJ22382 fi		2.3
417094	NM_006895	Hs.81182	histamine N-methyltransferase	Acyl-CoA_dh	2.3
403247			Target Exon		2.3
441916	AA993571		ESTs		2.3
422746	NM_004484	Hs.119651	glypican 3	Glypican,SS	2.3
416777	AF146760	Hs.79844	DKFZP564M1416 protein	SS,GTP_CDC,SS	2.3
409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fi	SS,TM	2.3
418956	AA234831		KIAA0788 protein	SS	2.3
410073	AW408163	Hs.58488	catenin (cadherin-associated p	Vinculin,Stathmin	2.3
419461	AI452601	Hs.288869	nuclear receptor subfamily 2,	hormone_rec,zf-C4,hormone	2.3
429319	AL023754	Hs.199068	similar to calcium/calmodulin	SS,pkinase	2.2
452123	AI267615	Hs.38022	ESTs	SS	2.2
453305	R39224	Hs.267997	EHM2 gene		2.2
416157	NM_003243	Hs.342874	transforming growth factor, be	zona_pellucida,SS,TM,zona	2.2
406637	U14966	Hs.180946	ribosomal protein L5	Ribosomal_L18p	2.2
414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA	p450	2.2
408915	NM_016651	Hs.48950	heptacellular carcinoma novel	SS	2.2
420929	AI694143	Hs.326248	programmed cell death 4	MA3,LRR	2.2
456972	AI054347	Hs.2017	ribosomal protein L38	SS,TM	2.2
409549	AB029015	Hs.54886	phospholipase C, epsilon 2	C2,PH,PI-PLC-Y,PI-PLC-X	2.2
410209	AI583661	Hs.60548	hypothetical protein PRO1635	SS,TM,Fork_head	2.2
449500	AW956345	Hs.12926	ESTs	SS,TM	2.2
447806	W03616	Hs.10432	ESTs, Weakly similar to I38022		2.1
441712	AW391927	Hs.7946	KIAA1288 protein		2.1
445025	AI768895	Hs.295727	ESTs, Weakly similar to ALUB_H	SS,BAG,UPF0001	2.1
444161	N52543	Hs.142940	ESTs	SS	2.1
427156	BE621719	Hs.173802	KIAA0603 gene product	SS,TM,TBC	2.1
436995	AI160015	Hs.125489	ESTs	SS,TM,RasGEF,actin,RasGEF	2.1
408443	N33937	Hs.10336	ESTs	SS	2.1
448274	AI268097	Hs.67317	Homo sapiens cDNA FLJ11775 fis		2.1
426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy	ZZ,CH,WW,spectrin,bZIP,SS	2.1
443906	AA348031	Hs.7913	ESTs		2.1

444815	AA151539	Hs.1227	aminolevulinate, delta-, dehyd	SS,ALAD	2.1
420728	AA767718	Hs.93581	hypothetical protein FLJ10512	SS,TM,Sema,PSI,ig	2.1
404245			NM_007116*:	fibrinogen_C,fn3,SS	2.1
436420	AA443966	Hs.31595	ESTs	SS,TM,PMP22_Claudin,SS,TM	2.1
410066	AL117664	Hs.58419	DKFZP586L2024 protein		2.0
414476	AA301867	Hs.76224	EGF-containing fibulin-like ex	EGF,TIL,SS	2.0
424137	AA335769	Hs.16262	ESTs		2.0
447659	AA017472	Hs.107260	hypothetical protein DKFZp586H	SS	2.0
444862	AI209158	Hs.143929	ESTs	SS,TM	2.0
426086	T94907	Hs.188572	ESTs	PH,CH,spectrin	2.0
436080	AI684710	Hs.201645	ESTs	SS,ATP-synt_C	2.0
424651	AI493206		ESTs	SS	2.0
432939	AL038924	Hs.279849	KIAA0438 gene product	zf-C3HC4,myosin_head,DIL,	2.0
449088	AI654048	Hs.196556	ESTs	SS,MACPF,sushi,ldl_recept	2.0
428642	NM_014899	Hs.10432	KIAA0878 protein	BTB,ras	2.0
419577	L36531	Hs.91296	integrin, alpha 8	TM,integrin_A,FG-GAP	2.0
450435	AI695975	Hs.201805	ESTs	laminin_B,laminin_EGF,lam	2.0
450696	AI654223	Hs.16026	hypothetical protein FLJ23191	SS	2.0
421255	BE326214	Hs.93813	ESTs	TM	2.0
432467	T03667	Hs.239388	Human DNA sequence from clone	SS	2.0
408654	BE018882	Hs.46721	UCC1 protein	SS,Ependymin,SS	2.0
412611	AA732036	Hs.164478	hypothetical protein FLJ21939		2.0
453355	AW295374	Hs.31412	myopodin		2.0
424665	AW368576	Hs.139851	caveolin 2	SS,TM,Caveolin,Caveolin	2.0
458147	AW752597		gb:IL3-CT0214-161299-045-B06 C	SS,TM,PMM	2.0
447566	N50432	Hs.102648	ESTs		2.0
414496	W73853		ESTs	SS,TM,pkinase,F5_F8_type_	2.0
425618	AW119112	Hs.9052	Homo sapiens cDNA: FLJ22042 fi	SS,TM	2.0
415166	NM_003652	Hs.78068	carboxypeptidase Z	Zn_carbOpept,Fz,Dioxygena	2.0
422157	AW957295	Hs.112318	6.2 kd protein	SS	2.0
450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp4	SH3	2.0
418919	AA232635		ESTs	SS,DUF25	2.0
444846	AI871055	Hs.148477	ESTs	SS,TM	2.0
418781	T41160	Hs.8404	ESTs		2.0

TABLE 24B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408468	106033_1	AI909712 AL039752 BE000369 AA376876 N75269 AA345398 AA349053 AW960062 R76169 R70638 AA054770 AI378587 AI338002 AI762398 N47873 AI066549 AI474112 AW450680 AA668668 R76114 AW242828 N58855 AW080313 AI378491 AI807102 AA417043 AI565444 AW263286 AW297099
410295	11922_2	AA741357 AI870000 W75997 H50726 AV658709 AI498817 AL037804 W67847 BE018553 AI033256 N76810 N31548 AI032084 N36278 AW075272 AI032081 R35753 W93372 AA700790 AI903697 N52985 R82468 AW580252 AL036760 AI052219 R36621 W07047 AA088621 AI249109 W68776 W69374 AA15
414496	145392_1	W73853 AA928112 W77887 AW889237 AA148524 AI749182 AI754442 AI338392 AI253102 AI079403 AI370541 AI697341 H97538 AW188021 AI927669 W72716 AI051402 AI188071 AI335900 N21488 AW770478 W92522 AI691028 AI913512 AI144448 W73819 AA604358 N28900 W95221 AI868132 H98
418919	180623_1	AA232635 AI373703 AA233330
418956	180862_1	AA234831 AI700302 AA906216 AA776957 R49415 AI420777 AA666394 AI830619 AA779469 AI972390 N40980 AI094453 AA826397 AA535994 AI868257 AI804295 AA897791 AA232893 AI348680 AI356232 AA235138 F31396 AW079977 H16405
424651	241981_1	AI493206 AA732315 AA344619 AA904035 AW952967 AA488889 AA635644 BE245127 AA669979 AA761874 H28767 AA910081 AA837086 AA766495 W76175 AI521825 AA746092 AA743152 AI478562 H88863
436772	426854_1	AW975688 AA731063 N67084
438780	46501_1	M64936 AI025512 AI382987 BE061777 AA089966 BE169930 T41176 AW594624 BE502415 AA121893 AI269283 T40311 AI684569 AA257011 AI079277 AI241318 BE327710 AW975215 AW896268 AA884990 BE327514
441916	528799_1	AA993571 AA971518 AI937262
444931	62567_1	AV652066 AA459880 T58512 T58561 AI651255 N49838 H87921 AW264447 AA428067 AA364094 AW955685 D62894 AW341452 AA243652 AI984618 AI816803 AI871252 AI376942 AI740496 AA452836 AI277917 AI149141 AA456147 AI784566 AI003975 AI245674 AI433703 AI200208 AI268985 AI38
451573	875588_1	AW130351 AW338699 AI803973
458147	488021_1	AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700

TABLE 24C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of *human chromosome 22*" Dunham, *et al.* (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
400829	8570385	Plus	152176-152616
403247	7656833	Minus	76626-77140
404245	7406725	Plus	36019-36282,37073-37813,38946-39314,40355-40651,42738-43028,43391-43696,45698-46030,51110-51415,52779-53072,54648-54935,55201-55509,55926-56240,56355-56672,57078-57401,59966-60262,62600-62926,63363-63686,66693-67025,68180-68497,68909-69232,71372-71695,720

Table 25A provides UnigeneID, UnigeneTitle, Pkey, and Exemplar Accession for sequences in Table 26. The information in Table 25A is linked by SEQ ID NO: to Table 26.

Table 25A:
Pkey: Unique Eos probeset identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number
UG ID: UniGene number
Title: UniGene title
SEQ ID NO: Sequence Identification number for sequences in Table 26

Pkey	Ex. Accn	UG ID	Title	SEQ ID NO
452838	U65011	Hs.30743	preferentially expressed antigen in mela	SEQ ID NO: 1-2
421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	SEQ ID NO: 3-4
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	SEQ ID NO: 5-6
458627	AW088642	Hs.97984	SRY (sex determining region Y)-box 17 (S	SEQ ID NO: 7-8
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	SEQ ID NO: 9-10
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	SEQ ID NO: 11-12
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	SEQ ID NO: 13-22
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	SEQ ID NO: 23-24
451110	AI955040	Hs.265398	PAR-6 beta (partitioning defective 6 h	SEQ ID NO: 25-26
428187	AI687303	Hs.285529	G protein-coupled receptor 49	SEQ ID NO: 27-28
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	SEQ ID NO: 29-30
433159	AB035898	Hs.150587	kinesin-like protein 2	SEQ ID NO: 31-32
426427	M86699	Hs.169840	TTK protein kinase	SEQ ID NO: 33-34
425371	D49441	Hs.155981	mesothelin	SEQ ID NO: 35-38
418506	AA084248	Hs.85339	G protein-coupled receptor 39	SEQ ID NO: 39-40
456546	AI690321	Hs.203845	KCNK15 potassium channel, subfamily K, m	SEQ ID NO: 41-42
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	SEQ ID NO: 43-44
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	SEQ ID NO: 45-46
424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	SEQ ID NO: 47-48
412078	X69699	Hs.73149	paired box gene 8	SEQ ID NO: 49-52
409178	BE393948	Hs.50915	kallikrein 5	SEQ ID NO: 53-54
448243	AW369771		integrin, beta 8	SEQ ID NO: 55-56
426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	SEQ ID NO: 57-58
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	SEQ ID NO: 59-60
431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	SEQ ID NO: 61-62
415539	AI733881	Hs.72472	BMP-R1B	SEQ ID NO: 63-64
423961	D13666	Hs.136348	periostin (OSF-2os)	SEQ ID NO: 65-66
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	SEQ ID NO: 67-68
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	SEQ ID NO: 69-70
409542	AA503020	Hs.36563	hypothetical protein FLJ22418	SEQ ID NO: 71-72
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	SEQ ID NO: 73-74
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	SEQ ID NO: 75-76
450375	AA009647		a disintegrin and metalloproteinase doma	SEQ ID NO: 77-78
426215	AW963419	Hs.155223	stanniocalcin 2	SEQ ID NO: 79-80
430044	AA464510	Hs.152812	ESTs	SEQ ID NO: 81
447033	AI357412	Hs.157601	ESTs	SEQ ID NO: 82-87
410418	D31382	Hs.63325	transmembrane protease, serine 4	SEQ ID NO: 88-89
411274	NM_002776	Hs.69423	kallikrein 10	SEQ ID NO: 90-91
422260	AA315993	Hs.105484	regenerating gene type IV	SEQ ID NO: 92-93
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	SEQ ID NO: 94-95
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	SEQ ID NO: 96-97
404977			Insulin-like growth factor 2 (somatomedi	SEQ ID NO: 98-99
427747	AW411425	Hs.180655	serine/threonine kinase 12	SEQ ID NO: 100-101
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	SEQ ID NO: 102-103
431846	BE019924	Hs.271580	uroplakin 1B	SEQ ID NO: 104-105
425465	L18964	Hs.1904	protein kinase C, iota	SEQ ID NO: 106-107
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	SEQ ID NO: 108-109
421451	AA291377	Hs.50831	ESTs	SEQ ID NO: 110-117
437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	SEQ ID NO: 118-119
411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	SEQ ID NO: 120-121
424078	AB006625	Hs.139033	paternally expressed 3	SEQ ID NO: 122-123
406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	SEQ ID NO: 124-125
428450	NM_014791	Hs.184339	KIAA0175 gene product	SEQ ID NO: 126-127
438167	R28363	Hs.24286	chemokine binding protein 2 (CCBP2), mRN	SEQ ID NO: 128-129
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SEQ ID NO: 130-131
430691	C14187	Hs.157208	aristaless-related homeobox protein ARX	SEQ ID NO: 132-133
408081	AW451597	Hs.167409	intron of basic-helix-loop-helix-PAS pro	SEQ ID NO: 134
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SEQ ID NO: 135-138
407792	AI077715	Hs.39384	putative secreted ligand homologous to f	SEQ ID NO: 139-140
428093	AW594506	Hs.104830	ESTs	SEQ ID NO: 141-144
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	SEQ ID NO: 145-148
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	SEQ ID NO: 149-150
431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	SEQ ID NO: 151-152
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	SEQ ID NO: 153-154
436972	AA284679	Hs.25640	claudin 3	SEQ ID NO: 155-156
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	SEQ ID NO: 157-158
410001	AB041036	Hs.57771	kallikrein 11	SEQ ID NO: 159-160

TABLE 25B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
448243	75629_1	AW369771 AW748174 AA290801 AA419198 AA044331 AA127909 AW995442 AI480343 AA044582 AW956159 AA373451 AA127965 AL134913 AW994956 BE622314 BE006298 BE006312 BE006305 BE006317 BE006303 AA043906 AA234175 AA479726
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

TABLE 25C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	Nt_position
404977	3738341	Minus	43081-43229
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 26

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_006115.1
Coding sequence: 236..1765

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1          11         21         31         41         51
|          |          |          |          |          |
GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCCT GCAGCCCCTC AGCACCGCTC     60
CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA    120
ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGACT    180
GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA    240
ACGAAGGCGT TTGTGGGGTT CCATTCAGAG CCGATACATC AGCATGAGTG TGTGGACAAG    300
CCCACGGAGA CTTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT    360
TGCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCCCGCCA CTCTTCATGG CAGCCTTTGA    420
CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC    480
TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA    540
TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAAC TTCAAGTGCT    600
GGATTTACGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG    660
TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAAGTAGA    720
TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCCAGTA GAGGTGCTCG TAGACCTGTT    780
CCTCAAGGAA GGTGCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA    840
GAAAAATGTA CTACGCCTGT GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA    900
TATCAAGATG ATCCTGAAAA TGGTGCAGCT GGACTCTATT GAAGATTTGG AAGTGACTTG    960
TACCTGGAAG CTACCCACCT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAATCT   1020
GCGTAGACTC CTCCTCTCCC ACATCCATGC ATCTTCCTAC ATTTCCCCGG AGAAGGAAGA   1080
GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA   1140
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Seq ID NO: 2 Protein sequence
Protein Accession #: NP_006106.1

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LTDVSPEPLQ ALLERASATL QDLVFDECGI TDDQLLALLP SLSHCSQLTT LSFYGNSISI    420
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Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 264..782

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Seq ID NO: 4 Protein sequence
Protein Accession #: Eos sequence

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Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: AB051390.
Coding sequence: 34..2457

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AGAAATGTAT AGACACCTCA TACTCAAATA AGAAACTGAC TTAAATGGTA CTTGTAATTA   2940
GCACTTGGTG AAAGCTGGAA GGAAGATAAA TAACACTAAA CTATGCTATT TGATTTTTCT   3000
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TGCTATCAGC TGATATTAGT AGCTTTGCAA CCCTGATAGA GTAAATAAAT TTTATGGGCG   3180
GGTGCCAAAT ACTGCTGTGA ATCTATTTGT ATAGTATCCA TGAATGAATT TATGGAAATA   3240
GATATTTGTG CAGCTCAATT TATGCAGAGA TTAAATGACA TCATAATACT GGATGAAAAC   3300
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ATAACCACTC CTTTCACAGT TTATTTTCTT CTCAAGCGTT TTCAAGATCT AGCATGTGGA   3420
TTTTAAAAGA TTTGCCCTCA TTAACAAGAA TAACATTTAA AGGAGATTGT TTCAAAATAT   3480
TTTTGCAAAT TGAGATAAGG ACAGAAAGAT TGAGAAACAT TGTATATTTT GCAAAAACAA   3540
GATGTTTGTA GCTGTTTCAG AGAGAGTACG GTATATTTAT GGTAATTTTA TCCACTAGCA   3600
AATCTTGATT TAGTTTGATA GTGTGTGGAA TTTTATTTTG AAGGATAAGA CCATGGGAAA   3660
ATTGTGGTAA AGACTGTTTG TACCCTTCAT GAAATAATTC TGAAGTTGCC ATCAGTTTTA   3720
CTAATCTTCT GTGAAATGCA TAGATATGCG CATGTTCAAC TTTTTATTGT GGTCTTATAA   3780
TTAAATGTAA AATTGAAAAT TCATTTGCTG TTTCAAAGTG TGATATCTTT CACAATAGCC   3840
TTTTTATAGT CAGTAATTCA GAATAATCAA GTTCATATGG ATAAATGCAT TTTTATTTCC   3900
TATTTCTTTA GGGAGTGCTA CAAATGTTTG TCACTTAAAT TTCAAGTTTC TGTTTTAATA   3960
GTTAACTGAC TATAGATTGT TTTCTATGCC ATGTATGTGC CACTTCTGAG AGTAGTAAAT   4020
GACTCTTTGC TACATTTTAA AAGCAATTGT ATTAGTAAGA ACTTTGTAAA TAAATACCTA   4080
AAACCCAAAA AAAAAAAAAA AAAAA
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Seq ID NO: 10 Protein sequence
Protein Accession #: Q9H8V3

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KQEELTKALK DIKVGFVKME SVEEFEGLDS PEFENVFVVT DFQDSVFNDL YKADCRVIGP    120
PVVLNCSQKG EPLPFSCRPL YCTSMMNLVL CFTGFRKKEE LVRLVTLVHH MGGVIRKDFN    180
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VKQEWFWGSI QMDARAGETM YLYEKANTPE LKKSVSMLSL NTPNSNRKRR RLKETLAQLS   360
RDTDVSPFPP RKRPSAEHSL SIGSLLDISN TPESSINYGD TPKSCTKSSK SSTPVPSKQS   420
ARWQVAKELY QTESNYVNIL ATIIQLFQVP LEEEGQRGGP ILAPEEIKTI FGSIPDIFDV   480
HTKIKDDLED LIVNWDESKS IGDIFLKYSK DLVKTYPPFV NFFEMSKETI IKCEKQKPRF   540
HAFLKINQAK PECGRQSLVE LLIRPVQRLP SVALLLNDLK KHTADENPDK STLEKAIGSL   600
KEVMTHINED KRKTEAQKQI FDVVYEVDGC PANLLSSHRS LVQRVETISL GEHPCDRGEQ   660
VTLFLFNDCL EIARKRHKVI GTFRSPHGQT RPPASLKHIH LMPLSQIKKV LDIRETEDCH   720
NAFALLVRPP TEQANVLLSF QMTSDELPKE NWLKMLCRHV ANTICKADAE NLIYTADPES   780
FEVNTKDMDS TLSRASRAIK KTSKKVTRAF SFSKTPKRAL RRALMTSHGS VEGRSPSSND   840
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Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: XM_044166
Coding sequence: 1..1576

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CGCCCTTCAG CTGGCTCTCG ATCAACTCTG CCTCCTGGGT TTGGGGGAGC CCCCCGCCCC    180
CAGGGCGGGC GAGGACGGGG GAGGTGGGGG GGGCGGCGCC CCCGCGCAGC CGACAGCCCC    240
CCCGCAGCCG GCGCCGCCGC CGCCGCCCGC GGCGCCCCCG GCCGCCCCGA CGACGGCCCC    300
CGCAGCGCAG ACGCCCCAGC CCCCCACCGC CCCCAAAGGG GCGAGCGACG CCAAGCTCTG    360
CGCTCTCTAC AAAGAGGCCG AGCTGCGCCT GAAGGGCAGC AGCAACACCA CGGAGTGTGT    420
TCCCGTGCCC ACCTCCGAGC ACGTGGCCGA GATCGTGGGC AGGCAAGGCT GCAAGATTAA    480
GGCCTTGAGG GCCAAGACCA ACACCTACAT CAAGACACCG GTGAGGGGCG AGGAACCAGT    540
GTTCATGGTG ACAGGGCGAC GGGAGGACGT GGCCACAGCC CGGCGGGAAA TCATCTCAGC    600
AGCGGAGCAC TTCTCCATGA TCCGTGCCTC CCGCAACAAG TCAGGCGCCG CCTTTGGTGT    660
GGCTCCTGCT CTGCCCGGCC AGGTGACCAT CCGTGTGCGG GTGCCCTACC GCGTGGTGGG    720
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CGTGGAGCGT GCGCGCGAGG AGATCGAGAC GCACATCGCG GTGCGCACTG GCAAGATCCT    900
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CTGGACCTGT TTTCCACTAA AGCCTTTTGG AAAGCGGTGA TTTGAGGGGC AAGGTGCTTA   1680
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GGAAGGAGGT CACAGCCAAG AAAACTGCCC TGTGACGACT TCCCTCCTTC CCGCCTATGT   3060
GAGCCATCCT GAGATGTCTG TACAATAGAA ACCAAACCAA ATGGGCACCC TCGGTTGCCG   3120
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CCCACCCTTA CCAATTGAGC CAAACCTAGA AACAAACACA AAACACGAAT AGTGAGAGAC   3300
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AGAAAACAAA AATAGCAAAA AAAAAAAAAA AAAGCAGTTC TTTATAATTT AATATTCTAT   3420
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Seq ID NO: 12 Protein sequence
Protein Accession #: XP_044166

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ALYKEAELRL KGSSNTTECV PVPTSEHVAE IVGRQGCKIK ALRAKTNTYI KTPVRGEEPV    180
FMVTGRREDV ATARREIISA AEHFSMIRAS RNKSGAAFGV APALPGQVTI RVRVPYRVVG    240
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KARAGPPGAH RSPATSAGPE LAGLPRRPPG EPLQGFSKLG GGGLRSPGGG RDCMVCFESE   480
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Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2982

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AACGAAACAG AAAAAACTAA AATCACTATA GTAAAAACCT TCAATGCTTC AGGCGTCAAA    240
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GGCACCTTAA CTGGAGTCCT GTCTCTAAGT GAATTAAAAC GCTCAGAGCT CAACAAAACC    420
CTGCAAACCC TAAGTGAGAC TTACTTTATA ATGTGTGCTA CAGCAGAGGC CCAAAGCACA    480
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TGCCCTTCCT CCCCAGAAGA GTTGGAAAAG CTTCAGTGTG ACCTGCAGGA TCCCATTGTC    660
TGTCTTGCTG ACCATCCACG TGGCCCACCA TTTTCTTCCA GCCAATCCAT CCCAGTGGTG    720
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TCAGACAATG GCTGCTCTGT CAAAGACAGG AGATTGAATG AAACCATCTG TACCTGTAGC   1740
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Seq ID NO: 14 Protein sequence
Protein Accession #: Eos sequence

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ALERVKIRPM EHCCCSVRIP CPSSPEELEK LQCDLQDPIV CLADHPRGPP FSSSQSIPVV    240
PRATVLSQVP KATSFAEPPD YSPVTHNVPS PIGEIQPLSP QPSAPIASSP AIDMPPQSET    300
ISSPMPQTHV SGTPPPVKAS FSSPTVSAPA NVNTTSAPPV QTDIVNTSSI SDLENQVLQM    360
EKALSLGSLE PNLAGEMINQ VSRLLHSPPD MLAPLAQRLL KVVDDIGLQL NFSNTTISLT    420
SPSLALAVIR VNASSFNTTT FVAQDPANLQ VSLETQAPEN SIGTITLPSS LMNNLPAHDM    480
ELASRVQFNF FETPALFQDP SLENLSLISY VISSSVANLT VRNLTRNVTV TLKHINPSQD    540
ELTVRCVFWD LGRNGGRGGW SDNGCSVKDR RLNETICTCS HLTSFGVLLD LSRTSVLPAQ    600
MMALTFITYI GCGLSSIFLS VTLVTYIAFE KIRRDYPSKI LIQLCAALLL LNLVFLLDSW    660
IALYKMQGLC ISVAVFLHYF LLVSFTWMGL EAFHMYLALV KVFNTYIRKY ILKFCIVGWG    720
VPAVVVTIIL TISPDNYGLG SYGKFPNGSP DDFCWINNNA VFYITVVGYF CVIFLLNVSM    780
FIVVLVQLCR IKKKKQLGAQ RKTSIQDLRS IAGLTFLLGI TWGFAFFAWG PVNVTFMYLF    840
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SSSSNSLQSS SNSTNSTTLL VNNDCSVHAS GNGNASTERN GVSFSVQNGD VCLHDFTGKQ    960
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Seq ID NO: 15 DNA sequence

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Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2904
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AACGAAACAG AAAAAACTAA AATCACTATA GTAAAAACCT TCAATGCTTC AGGCGTCAAA    240
CCCCAGAGAA ATATCTGCAA TTTGTCATCT ATTTGCAATG ACTCAGCATT TTTTAGAGGT    300
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GGCACCTTAA CTGGAGTCCT GTCTCTAAGT GAATTAAACA CATTAAATTG TACATTCACA    420
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CGTGGCCCAC CATTTTCTTC CAGCCAATCC ATCCCAGTGG TGCCTCGGGC CACTGTGCTT    660
TCCCAGGTCC CCAAAGCTAC CTCTTTTGCT GAGCCTCCAG ATTATTCACC TGTGACCCAC    720
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Seq ID NO: 16 Protein sequence
Protein Accession #: Eos sequence
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GTTACTTTAA GCTTACTCCC TTCAAACGAA ACAGGCGTCA AACCCCAGAG AAATATCTGC    240
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Protein Accession #: Eos sequence

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IRPMEHCCCS VRIPCPSSPE ELEKLQCDLQ DPIVCLADHP RGPPFSSSQS IPVVPRATVL    240
SQVPKATSFA EPPDYSPVTH NVPSPIGEIQ PLSPQPSAPI ASSPAIDMPP QSETISSPMP    300
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PSSNEVETTS LNDVTLSLLP SNETGVKPQR NICNLSSICN DSAFFRGEIM FQYDKESTVP   120
QNQHITNGTL TGVLSLSELK RSELNKTLQT LSETYFIMCA TAEAQSTLNC TFTIKLNNTM   180
NACAVIAALE RVKIRPMEHC CCSVRIPCPS SPEELEKLQC DLQDPIVCLA DHPRGPPFSS   240
SQSIPVVPRA TVLSQVPKAT SFAEPPDYSP VTHNVPSPIG EIQPLSPQPS APIASSPAID   300
MPPQSETISS PMPQTHVSGT PPPVKASPSS PTVSAPANVN TTSAPPVQTD IVNTSSISDL   360
ENQVLQMEKA LSLGSLEPNL AGEMINQVSR LLHSPPDMLA PLAQRLLKVV DDIGLQLNFS   420
NTTISLTSPS LALAVIRVNA SSFNTTTFVA QDPANLQVSL ETQAPENSIG TITLPSSLMN   480
NLPAHDMELA SRVQFNFFET PALFQDPSLE NLSLISYVIS SSVANLTVRN LTRNVTVTLK   540
HINPSQDELT VRCVFWDLGR NGGRGGWSDN GCSVKDRRLN ETICTCSHLT SFGVLLDLSR   600
TSVLPAQMMA LTFITYIGCG LSSIPLSVTL VTYIAFEKIR RDYPSKILIQ LCAALLLLNL   660
VFLLDSWIAL YKMQGLCISV AVFLHYFLLV SFTWMGLEAF HMYLALVKVF NTYIRKYILK   720
FCIVGWGVPA VVVTIILTIS PDNYGLGSYG KFPNGSPDDF CWINNNAVFY ITVVGYFCVI   780
FLLNVSMFIV VLVQLCRIKK KKQLGAQRKT SIQDLRSIAG LTFLLGITWG FAFFAWGPVN   840
VTFMYLFAIF NTLQGFFIFI FYCVAKENVR KQWRRYLCCG KLRLAENSDW SKTATNGLKK   900
QTVNQGVSSS SNSLQSSSNS TNSTTLLVNN DCSVHASGNG NASTERNGVS FSVQNGDVCL   960
HDFTGKQHMF NEKEDSCNGK GRMALRRTSK RGSLHFIEQM
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Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67..363

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1          11         21         31         41         51
|          |          |          |          |          |
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GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC     60
AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC    120
ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA    180
CCTGTTAATC CAAGGTCTTT AGAAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA    240
CGTGTTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA    300
TCGAAGGCCA TCAAGAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT    360
TAAAACCAGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG    420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA    480
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAAATCAGC TGCTACTACT CCTGTAGGAA    540
GGTTAATGTT CATCATCCTA AGCTATTCAG TAATAACTCT ACCCTGGCAC TATAATGTAA    600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCTGACC CTGCTTCAAA TATTTCCCTC    660
ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAATTC    720
TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTTTAAAG AATGCTCTTT    780
ACTTCATGGA CTTCCACTGC CATCCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA    840
CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT    900
CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT    960
TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA   1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG   1080
TTTTCAAATA AAAATGAGGT ACTCTCCTGG AAATATTAAG
```

Seq ID NO: 24 Protein sequence
Protein Accession #: NP_001556.1

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1          11         21         31         41         51
|          |          |          |          |          |
MNQTAILICC LIFLTLSGIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV     60
EIIATMKKKG EKRCLNPESK AIKNLLKAVS KEMSKRSP
```

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: XM_030559
Coding sequence: 1..1119

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAACCGCA GCCACCGGCA CGGGGCGGGC AGCGGCTGCC TGGGCACTAT GGAGGTGAAG     60
AGCAAGTTTG GAGCTGAATT TCGTCGGTTT TCGCTGGAAA GATCAAAACC TGGAAAATTT    120
GAGGAGTTTT ATGGATTACT ACAACATGTT CATAAGATCC CCAATGTTGA CGTTTTGGTA    180
GGCTATGCAG ACATCCATGG AGACTTACTA CCTATAAATA ATGATGATAA TTATCACAAA    240
GCTGTTTCAA CGGCCAATCC ACTGCTTAGG ATATTTATAC AAAAGAAGGA AGAAGCAGAC    300
TACAGTGCCT TTGGTACAGA CACGCTAATA AAGAAGAAGA ATGTTTTAAC CAACGTATTG    360
CGTCCTGACA ACCATAGAAA AAAGCCACAT ATAGTCATTA GTATGCCCCA AGACTTTAGA    420
CCTGTGTCTT CTATTATAGA CGTGGATATT CTCCCAGAAA CGCATCGTAG GGTACGTCTT    480
TACAAATACG GCACGGAGAA ACCCCTAGGA TTCTACATCC GGGATGGCTC CAGTGTCAGG    540
GTAACACCAC ATGGCTTAGA AAAGGTTCCA GGGATCTTTA TATCCAGGCT TGTCCCAGGA    600
GGTCTGGCTC AAAGTACAGG ACTATTAGCT GTTAATGATG AAGTTTTAGA AGTTAATGGC    660
ATAGAAGTTT CAGGGAAGAG CCTTGATCAA GTAACAGACA TGATGATTGC AAATAGCCGT    720
AACCTCATCA TAACAGTGAG ACCGGCAAAC CAGAGGAATA ATGTTGTGAG GAACAGTCGG    780
ACTTCTGGCA GTTCCGGTCA GTCTACTGAT AACAGCCTTC TTGGCTACCC ACAGCAGATT    840
GAACCAAGCT TTGAGCCAGA GGATGAAGAC AGCGAAGAAG ATGACATTAT CATTGAAGAC    900
AATGGAGTGC CACAGCAGAT TCCAAAAGCT GTTCCTAATA CTGAGAGCCT GGAGTCATTA    960
ACACAGATAG AGCTAAGCTT TGAGTCTGGA CAGAATGGCT TTATTCCCTC TAATGAAGTG   1020
AGCTTAGCAG CCATAGCAAG CAGCTCAAAC ACGGAATTTG AAACACATGC TCCAGATCAA   1080
AAACTCTTAG AAGAAGATGG AACAATCATA ACATTATGA
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Seq ID NO: 26 Protein sequence
Protein Accession #: XP_030559

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1          11         21         31         41         51
|          |          |          |          |          |
MNRSHRHGAG SGCLGTMEVK SKFGAEFRRF SLERSKPGKF EEFYGLLQHV HKIPNVDVLV     60
GYADIHGDLL PINNDDNYHK AVSTANPLLR IFIQKKEEAD YSAFGTDTLI KKKNVLTNVL    120
RPDNHRKKPH IVISMPQDFR PVSSIIDVDI LPETHRRVRL YKYGTEKPLG FYIRDGSSVR    180
VTPHGLEKVP GIFISRLVPG GLAQSTGLLA VNDEVLEVNG IEVSGKSLDQ VTDMMIANSR    240
NLIITVRPAN QRNNVVRNSR TSGSSGQSTD NSLLGYPQQI EPSFEPEDED SEEDDIIIED    300
NGVPQQIPKA VPNTESLESL TQIELSFESG QNGFIPSNEV SLAAIASSSN TEFETHAPDQ    360
KLLEEDGTII TL
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Seq ID NO: 27 DNA sequence
Nucleic Acid Accession #: NM_003667.1
Coding sequence: 1..2651

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGACACCT CCCGGCTCGG TGTGCTCCTG TCCTTGCCTG TGCTGCTGCA GCTGGCGACC     60
GGGGGCAGCT CTCCCAGGTC TGGTGTGTTG CTGAGGGGCT GCCCCACACA CTGTCATTGC    120
GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTCGGAGCTG    180
CCTTCCAACC TCAGCGTCTT CACCTCCTAC CTAGACCTCA GTATGAACAA CATCAGTCAG    240
CTGCTCCCGA ATCCCCTGCC CAGTCTCCGC TTCCTGGAGG AGTTACGTCT TGCGGGAAAC    300
GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT ACAGTCTTAA AGTTCTTATG    360
CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC TGCAGAATTT GCGAAGCCTT    420
CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC CCCCAAGCTG TTTCAGTGGC    480
CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT TAACAGAAAT CCCCGTCCAG    540
GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG CCCTGAACAA AATACACCAC    600
ATACCAGACT ATGCCTTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAAT    660
AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT    720
TTAAATTACA ATAACCTTGA TGAATTCCCC ACTGCAATTA GGACACTCTC CAACCTTAAA    780
GAACTACATT TCTATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA    840
CCTGAACTAA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACTGAATT TCCTGATTTA    900
ACTGGAACTG CAAACCTGGA GAGTCTGACT TTAACTGGAG CACAGATCTC ATCTCTTCCT    960
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CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA  1020
GAAGATTTAC CCAGTTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT  1080
GAAATCTACG AAATTAAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATCGCTGAAT  1140
TTGGCTTGGA ACAAAATTGC TATTATTCAC CCCAATGCAT TTTCCACTTT GCCATCCCTA  1200
ATAAAGCTGG ACCTATCGTC CAACCTCCTG TCGTCTTTTC CTATAACTGG GTTACATGGT  1260
TTAACTCACT TAAAATTAAC AGGAAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC  1320
TTTCCAGAAC TCAAGGTTAT AGAAATGCCT TATGCTTACC AGTGCTGTGC ATTTGGAGTG  1380
TGTGAGAATG CCTATAAGAT TTCTAATCAA TGGAATAAAG GTGACAACAG CAGTATGGAC  1440
GACCTTCATA AGAAAGATGC TGGAATGTTT CAGGCTCAAG ATGAACGTGA CCTTGAAGAT  1500
TTCCTGCTTG ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCAGTG TTCACCTTCC  1560
CCAGGCCCCT TCAAACCCTG TGAACACCTG CTTGATGGCT GGCTGATCAG AATTGGAGTG  1620
TGGACCATAG CAGTTCTGGC ACTTACTTGT AATGCTTTGG TGACTTCAAC AGTTTTCAGA  1680
TCCCCTCTGT ACATTTCCCC CATTAAACTG TTAATTGGGG TCATCGCAGC AGTGAACATG  1740
CTCACGGGAG TCTCCAGTGC CGTGCTGGCT GGTGTGGATG CGTTCACTTT TGGCAGCTTT  1800
GCACGACATG GTGCCTGGTG GGAGAATGGG GTTGGTTGCC ATGTCATTGG TTTTTTGTCC  1860
ATTTTTGCTT CAGAATCATC TGTTTTCCTG CTTACTCTGG CAGCCCTGGA GCGTGGGTTC  1920
TCTGTGAAAT ATTCTGCAAA ATTTGAAACG AAAGCTCCAT TTTCTAGCCT GAAAGTAATC  1980
ATTTTGCTCT GTGCCCTGCT GGCCTTGACC ATGGCCGCAG TTCCCCTGCT GGGTGGCAGC  2040
AAGTATGGCG CCTCCCCTCT CTGCCTGCCT TTGCCTTTTG GGAGCCCAG CACCATGGGC  2100
TACATGGTCG CTCTCATCTT GCTCAATTCC CTTTGCTTCC TCATGATGAC CATTGCCTAC  2160
ACCAAGCTCT ACTGCAATTT GGACAAGGGA GACCTGGAGA ATATTTGGGA CTGCTCTATG  2220
GTAAAACACA TTGCCCTGTT GCTCTTCACC AACTGCATCC TAAACTGCCC TGTGGCTTTC  2280
TTGTCCTTCT CCTCTTTAAT AAACCTTACA TTTATCAGTC CTGAAGTAAT TAAGTTTATC  2340
CTTCTGGTGG TAGTCCCACT TCCTGCATGT CTCAATCCCC TTCTCTACAT CTTGTTCAAT  2400
CCTCACTTTA AGGAGGATCT GGTGAGCCTG AGAAAGCAAA CCTACGTCTG GACAAGATCA  2460
AAACACCCAA GCTTGATGTC AATTAACTCT GATGATGTCG AAAAACAGTC CTGTGACTCA  2520
ACTCAAGCCT TGGTAACCTT TACCAGCTCC AGCATCACTT ATGACCTGCC TCCCAGTTCC  2580
GTGCCATCAC CAGCTTATCC AGTGACTGAG AGCTGCCATC TTTCCTCTGT GGCATTTGTC  2640
CCATGTCTTA A
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Seq ID NO: 28 Protein sequence
Protein Accession #: NP_003658.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDTSRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL    60
PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLM   120
LQNNQLRHVP TEALQNLRSL QSLRLDANHI SYVPPSCFSG LHSLRHLWLD DNALTEIPVQ   180
APRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD   240
LNYNNLDEFP TAIRTLSNLK ELHFYDNPIQ FVGRSAFQHL PELRTLTLNG ASQITEFPDL   300
TGTANLESLT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSFSVCQ KLQKIDLRHN   360
EIYEIKVDTF QQLLSLRSLN LAWNKIAIIH PNAFSTLPSL IKLDLSSNLL SSFPITGLHG   420
LTHLKLTGNH ALQSLISSEN FPELKVIEMP YAYQCCAFGV CENAYKISNQ WNKGDNSSMD   480
DLHKKDAGMF QAQDERDLED FLLDFEEDLK ALHSVQCSPS PGPFKPCEHL LDGWLIRIGV   540
WTIAVLALTC NALVTSTVFR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDAFTFGSF   600
ARHGAWWENG VGCHVIGFLS IFASESSVFL LTLAALERGF SVKYSAKFET KAPFSSLKVI   660
ILLCALLALT MAAVPLLGGS KYGASPLCLP LPFGEPSTMG YMVALILLNS LCFLMMTIAY   720
TKLYCNLDKG DLENIWDCSM VKHIALLLFT NCILNCPVAF LSFSSLINLT FISPEVIKFI   780
LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS   840
TQALVTFTSS SITYDLPPSS VPSPAYPVTE SCHLSSVAFV PCL
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Seq ID NO: 29 DNA sequence
Nucleic Acid Accession #: NM_002497.1
Coding sequence: 135..1472

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGTA GGGGTGGCGG GTCAGTGCTG CTCGGGGGCT TCTCCATCCA GGTCCCTGGA    60
GTTCCTGGTC CCTGGAGCTC CGCACTTGGC GCGCAACCTG CGTGAGGCAG CGCGACTCTG   120
GCGACTGGCC GGCCATGCCT TCCCGGGCTG AGGACTATGA AGTGTTGTAC ACCATTGGCA   180
CAGGCTCCTA CGGCCGCTGC CAGAAGATCC GGAGGAAGAG TGATGGCAAG ATATTAGTTT   240
GGAAAGAACT TGACTATGGC TCCATGACAG AAGCTGAGAA ACAGATGCTT GTTTCTGAAG   300
TGAATTTGCT TCGTGAACTG AAACATCCAA ACATCGTTCG TTACTATGAT CGGATTATTG   360
ACCGGACCAA TACAACACTG TACATTGTAA TGGAATATTG TGAAGGAGGG GATCTGGCTA   420
GTGTAATTAC AAAGGGAACC AAGGAAAGGC AATACTTAGA TGAAGAGTTT GTTCTTCGAG   480
TGATGACTCA GTTGACTCTG GCCCTGAAGG AATGCCACAG ACGAAGTGAT GGTGGTCATA   540
CCGTATTGCA TCGGGATCTT AAACCAGCCA ATGTTTTCCT GGATGGCAAG CAAAACGTCA   600
AGCTTGGAGA CTTTGGGCTA GCTAGAATAT TAAACCATGA CACGAGTTTT GCAAAAACAT   660
TTGTTGGCAC ACCTTATTAC ATGTCTCCTG AACAAATGAA TCGCATGTCC TACAATGAGA   720
AATCAGATAT CTGGTCATTG GGCTGCTTGC TGTATGAGTT ATGTGCATTA ATGCCTCCAT   780
TTACAGCTTT TAGCCAGAAA GAACTCGCTG GGAAAATCAG AGAAGGCAAA TTCAGGCGAA   840
TTCCATACCG TTACTCTGAT GAATTGAATG AAATTATTAC GAGGATGTTA AACTTAAAGG   900
ATTACCATCG ACCTTCTGTT GAAGAAATTC TTGAGAACCC TTTAATAGCA GATTTGGTTG   960
CAGACGAGCA AAGAAGAAAT CTTGAGAGAA GAGGGCGACA ATTAGGAGAG CCAGAAAAAT  1020
CGCAGGATTC CAGCCCTGTA TTGAGTGAGC TGAAACTGAA GGAAATTCAG TTACAGGAGC  1080
GAGAGCGAGC TCTCAAAGCA AGAGAAGAAA GATTGGAGCA GAAAGAACAG GAGCTTTGTG  1140
TTCGTGAGAG ACTAGCAGAG GACAAACTGG CTAGAGCAGA AAATCTGTTG AAGAACTACA  1200
GCTTGCTAAA GGAACGGAAG TTCCTGTCTC TGGCAAGTAA TCCAGAACTT CTTAATCTTC  1260
CATCCTCAGT AATTAAGAAG AAAGTTCATT TCAGTGGGGA AAGTAAAGAG AACATCATGA  1320
GGAGTGAGAA TTCTGAGAGT CAGCTCACAT CTAAGTCCAA GTGCAAGGAC CTGAAGAAAA  1380
GGCTTCACGC TGCCCAGCTG CGGGCTCAAG CCCTGTCAGA TATTGAGAAA AATTACCAAC  1440
TGAAAAGCAG ACAGATCCTG GGCATGCGCT AGCCAGGTAG AGAGACACAG AGCTGTGTAC  1500
AGGATGTAAT ATTACCAACC TTTAAAGACT GATATTCAAA TGCTGTAGTG TTGAATACTT  1560
GGCCCCATGA GCCATGCCTT TCTGTATAGT ACACATGATA TTTCGGAATT GGTTTTACTG  1620
TTCTTCAGCA ACTATTGTAC AAAATGTTCA CATTTAATTT TTCTTTCTTC TTTTAAGAAC  1680
ATATTATAAA AAGAATACTT TCTTGGTTGG GCTTTTAATC CTGTGTGTGA TTACTAGTAG  1740
GAACATGAGA TGTGACATTC TAAATCTTGG GAGAAAAAAT AATATTAGGA AAAAAATATT  1800
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TATGCAGGAA GAGTAGCACT CACTGAATAG TTTTAAATGA CTGAGTGGTA TGCTTACAAT  1860
TGTCATGTCT AGATTTAAAT TTTAAGTCTG AGATTTTAAA TGTTTTTGAG CTTAGAAAAC  1920
CCAGTTAGAT GCAATTTGGT CATTAATACC ATGACATCTT GCTTATAAAT ATTCCATTGC  1980
TCTGTAGTTC AAATCTGTTA GCTTTGTGAA AATTCATCAC TGTGATGTTT GTATTCTTTT  2040
TTTTTTTCTG TTTAACAGAA TATGAGCTGT CTGTCATTTA CCTACTTCTT TCCCACTAAA  2100
TAAAAGAATT CTTCAGTTA
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Seq ID NO: 30 Protein sequence
Protein Accession #: NP_002488.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPSRAEDYEV LYTIGTGSYG RCQKIRRKSD GKILVWKELD YGSMTEAEKQ MLVSEVNLLR    60
ELKHPNIVRY YDRIIDRTNT TLYIVMEYCE GGDLASVITK GTKERQYLDE EFVLRVMTQL   120
TLALKECHRR SDGGHTVLHR DLKPANVFLD GKQNVKLGDF GLARILNHDT SFAKTFVGTP   180
YYMSPEQMNR MSYNEKSDIW SLGCLLYELC ALMPPFTAFS QKELAGKIRE GKFRRIPYRY   240
SDELNEIITR MLNLKDYHRP SVEEILENPL IADLVADEQR RNLERRGRQL GEPEKSQDSS   300
PVLSELKLKE IQLQERERAL KAREERLEQK EQELCVRERL AEDKLARAEN LLKNYSLLKE   360
RKFLSLASNP ELLNLPSSVI KKKVHFSGES KENIMRSENS ESQLTSKSKC KDLKKRLHAA   420
QLRAQALSDI EKNYQLKSRQ ILGMR
```

Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: NM_020242
Coding sequence: 72..4240

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1          11         21         31         41         51
|          |          |          |          |          |
CAGTCGCGCG CGGTGCAGTC GGGAGGTGGA GGCACCGGCT GCATTGTTTT CGGGATCGAG    60
GGGTGAGGGC GCTATGGCAC CCGGCTGCAA AACTGAGTTA CGCAGCGTGA CAAATGGTCA   120
GTCTAACCAA CCAAGTAATG AAGGTGATGC CATCAAAGTT TTTGTGCGAA TTCGTCCTCC   180
TGCAGAAAGA TCTGGGTCAG CTGATGGAGA GCAGAACTTA TGCTTATCTG TGCTGTCCTC   240
CACGAGTCTC CGGCTGCACT CCAACCCTGA GCCCAAGACC TTCACGTTTG ATCATGTTGC   300
AGATGTGGAT ACCACTCAGG AATCTGTATT TGCAACTGTG GCTAAAAGCA TTGTGGAGTC   360
TTGCATGAGC GGTTATAATG GTACCATCTT TGCATATGGA CAGACTGGCT CAGGGAAGAC   420
ATTTACTATG ATGGGACCAT CTGAATCTGA TAATTTTTCT CATAACCTGA GAGGAGTAAT   480
CCCACGAAGT TTTGAATATT TGTTTTCCTT AATTGATCGT GAAAAAGAAA AGGCTGGAGC   540
TGGAAAGAGT TTCCTTTGTA AGTGTTCCTT TATTGAAATC TACAACGAGC AGATATATGA   600
TCTACTGGAC TCTGCATCGG CTGGACTGTA CTTAAGGGAG CATATCAAGA AGGGAGTCTT   660
TGTTGTTGGT GCGGTGGAGC AGGTGGTAAC CTCAGCTGCT GAAGCCTATC AGGTGCTGTC   720
TGGAGGATGG AGGAATAGAC GTGTGGCATC AACATCAATG AACAGAGAAT CGTCTAGGTC   780
TCATGCCGTC TTTACAATTA CAATAGAGTC AATGGAGAAA AGTAATGAGA TTGTGAATAT   840
ACGGACCTCC CTACTCAACC TGGTGGATTT AGCAGGATCT GAAAGGCAAA AAGATACCCA   900
TGCAGAAGGG ATGAGATTGA AGGAAGCAGG TAACATAAAT CGATCATTGA GCTGCCTGGG   960
CCAAGTGATT ACAGCACTTG TCGACGTGGG TAATGGAAAA CAGAGACATG TTTGCTACAG  1020
AGACTCCAAA CTTACCTTCT TACTACGGGA TTCCCTTGGA GGTAATGCCA AAACAGCCAT  1080
AATTGCAAAT GTTCATCCTG GATCCAGGTG TTTTGGGGAA ACCCTATCAA CACTTAACTT  1140
TGCTCAAAGA GCCAAGCTGA TTAAAAACAA GGCAGTAGTA AATGAAGACA CCCAAGGAAA  1200
TGTGAGCCAG CTCCAAGCTG AAGTGAAGAG GCTCAAAGAA CAACTGGCGG AGCTTGCTTC  1260
AGGACAGACA CCACCAGAAA GCTTCCTGAC CAGAGACAAA AAGAAGACTA ACTATATGGA  1320
GTATTTCCAG GAAGCAATGT TATTCTTTAA GAAATCTGAA CAGGAAAAGA AGTCTCTGAT  1380
AGAAAAAGTT ACCCAATTAG AAGACCTCAC CCTCAAAAAG GAAAAATTTA TTCAATCTAA  1440
TAAAATGATT GTGAAATTCC GAGAGGATCA AATAATACGC TTGGAAAAGC TCCACAAGGA  1500
ATCCCGGGGA GGTTTTCTGC CTGAGGAGCA GGATCGTTTG CTCTCAGAAT TAAGGAATGA  1560
GATTCAAACT CTGCGAGAAC AAATAGAGCA CCACCCCAGA GTTGCAAAGT ATGCTATGGA  1620
AAATCATTCC CTCAGGGAGG AGAATAGAAG ACTGAGATTA TTAGAGCCTG TGAAAAGAGC  1680
TCAAGAAATG GATGCCCAGA CCATTGCAAA ACTAGAAAAA GCTTTCTCTG AAATAAGTGG  1740
CATGGAGAAA AGTGACAAAA ATCAGCAAGG ATTTTCACCT AAAGCTCAGA AAGAGCCATG  1800
TTTGTTTGCA AACACTGAGA AGTTAAAAGC ACAACTCCTG CAAATTCAGA CAGAGCTGAA  1860
TAATTCAAAG CAAGAATATG AAGAATTCAA AGAACTTACT AGGAAAAGGC AGCTAGAATT  1920
GGAATCAGAG CTTCAGTCTT TGCAAAAAGC GAACCTTAAT CTTGAAAACC TTTTGGAAGC  1980
AACAAAAGCC TGCAAGCGGC AAGAAGTTTC TCAGCTGAAT AAAATTCATG CTGAAACACT  2040
TAAGATTATA ACTACACCAA CCAAGGCCTA CCAACTTCAT TCCCGACCAG TACCAAAATT  2100
AAGCCCTGAA ATGGGAAGCT TTGGCTCTCT ATACACTCAG AATTCTAGCA TATTAGATAA  2160
TGATATATTA AATGAGCCAG TTCCTCCTGA GATGAATGAA CAAGCTTTTG AGGCCATTTC  2220
TGAAGAGCTT AGAACAGTGC AGGAACAAAT GAGTGCTCTT CAAGCCAAAC TGGATGAAGA  2280
AGAGCATAAA AACCTAAAGC TTCAGCAGCA TGTTGACAAA CTGGAACATC ATTCTACCCA  2340
AATGCAGGAG CTTTTCTCAT CAGAAAGAAT TGATTGGACC AAACAGCAGG AAGAGCTTCT  2400
CTCACAGTTG AATGTCCTTG AAAAGCAGCT TCAAGAGACT CAAACTAAAA ATGACTTTTT  2460
GAAAAGTGAG GTACATGACC TGCGAGTAGT CCTTCATTCT GCTGACAAGG AGCTTTCTTC  2520
AGTGAAATTG GAATATAGTT CATTCAAAAC GAATCAGGAG AAAGAATTCA ACAAACTTTC  2580
TGAAAGACAC ATGCATGTAC AGCTTCAATT AGATAATCTC AGGTTAGAAA ACGAAAAGCT  2640
GCTTGAGAGC AAAGCCTGCC TACAGGATTC CTATGACAAC TTACAAGAAA TAATGAAATT  2700
TGAGATTGAC CAACTTTCAA GAAACCTCCA AAACTTCAAA AAAGAAAATG AAACTCTGAA  2760
ATCTGATCTG AATAATTTGA TGGAGCTTCT TGAGGCAGAA AAAGAACGCA ATAACAAATT  2820
ATCATTACAG TTTGAAGAAG ATAAAGAAAA CAGTTCTAAA GAAATCTTAA AAGTTCTTGA  2880
GGCTGTACGT CAGGAGAAAC AGAAAGAGAC GGCCAAGTGT GAGCAGCAGA TGGCAAAAGT  2940
ACAGAAACTA GAAGAGAGCT TGCTTGCTAC TGAAAAAGTG ATCAGTTCCC TGGAAAAGTC  3000
TAGAGATTCT GATAAGAAAG TTGTAGCTGA CCTCATGAAC CAGATCCAGG AGCTAAGAAC  3060
ATCGGTCTGT GAGAAAACAG AAACTATAGA CACCCTGAAA CAAGAACTGA AGGACATAAA  3120
TTGCAAATAC AACTCTGCTT TGGTTGACAG AGAAGAGAGC AGAGTGTTGA TCAAGAAGCA  3180
GGAAGTGGAT ATTCTGGATC TGAAAGAAAC CCTTAGGCTG AGAATACTTT CTGAGGACAT  3240
AGAGAGGGAT ATGCTCTGTG AGGACCTGGC TCATGCCACT GAGCAGCTGA ACATGCTCAC  3300
AGAGGCCTCA AAAAAACACT CGGGGCTGCT GCAGTCTGCC CAGGAAGAAC TGACCAAGAA  3360
GGAAGCCCTG ATTCAGGAAC TTCAGCACAA GCTAAACCAA AAGAAAGAGG AAGTAGAACA  3420
GAAGAAGAAT GAATATAACT TCAAAATGAG GCAACTAGAA CATGTGATGG ATTCTGCTGC  3480
TGAGGATCCC CAGAGTCCTA AGACACCACC TCACTTTCAA ACACATTTGG CAAAACTCCT  3540
GGAAACACAA GAACAAGAGA TAGAAGATGG AAGAGCCTCT AAGACTTCTT TGGAACACCT  3600
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TGTAACAAAG CTAAATGAAG ACAGAGAAGT CAAAAATGCT GAAATCCTCA GAATGAAGGA  3660
GCAGTTGCGT GAAATGGAAA ACCTACGCCT GGAAAGTCAG CAGTTAATAG AGAAAAACTG  3720
GCTCCTGCAA GGTCAGCTGG ATGATATTAA AAGACAAAAG GAAAACAGTG ATCAGAATCA  3780
TCCAGATAAT CAACAGCTGA AGAATGAACA AGAAGAAAGT ATCAAAGAAA GACTTGCAAA  3840
AAGTAAAATA GTTGAAGAAA TGCTGAAAAT GAAAGCAGAC CTAGAAGAAG TCCAAAGTGC  3900
CCTTTACAAC AAAGAGATGG AATGCCTTAG AATGACTGAT GAAGTCGAAC GAACCCAAAC  3960
TTTGGAGTCT AAAGCATTCC AGGAAAAAGA ACAACTGAGA TCAAAGCTGG AAGAAATGTA  4020
TGAAGAAAGA GAGAGAACAT CCCAGGAGAT GGAAATGTTA AGGAAGCAGG TGGAGTGTCT  4080
TGCTGAGGAA AATGGAAAGT TGGTAGGTCA CCAAAATTTG CATCAGAAGA TTCAGTACGT  4140
AGTGCGACTA AAGAAGGAAA ATGTCAGGCT TGCTGAGGAG ACAGAAAAGT TGCGTGCCGA  4200
AAATGTATTT TTAAAAGAAA AGAAAAGAAG TGAATCTTGA GGATTCCGGT CAGCTACCTA  4260
GGCATCACCT TGTTTGAAGA TGTTTCTTCT CTTTTACAAG TAAGACCTAC TCCTGGCCAC  4320
TTAGGAGAGC TGAATTTATG GACCTTAATT ATTAAATGTT TATAAGGTGG TGGTAACCAC  4380
CTCAAGTTTC TGATGAACAT TCTGCATCCA TATACACCCT GTGACAGTCA GCAGTCTGCT  4440
ATTAAGTGGC CTACTTCAAG GCTTTGAATC AACTTAAGGG AAAACCTTTT GTCTTTGTAA  4500
AAATAAAAGC CTGTAGCTAA GGTTTACAGT GGACATTAGC CAGATCATTT TCTTCTTAGA  4560
TTATGCCATA ATCTCCTTTG ATTCTTATGG AAGTTCTAAC AATATATGGT GGTTCCAACA  4620
CCTGCAGTGA GTTTAATGAC TGACTTAGTA GCAGGTACAA GAAGCAAACT TGTTAATATA  4680
GATTATTTTT GTATTCTTAC TTTAGGTATT TTACTTGAGC ATTTTCCATG ACTGTAAATA  4740
AAGCCATTTT TTAAGATAAA AAAAAAAAAA AAAAA
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Seq ID NO: 32 Protein sequence
Protein Accession #: NP_064627
1          11         21         31         41         51
|          |          |          |          |          |
MAPGCKTELR SVTNGQSNQP SNEGDAIKVF VRIRPPAERS GSADGEQNLC LSVLSSTSLR    60
LHSNPEPKTF TFDHVADVDT TQESVFATVA KSIVESCMSG YNGTIFAYGQ TGSGKTFTMM   120
GPSESDNFSH NLRGVIPRSF EYLFSLIDRE KEKAGAGKSF LCKCSFIEIY NEQIYDLLDS   180
ASAGLYLREH IKKGVFVVGA VEQVVTSAAE AYQVLSGGWR NRRVASTSMN RESSRSHAVF   240
TITIESMEKS NEIVNIRTSL LNLVDLAGSE RQKDTHAEGM RLKEAGNINR SLSCLGQVIT   300
ALVDVGNGKQ RHVCYRDSKL TFLLRDSLGG NAKTAIIANV HPGSRCFGET LSTLNFAQRA   360
KLIKNKAVVN EDTQGNVSQL QAEVKRLKEQ LAELASGQTP PESFLTRDKK KTNYMEYFQE   420
AMLFFKKSEQ EKKSLIEKVT QLEDLTLKKE KFIQSNKMIV KFREDQIIRL EKLHKESRGG   480
FLPEEQDRLL SELRNEIQTL REQIEHHPRV AKYAMENHSL REENRRLRLL EPVKRAQEMD   540
AQTIAKLEKA FSEISGMEKS DKNQQGFSPK AQKEPCLFAN TEKLKAQLLQ IQTELNNSKQ   600
EYEEFKELTR KRQLELESEL QSLQKANLNL ENLLEATKAC KRQEVSQLNK IHAETLKIIT   660
TPTKAYQLHS RPVPKLSPEM GSFGSLYTQN SSILDNDILN EPVPPEMNEQ AFEAISEELR   720
TVQEQMSALQ AKLDEEEHKN LKLQQHVDKL EHHSTQMQEL FSSERIDWTK QQEELLSQLN   780
VLEKQLQETQ TKNDFLKSEV HDLRVVLHSA DKELSSVKLE YSSFKTNQEK EFNKLSERHM   840
HVQLQLDNLR LENEKLLESK ACLQDSYDNL QEIMKFEIDQ LSRNLQNFKK ENETLKSDLN   900
NLMELLEAEK ERNNKLSLQF EEDKENSSKE ILKVLEAVRQ EKQKETAKCE QQMAKVQKLE   960
ESLLATEKVI SSLEKSRDSD KKVVADLMNQ IQELRTSVCE KTETIDTLKQ ELKDINCKYN  1020
SALVDREESR VLIKKQEVDI LDLKETLRLR ILSEDIERDM LCEDLAHATE QLNMLTEASK  1080
KHSGLLQSAQ EELTKKEALI QELQHKLNQK KEEVEQKKNE YNFKMRQLEH VMDSAAEDPQ  1140
SPKTPPHFQT HLAKLLETQE QEIEDGRASK TSLEHLVTKL NEDREVKNAE ILRMKEQLRE  1200
MENLRLESQQ LIEKNWLLQG QLDDIKRQKE NSDQNHPDNQ QLKNEQEESI KERLAKSKIV  1260
EEMLKMKADL EEVQSALYNK EMECLRMTDE VERTQTLESK AFQEKEQLRS KLEEMYEERE  1320
RTSQEMEMLR KQVECLAEEN GKLVGHQNLH QKIQYVVRLK KENVRLAEET EKLRAENVFL  1380
KEKKRSES
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Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: BC000633.1
Coding sequence: 1..2574
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|          |          |          |          |          |
ATGGAATCCG AGGATTTAAG TGGCAGAGAA TTGACAATTG ATTCCATAAT GAACAAAGTG    60
AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACTAAG CTTGAATAAA   120
ATTTCTGCTG ATACTACAGA TAACTCGGGA ACTGTTAACC AAATTATGAT GATGGCAAAC   180
AACCCAGAGG ACTGGTTGAG TTTGTTGCTC AAACTAGAGA AAAACAGTGT TCCGCTAAGT   240
GATGCTCTTT TAAATAAATT GATTGGTCGT TACAGTCAAG CAATTGAAGC GCTTCCCCCA   300
GATAAATATG GCCAAAATGA GAGTTTTGCT AGAATTCAAG TGAGATTTGC TGAATTAAAA   360
GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAACTGCAAG   420
AAATTTGCTT TTGTTCATAT ATCTTTTGCA CAATTTGAAC TGTCACAAGG TAATGTCAAA   480
AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCACT AGAAATGCTG   540
GAAATTGCCC TGCGGAATTT AAACCTCCAA AAAAAGCAGC TGCTTTCAGA GGAGGAAAAG   600
AAGAATTTAT CAGCATCTAC GGTATTAACT GCCCAAGAAT CATTTTCCGG TTCACTTGGG   660
CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT   720
TTATATGGAG AGAACATGCC ACCACAAGAT GCAGAAATAG GTTACCGGAA TTCATTGAGA   780
CAAACTAACA AAACTAAACA GTCATGCCCA TTTGGAAGAG TCCCAGTTAA CCTTCTAAAT   840
AGCCCAGATT GTGATGTGAA GACAGATGAT TCAGTTGTAC CTTGTTTTAT GAAAAGACAA   900
ACCTCTAGAT CAGAATGCCG AGATTTGGTT GTGCCTGGAT CTAAACCAAG TGGAAATGAT   960
TCCTGTGAAT TAAGAAATTT AAAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGGTG  1020
TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCCTGAA GAATAAAACG  1080
GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGGTTCCA  1140
GAGAGTAACC AGAAACAGTG GCAATCTAAG AGAAAGTCAG AGTGTATTAA CCAGAATCCT  1200
GCTGCATCTT CAAATCACTG GCAGATTCCG GAGTTAGCCC GAAAAGTTAA TACAGAGCAG  1260
AAACATACCA CTTTTGAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA  1320
ACATCTAAAT GGTTTGACCC AAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGGAT  1380
GATTACATGA GCTGTTTTAG AACTCCAGTT GTAAAGAATG ACTTTCCACC TGCTTGTCAG  1440
TTGTCAACAC CTTATGGCCA ACCTGCCTGT TTCCAGCAGC AACAGCATCA AATACTTGCC  1500
ACTCCACTTC AAAATTTACA GGTTTTAGCA TCTTCTTCAG CAAATGAATG CATTTCGGTT  1560
AAAGGAAGAA TTTATTCCAT TTTAAAGCAG ATAGGAAGTG GAGGTTCAAG CAAGGTATTT  1620
CAGGTGTTAA ATGAAAAGAA ACAGATATAT GCTATAAAAT ATGTGAACTT AGAAGAAGCA  1680
GATAACCAAA CTCTTGATAG TTACCGGAAC GAAATAGCTT ATTTGAATAA ACTACAACAA  1740
CACAGTGATA AGATCATCCG ACTTTATGAT TATGAAATCA CGGACCAGTA CATCTACATG  1800
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GTAATGGAGT GTGGAAATAT TGATCTTAAT AGTTGGCTTA AAAAGAAAAA ATCCATTGAT  1860
CCATGGGAAC GCAAGAGTTA CTGGAAAAAT ATGTTAGAGG CAGTTCACAC AATCCATCAA  1920
CATGGCATTG TTCACAGTGA TCTTAAACCA GCTAACTTTC TGATAGTTGA TGGAATGCTA  1980
AAGCTAATTG ATTTTGGGAT TGCAAACCAA ATGCAACCAG ATACAACAAG TGTTGTTAAA  2040
GATTCTCAGG TTGGCACAGT TAATTATATG CCACCAGAAG CAATCAAAGA TATGTCTTCC  2100
TCCAGAGAGA ATGGGAAATC TAAGTCAAAG ATAAGCCCCA AAAGTGATGT TTGGTCCTTA  2160
GGATGTATTT TGTACTATAT GACTTACGGG AAAACACCAT TTCAGCAGAT AATTAATCAG  2220
ATTTCTAAAT TACATGCCAT AATTGATCCT AATCATGAAA TTGAATTTCC CGATATTCCA  2280
GAGAAAGATC TTCAAGATGT GTTAAAGTGT TGTTTAAAAA GGGACCCAAA ACAGAGGATA  2340
TCCATTCCTG AGCTCCTGGC TCATCCCTAT GTTCAAATTC AAACTCATCC AGTTAACCAA  2400
ATGGCCAAGG GAACCACTGA AGAAATGAAA TATGTTCTGG GCCAACTTGT TGGTCTGAAT  2460
TCTCCTAACT CCATTTTGAA AGCTGCTAAA ACTTTATATG AACACTATAG TGGTGGTGAA  2520
AGTCATAATT CTTCATCCTC CAAGACTTTT GAAAAAAAAA GGGGAAAAAA ATGA
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Seq ID NO: 34 Protein sequence:
Protein Accession #: AAH00633.1

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1          11         21         31         41         51
|          |          |          |          |          |
MESEDLSGRE LTIDSIMNKV RDIKNKFKNE DLTDELSLNK ISADTTDNSG TVNQIMMMAN    60
NPEDWLSLLL KLEKNSVPLS DALLNKLIGR YSQAIEALPP DKYGQNESFA RIQVRFAELK   120
AIQEPDDARD YFQMARANCK KFAFVHISFA QFELSQGNVK KSKQLLQKAV ERGAVPLEML   180
EIALRNLNLQ KKQLLSEEEK KNLSASTVLT AQESFSGSLG HLQNRNNSCD SRGQTTKARF   240
LYGENMPPQD AEIGYRNSLR QTNKTKQSCP FGRVPVNLLN SPDCDVKTDD SVVPCFMKRQ   300
TSRSECRDLV VPGSKPSGND SCELRNLKSV QNSHFKEPLV SDEKSSELII TDSITLKNKT   360
ESSLLAKLEE TKEYQEPEVP ESNQKQWQSK RKSECINQNP AASSNHWQIP ELARKVNTEQ   420
KHTTFEQPVF SVSKQSPPIS TSKWFDPKSI CKTPSSNTLD DYMSCFRTPV VKNDFPPACQ   480
LSTPYGQPAC FQQQQHQILA TPLQNLQVLA SSSANECISV KGRIYSILKQ IGSGGSSKVF   540
QVLNEKKQIY AIKYVNLEEA DNQTLDSYRN EIAYLNKLQQ HSDKIIRLYD YEITDQYIYM   600
VMECGNIDLN SWLKKKKSID PWERKSYWKN MLEAVHTIHQ HGIVHSDLKP ANFLIVDGML   660
KLIDFGIANQ MQPDTTSVVK DSQVGTVNYM PPEAIKDMSS SRENGKSKSK ISPKSDVWSL   720
GCILYYMTYG KTPFQQIINQ ISKLHAIIDP NHEIEFPDIP EKDLQDVLKC CLKRDPKQRI   780
SIPELLAHPY VQIQTHPVNQ MAKGTTEEMK YVLGQLVGLN SPNSILKAAK TLYEHYSGGE   840
SHNSSSSKTF EKKRGKK
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Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: NM_005823.2
Coding sequence: 85..1953

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1          11         21         31         41         51
|          |          |          |          |          |
TGGCCACTCC CGTCTGCTGT GACGCGCGGA CAGAGAGCTA CCGGTGGACC CACGGTGCCT    60
CCCTCCCTGG GATCTACACA GACCATGGCC TTGCCAACGG CTCGACCCCT GTTGGGGTCC   120
TGTGGGACCC CCGCCCTCGG CAGCCTCCTG TTCCTGCTCT TCAGCCTCGG ATGGGTGCAG   180
CCCTCGAGGA CCCTGGCTGG AGAGACAGGG CAGGAGGCTG CACCCCTGGA CGGAGTCCTG   240
GCCAACCCAC CTAACATTTC CAGCCTCTCC CCTCGCCAAC TCCTTGGCTT CCCGTGTGCG   300
GAGGTGTCCG GCCTGAGCAC GGAGCGTGTC CGGGAGCTGG CTGTGGCCTT GGCACAGAAG   360
AATGTCAAGC TCTCAACAGA GCAGCTGCGC TGTCTGGCTC ACCGGCTCTC TGAGCCCCCC   420
GAGGACCTGG ACGCCCTCCC ATTGGACCTG CTGCTATTCC TCAACCCAGA TGCGTTCTCG   480
GGGCCCCAGG CCTGCACCCG TTTCTTCTCC CGCATCACGA AGGCCAATGT GGACCTGCTC   540
CCGAGGGGGG CTCCCGAGCG ACAGCGGCTG CTGCCTGCGG CTCTGGCCTG CTGGGGTGTG   600
CGGGGGTCTC TGCTGAGCGA GGCTGATGTG CGGGCTCTGG GAGGCCTGGC TTGCGACCTG   660
CCTGGGCGCT TTGTGGCCGA GTCGGCCGAA GTGCTGCTAC CCCGGCTGGT GAGCTGCCCG   720
GGACCCCTGG ACCAGGACCA GCAGGAGGCA GCCAGGGCGG CTCTGCAGGG CGGGGGACCC   780
CCCTACGGCC CCCCGTCGAC ATGGTCTGTC TCCACGATGG ACGCTCTGCG GGGCCTGCTG   840
CCCGTGCTGG GCCAGCCCAT CATCCGCAGC ATCCCGCAGG GCATCGTGGC CGCGTGGCGG   900
CAACGCTCCT CTCGGGACCC ATCCTGGCGG CAGCCTGAAC GGACCATCCT CCGGCCGCGG   960
TTCCGGCGGG AAGTGGAGAA GACAGCCTGT CCTTCAGGCA AGAAGGCCCG CGAGATAGAC  1020
GAGAGCCTCA TCTTCTACAA GAAGTGGGAG CTGGAAGCCT GCGTGGATGC GGCCCTGCTG  1080
GCCACCCAGA TGGACCGCGT GAACGCCATC CCCTTCACCT ACGAGCAGCT GGACGTCCTA  1140
AAGCATAAAC TGGATGAGCT CTACCCACAA GGTTACCCCG AGTCTGTGAT CCAGCACCTG  1200
GGCTACCTCT TCCTCAAGAT GAGCCCTGAG GACATTCGCA AGTGGAATGT GACGTCCCTG  1260
GAGACCCTGA AGGCTTTGCT TGAAGTCAAC AAAGGGCACG AAATGAGTCC TCAGGTGGCC  1320
ACCCTGATCG ACCGCTTTGT GAAGGGAAGG GGCCAGCTAG ACAAAGACAC CCTAGACACC  1380
CTGACCGCCT TCTACCCTGG GTACCTGTGC TCCCTCAGCC CCGAGGAGCT GAGCTCCGTG  1440
CCCCCCAGCA GCATCTGGGC GGTCAGGCCC CAGGACCTGG ACACGTGTGA CCCAAGGCAG  1500
CTGGACGTCC TCTATCCCAA GGCCCGCCTT GCTTTCCAGA ACATGAACGG GTCCGAATAC  1560
TTCGTGAAGA TCCAGTCCTT CCTGGGTGGG GCCCCCACGG AGGATTTGAA GGCGCTCAGT  1620
CAGCAGAATG TGAGCATGGA CTTGGCCACG TTCATGAAGC TGCGGACGGA TGCGGTGCTG  1680
CCGTTGACTG TGGCTGAGGT GCAGAAACTT CTGGGACCCC ACGTGGAGGG CCTGAAGGCG  1740
GAGGAGCGGC ACCGCCCGGT GCGGGACTGG ATCCTACGGC AGCGGCAGGA CGACCTGGAC  1800
ACGCTGGGGC TGGGGCTACA GGGCGGCATC CCCAACGGCT ACCTGGTCCT AGACCTCAGC  1860
GTGCAAGAGG CCCTCTCGGG GACGCCCTGC CTCCTAGGAC CTGGACCTGT TCTCACCGTC  1920
CTGGCACTGC TCCTAGCCTC CACCCTGGCC TGAGGGCCCC ACTCCCTTGC TGGCCCCAGC  1980
CCTGCTGGGG ATCCCCGCCT GGCCAGGAGC AGGCACGGGT GATCCCCGTT CCACCCCAAG  2040
AGAACTCGCG CTCAGTAAAC GGGAACATGC CCCCTGCAGA CACGT
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Seq ID NO: 36 Protein sequence
Protein Accession #: NP_005814.1

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1          11         21         31         41         51
|          |          |          |          |          |
MALPTARPLL GSCGTPALGS LLFLLFSLGW VQPSRTLAGE TGQEAAPLDG VLANPPNISS    60
LSPRQLLGFP CAEVSGLSTE RVRELAVALA QKNVKLSTEQ LRCLAHRLSE PPEDLDALPL   120
DLLLFLNPDA FSGPQACTRF FSRITKANVD LLPRGAPERQ RLLPAALACW GVRGSLLSEA   180
DVRALGGLAC DLPGRFVAES AEVLLPRLVS CPGPLDQDQQ EAARAALQGG GPPYGPPSTW   240
SVSTMDALRG LLPVLGQPII RSIPQGIVAA WRQRSSRDPS WRQPERTILR PRFRREVEKT   300
ACPSGKKARE IDESLIFYKK WELEACVDAA LLATQMDRVN AIPFTYEQLD VLKHKLDELY   360
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PQGYPESVIQ HLGYLFLKMS PEDIRKWNVT SLETLKALLE VNKGHEMSPQ VATLIDRFVK   420
GRGQLDKDTL DTLTAFYPGY LCSLSPEELS SVPPSSIWAV RPQDLDTCDP RQLDVLYPKA   480
RLAFQNMNGS EYFVKIQSFL GGAPTEDLKA LSQQNVSMDL ATFMKLRTDA VLPLTVAEVQ   540
KLLGPHVEGL KAEERHRPVR DWILRQRQDD LDTLGLGLQG GIPNGYLVLD LSVQEALSGT   600
PCLLGPGPVL TVLALLLAST LA
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Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_013404.1
Coding sequence: 89..1975

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1          11         21         31         41         51
|          |          |          |          |          |
TGGCCGGCCA CTCCCGTCTG CTGTGACGCG CGGACAGAGA GCTACCGGTG GACCCACGGT     60
GCCTCCCTCC CTGGGATCTA CACAGACCAT GGCCTTGCAA CGGCTCGACC CCTGTTGGTC    120
CTGTGGGGAC CGCCCTGGCA GCCTCCTGTT CCTGCTCTTC AGCCTCGGAT GGGTGCATCC    180
CGCGAGGACC CTGGCTGGAG AGACAGGGAC GGAGTCTGCC CCCCTGGGGG GAGTCCTGAC    240
AACCCCCCAT AACATTTCCA GCCTCTCCCC TCGCCAACTC CTTGGCTTCC CGTGTGCGGA    300
GGTGTCCGGC CTGAGCACGG AGCGTGTCCG GGAGCTGGCT GTGGCCTTGG CACAGAAGAA    360
TGTCAAGCTC TCAACAGAGC AGCTGCGCTG TCTGGCTCAC CGGCTCTCTG AGCCCCCCGA    420
GGACCTGGAC GCCCTCCCAT TGGACCTGCT GCTATTCCTC AACCCAGATG CGTTCTCGGG    480
GCCCCAGGCC TGCACCCGTT TCTTCTCCCG CATCACGAAG GCCAATGTGG ACCTGCTCCC    540
GAGGGGGGCT CCCGAGCGAC AGCGGCTGCT GCCTGCGGCT CTGGCCTGCT GGGGTGTGCG    600
GGGGTCTCTG CTGAGCGAGG CTGATGTGCG GGCTCTGGGA GGCCTGGCTT GCGACCTGCC    660
TGGGCGCTTT GTGGCCGAGT CGGCCGAAGT GCTGCTACCC CGGCTGGTGA GCTGCCCGGG    720
ACCCCTGGAC CAGGACCAGC AGGAGGCAGC CAGGGCGGCT CTGCAGGGCG GGGGACCCCC    780
CTACGGCCCC CCGTCGACAT GGTCTGTCTC CACGATGGAC GCTCTGCGGG GCCTGCTGCC    840
CGTGCTGGGC CAGCCCATCA TCCGCAGCAT CCCGCAGGGC ATCGTGGCCG CGTGGCGGCA    900
ACGCTCCTCT CGGGACCCAT CCTGGCGGCA GCCTGAACGG ACCATCCTCC GGCCGCGGTT    960
CCGGCGGGAA GTGGAGAAGA CAGCCTGTCC TTCAGGCAAG AAGGCCCGCG AGATAGACGA   1020
GAGCCTCATC TTCTACAAGA AGTGGGAGCT GGAAGCCTGC GTGGATGCGG CCCTGCTGGC   1080
CACCCAGATG GACCGCGTGA ACGCCATCCC CTTCACCTAC GAGCAGCTGG ACGTCCTAAA   1140
GCATAAACTG GATGAGCTCT ACCCACAAGG TTACCCCGAG TCTGTGATCC AGCACCTGGG   1200
CTACCTCTTC CTCAAGATGA GCCCTGAGGA CATTCGCAAG TGGAATGTGA CGTCCCTGGA   1260
GACCCTGAAG GCTTTGCTTG AAGTCGACAA AGGGCACGAA ATGAGTCCTC AGGCTCCTCG   1320
GCGGCCCCTC CCACAGGTGG CCACCCTGAT CGACCGCTTT GTGAAGGGAA GGGGCCAGCT   1380
AGACAAAGAC ACCCTAGACA CCCTGACCGC CTTCTACCCT GGGTACCTGT GCTCCCTCAG   1440
CCCCGAGGAG CTGAGCTCCG TGCCCCCCAG CAGCATCTGG GCGGTCAGGC CCCAGGACCT   1500
GGACACGTGT GACCCAAGGC AGCTGGACGT CCTCTATCCC AAGGCCCGCC TTGCTTTCCA   1560
GAACATGAAC GGGTCCGAAT ACTTCGTGAA GATCCAGTCC TTCCTGGGTG GGGCCCCCAC   1620
GGAGGATTTG AAGGCGCTCA GTCAGCAGAA TGTGAGCATG GACTTGGCCA CGTTCATGAA   1680
GCTGCGGACG GATGCGGTGC TGCCGTTGAC TGTGGCTGAG GTGCAGAAAC TTCTGGGACC   1740
CCACGTGGAG GGCCTGAAGG CGGAGGAGCG GCACCGCCCG GTGCGGGACT GGATCCTACG   1800
GCAGCGGCAG GACGACCTGG ACACGCTGGG GCTGGGGCTA CAGGGCGGCA TCCCCAACGG   1860
CTACCTGGTC CTAGACCTCA GCGTGCAAGA GACCCTCTCG GGACGCCCCT GCCTCCTAGG   1920
ACCTGGACCT GTTCTCACCG TCCTGGCACT GCTCCTAGCC TCCACCCTGG CCTGAGGGCC   1980
CCACTCCCTT GCTGGCCCCA GCCCTGCTGG GGATCCCCGC CTGGCCAGGA GCAGGCACGG   2040
GTGATCCCCG TTCCACCCCA AGAGAACTCG CGCTCAGTAA ACGGGAACAT GCCCCCTGCA   2100
GACACGT
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Seq ID NO: 38 Protein sequence
Protein Accession #: NP_037536.1

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1          11         21         31         41         51
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MALQRLDPCW SCGDRPGSLL FLLFSLGWVH PARTLAGETG TESAPLGGVL TTPHNISSLS     60
PRQLLGFPCA EVSGLSTERV RELAVALAQK NVKLSTEQLR CLAHRLSEPP EDLDALPLDL    120
LLFLNPDAFS GPQACTRFFS RITKANVDLL PRGAPERQRL LPAALACWGV RGSLLSEADV    180
RALGGLACDL PGRFVAESAE VLLPRLVSCP GPLDQDQQEA ARAALQGGGP PYGPPSTWSV    240
STMDALRGLL PVLGQPIIRS IPQGIVAAWR QRSSRDPSWR QPERTILRPR FRREVEKTAC    300
PSGKKAREID ESLIFYKKWE LEACVDAALL ATQMDRVNAI PFTYEQLDVL KHKLDELYPQ    360
GYPESVIQHL GYLFLKMSPE DIRKWNVTSL ETLKALLEVD KGHEMSPQAP RRPLPQVATL    420
IDRFVKGRGQ LDKDTLDTLT AFYPGYLCSL SPEELSSVPP SSIWAVRPQD LDTCDPRQLD    480
VLYPKARLAF QNMNGSEYFV KIQSFLGGAP TEDLKALSQQ NVSMDLATFM KLRTDAVLPL    540
TVAEVQKLLG PHVEGLKAEE RHRPVRDWIL RQRQDDLDTL GLGLQGGIPN GYLVLDLSVQ    600
ETLSGTPCLL GPGPVLTVLA LLLASTLA
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Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_001508.1
Coding sequence: 1..1362

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1          11         21         31         41         51
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ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC     60
CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC    120
TTCGTGATGG GCCTTCTGGG GAACAGCGTC ACCATTCGGG TCACCCAGGT GCTGCAGAAG    180
AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC    240
TTGGTGTTCC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC    300
ACGTCCAGCT ACACCCTGTC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC    360
GCTACGCTGC TGCACGTGCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC    420
TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG    480
GTCACCTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCCTG    540
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG    600
CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC    660
CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC    720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC    780
ACGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG    840
ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG    900
ATTCGGAGGA TCATGGCTGC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG    960
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GCGTACATGA TCCTCCTCCC CTTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCATCAAC  1020
CCGCTCCTGT ACACGGTGTC CTCGCAGCAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC  1080
TGCCGCCTGT CGCTGCAGCA CGCCAACCAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC  1140
ACCACCGACA GCGCCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC  1200
TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG  1260
TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC  1320
AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA
```

Seq ID NO: 40 Protein sequence
Protein Accession #: NP_001499.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSV TIRVTQVLQK   60
KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY  120
ATLLHVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL  180
VNVPSHRGLT CNRSSTRHHE QPETSNMSIC TNLSSRWTVF QSSIFGAFVV YLVVLLSVAF  240
MCWNMMQVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCWMPNQ  300
IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC  360
CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPQ  420
SKSQSLSLES LEPNSGAKPA NSAAENGFQE HEV
```

Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_022358
Coding sequence: 65..1057

```
1          11         21         31         41         51
|          |          |          |          |          |
GGAGCGCGCG GTCCGGGCAC ACGGAGCAGG TTGGGACCGC GGCGGGTACC GGGGCCGGGG   60
CGCCATGCGG AGGCCGAGCG TGCGCGCGGC CGGGCTGGTC CTGTGCACCC TGTGTTACCT  120
GCTGGTGGGC GCTGCTGTCT TCGACGCGCT CGAGTCCGAG GCGGAAAGCG GCCGCCAGCG  180
ACTGCTGGTC CAGAAGCGGG GCGCTCTCCG GAGGAAGTTC GGCTTCTCGG CCGAGGACTA  240
CCGCGAGCTG GAGCGCCTGG CGCTCCAGGC TGAGCCCCAC CGCGCCGGCC GCCAGTGGAA  300
GTTCCCCGGC TCCTTCTACT TCGCCATCAC CGTCATCACT ACCATCGGGT ACGGCCACGC  360
CGCGCCGGGT ACGGACTCCG GCAAGGTCTT CTGCATGTTC TACGCGCTCC TGGGCATCCC  420
GCTGACGCTG GTCACTTTCC AGAGCCTGGG CGAACGGCTG AACGCGGTGG TGCGGCGCCT  480
CCTGTTGGCG GCCAAGTGCT GCCTGGGCCT GCGGTGGACG TGCGTGTCCA CGGAGAACCT  540
GGTGGTGGCC GGGCTGCTGG CGTGTGCCGC CACCCTGGCC CTCGGGGCCG TCGCCTTCTC  600
GCACTTCGAG GGCTGGACCT TCTTCCACGC CTACTACTAC TGCTTCATCA CCCTCACCAC  660
CATCGGCTTC GGCGACTTCG TGGCACTGCA GAGCGGCGAG GCGCTGCAGA GGAAGCTCCC  720
CTACGTGGCC TTCAGCTTCC TCTACATCCT CCTGGGGCTC ACGGTCATTG GCGCCTTCCT  780
CAACCTGGTG GTCCTGCGCT TCCTCGTTGC CAGCGCCGAC TGGCCCGAGC GCGCTGCCCG  840
CCCCCCCAGC CCGCGCCCCC CGGGGGCGCC CGAGAGCCGT GGCCTCTGGC TGCCCCGCCG  900
CCCGGCCCGC TCCGTGGGCT CCGCCTCTGT CTTCTGCCAC GTGCACAAGC TGGAGAGGTG  960
CGCCCGCGAC AACCTGGGCT TTTCGCCCCC CTCGAGCCCG GGGGTCGTGC GTGGCGGGCA 1020
GGCTCCCAGG CCTGGGGCCC GGTGGAAGTC CATCTGACAA CCCCACCCAG GCCAGGGTCG 1080
AATCTGGAAT GGGAGGGTCT GGCTTCAGCT ATCAGGGCAC CCTCCCCAGG GATTGGAAAC 1140
GGATGACGGG CCTCTAGGCG GTCTTCTGCC ACGAGCAGTT TCTCATTACT GTCTGTGGCT 1200
AAGTCCCCTC CCTCCTTTCC AAAAATATAT TACAGTCACA CCATAAAAAA AAAAAAAAAA 1260
AAAAAAAAAA AAAAAAAAAA AAAAAA
```

Seq ID NO: 42 Protein sequence
Protein Accession #: NP_071753

```
1          11         21         31         41         51
|          |          |          |          |          |
MRRPSVRAAG LVLCTLCYLL VGAAVFDALE SEAESGRQRL LVQKRGALRR KFGFSAEDYR   60
ELERLALQAE PHRAGRQWKF PGSFYFAITV ITTIGYGHAA PGTDSGKVFC MFYALLGIPL  120
TLVTFQSLGE RLNAVVRRLL LAAKCCLGLR WTCVSTENLV VAGLLACAAT LALGAVAFSH  180
FEGWTFFHAY YYCFITLTTI GFGDFVALQS GEALQRKLPY VAFSFLYILL GLTVIGAFLN  240
LVVLRFLVAS ADWPERAARP PSPRPPGAPE SRGLWLPRRP ARSVGSASVF CHVHKLERCA  300
RDNLGFSPPS SPGVVRGGQA PRPGARWKSI
```

Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: NM_000869.1
Coding sequence: 220..1656

```
1          11         21         31         41         51
|          |          |          |          |          |
GGAAACATGA TCCAGCTGAA GGACTGATTG CAGGAAAACT TGGCAGCTCC CCAACCTTGG   60
TGGCCCAGGG AGTGTGAGGC TGCAGCCTCA GAAGGTGTGA GCAGTGGCCA CGAGAGGCAG  120
GCTGGCTGGG ACATGAGGTT GGCAGAGGGC AGGCAAGCTG GCCCTTGGTG GGCCTCGCCC  180
TGAGCACTCG GAGGCACTCC TATGCTTGGA AAGCTCGCTA TGCTGCTGTG GGTCCAGCAG  240
GCGCTGCTCG CCTTGCTCCT CCCCACACTC CTGGCACAGG GAGAAGCCAG GAGGAGCCGA  300
AACACCACCA GGCCCGCTCT GCTGAGGCTG TCGGATTACC TTTTGACCAA CTACAGGAAG  360
GGTGTGCGCC CCGTGAGGGA CTGGAGGAAG CCAACCACCG TATCCATTGA CGTCATTGTC  420
TATGCCATCC TCAACGTGGA TGAGAAGAAT CAGGTGCTGA CCACCTACAT CTGGTACCGG  480
CAGTACTGGA CTGATGAGTT TCTCCAGTGG AACCCTGAGG ACTTTGACAA CATCACCAAG  540
TTGTCCATCC CCACGGACAG CATCTGGGTC CCGGACATTC TCATCAATGA GTTCGTGGAT  600
GTGGGGAAGT CTCCAAATAT CCCGTACGTG TATATTCGGC ATCAAGGCGA AGTTCAGAAC  660
TACAAGCCCC TTCAGGTGGT GACTGCCTGT AGCCTCGACA TCTACAACTT CCCCTTCGAT  720
GTCCAGAACT GCTCGCTGAC CTTCACCAGT TGGCTGCACA CCATCCAGGA CATCAACATC  780
TCTTTGTGGC GCTTGCCAGA AAAGGTGAAA TCCGACAGGA GTGTCTTCAT GAACCAGGGA  840
GAGTGGGAGT TGCTGGGGGT GCTGCCCTAC TTTCGGGAGT TCAGCATGGA AAGCAGTAAC  900
TACTATGCAG AAATGAAGTT CTATGTGGTC ATCCGCCGGC GGCCCCTCTT CTATGTGGTC  960
AGCCTGCTAC TGCCCAGCAT CTTCCTCATG GTCATGGACA TCGTGGGCTT CTACCTGCCC 1020
CCCAACAGTG GCGAGAGGGT CTCTTTCAAG ATTACACTCC TCCTGGGCTA CTCGGTCTTC 1080
CTGATCATCG TTTCTGACAC GCTGCCGGCC ACTGCCATCG GCACTCCTCT CATTGGTGTC 1140
TACTTTGTGG TGTGCATGGC TCTGCTGGTG ATAAGTTTGG CCGAGACCAT CTTCATTGTG 1200
```

```
CGGCTGGTGC ACAAGCAAGA CCTGCAGCAG CCCGTGCCTG CTTGGCTGCG TCACCTGGTT  1260
CTGGAGAGAA TCGCCTGGCT ACTTTGCCTG AGGGAGCAGT CAACTTCCCA GAGGCCCCCA  1320
GCCACCTCCC AAGCCACCAA GACTGATGAC TGCTCAGCCA TGGGAAACCA CTGCAGCCAC  1380
ATGGGAGGAC CCCAGGACTT CGAGAAGAGC CCGAGGGACA GATGTAGCCC TCCCCCACCA  1440
CCTCGGGAGG CCTCGCTGGC GGTGTGTGGG CTGCTGCAGG AGCTGTCCTC CATCCGGCAA  1500
TTCCTGGAAA AGCGGGATGA GATCCGAGAG GTGGCCCGAG ACTGGCTGCG CGTGGGCTCC  1560
GTGCTGGACA AGCTGCTATT CCACATTTAC CTGCTAGCGG TGCTGGCCTA CAGCATCACC  1620
CTGGTTATGC TCTGGTCCAT CTGGCAGTAC GCTTGAGTGG GTACAGCCCA GTGGAGGAGG  1680
GGGTACAGTC CTGGTTAGGT GGGGACAGAG GATTTCTGCT TAGGCCCCTC AGGACCCAGG  1740
GAATGCCAGG GACATTTTCA AGACACAGAC AAAGTCCCGT GCCCTGTTTC CAATGCCAAT  1800
TCATCTCAGC AATCACAAGC CAAGGTCTGA ACCCTTCCAC CAAAAACTGG GTGTTCAAGG  1860
CCCTTACACC CTTGTCCCAC CCCCAGCAGC TCACCATGGC TTTAAAACAT GCTCTCTTAG  1920
ATCAGGAGAA ACTCGGGCAC TCCCTAAGTC CACTCTAGTT GTGGACTTTT CCCCATTGAC  1980
CCTCACCTGA ATAAGGGACT TTGGAATTCT GCTTCTCTTT CACAACTTTG CTTTTAGGTT  2040
GAAGGCAAAA CCAACTCTCT ACTACACAGG CCTGATAACT CTGTACGAGG CTTCTCTAAC  2100
CCCTAGTGTC TTTTTTTTCT TCACCTCACT TGTGGCAGCT TCCCTGAACA CTCATCCCCC  2160
ATCAGATGAT GGGAGTGGGA AGAATAAAAT GCAGTGAAAC CC
```

Seq ID NO: 44 Protein sequence
Protein Accession #: NP_000860.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLLWVQQALL ALLLPTLLAQ GEARRSRNTT RPALLRLSDY LLTNYRKGVR PVRDWRKPTT   60
VSIDVIVYAI LNVDEKNQVL TTYIWYRQYW TDEFLQWNPE DFDNITKLSI PTDSIWVPDI  120
LINEFVDVGK SPNIPYVYIR HQGEVQNYKP LQVVTACSLD IYNFPFDVQN CSLTFTSWLH  180
TIQDINISLW RLPEKVKSDR SVFMNQGEWE LLGVLPYFRE FSMESSNYYA EMKFYVVIRR  240
RPLFYVVSLL LPSIFLMVMD IVGFYLPPNS GERVSFKITL LLGYSVFLII VSDTLPATAI  300
GTPLIGVYFV VCMALLVISL AETIFIVRLV HKQDLQQPVP AWLRHLVLER IAWLLCLREQ  360
STSQRPPATS QATKTDDCSA MGNHCSHMGG PQDFEKSPRD RCSPPPPPRE ASLAVCGLLQ  420
ELSSIRQFLE KRDEIREVAR DWLRVGSVLD KLLFHIYLLA VLAYSITLVM LWSIWQYA
```

Seq ID NO: 45 DNA sequence
Nucleic Acid Accession #: NM_015507
Coding sequence: 241..1902

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1          11         21         31         41         51
|          |          |          |          |          |
CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCCTCCCC AGGCCGCGAG    60
CGCCCCTGCC GCGGTGCCTG GCCTCCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACTG   120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG   180
GGGTCCGGCC GGCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCGAGA   240
ATGCCTCTGC CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC   300
GGGAACGCGG CCAGTGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC   360
TGTCACTATG GAACTAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC   420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC   480
AGATGCTTTC CAGGATACAC CGGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG   540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC   600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG   660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC   720
TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT   780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC   840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA   900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA   960
GGGTCCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT  1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC  1080
AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAAATTAA AAATGTTACC  1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACTTGC AGCCCTTCAA CTATGAAGAG  1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA  1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA  1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT  1380
CTGGTCCAAA GGAAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT  1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC  1500
TGGAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA  1560
GGTCACAAGA AAGACATTGG CCGATTGAAA CTTCTCCTAC CTGACCTGCA ACCCCAAAGC  1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCGGAGACA AAGTCGGGAA ACTTCGAGTG  1680
TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG  1740
TGGAAGACAG GGAAAATTCA GTTGTATCAA GGAACTGATG CTACCAAAAG CATCATTTTT  1800
GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT  1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT  1920
TTGACTTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT  1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT  2040
TCTTGTATAA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA  2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT  2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA  2220
TAGAAAAAAA AGCACAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC  2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT  2340
TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAAAAA AAAAAAAA
```

Seq ID NO: 46 Protein sequence
Protein Accession #: NP_056322

```
1          11         21         31         41         51
|          |          |          |          |          |
MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRRNSKGV   60
CEATCEPGCK FGECVGPNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRCV NTHGSYKCFC  120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS  180
GKVICPYNRR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFNTQ  240
```

GSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLLAHKNSM KKKAKIKNVT 300
PEPTRTPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360
SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD 420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFDYRL AGDKVGKLRV 480
FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGKTG EIAVDGVLLV 540
SGLCPDSLLS VDD

Seq ID NO: 47 DNA sequence
Nucleic Acid Accession #: NM_005046
Coding sequence: 16..777

1 11 21 31 41 51
GGATTTCCGG GCTCCATGGC AAGATCCCTT CTCCTGCCCC TGCAGATCCT ACTGCTATCC 60
TTAGCCTTGG AAACTGCAGG AGAAGAAGCC CAGGGTGACA AGATTATTGA TGGCGCCCCA 120
TGTGCAAGAG GCTCCCACCC ATGGCAGGTG GCCCTGCTCA GTGGCAATCA GCTCCACTGC 180
GGAGGCGTCC TGGTCAATGA GCGCTGGGTG CTCACTGCCG CCCACTGCAA GATGAATGAG 240
TACACCGTGC ACCTGGGCAG TGATACGCTG GGCGACAGGA GAGCTCAGAG GATCAAGGCC 300
TCGAAGTCAT TCCGCCACCC CGGCTACTCC ACACAGACCC ATGTTAATGA CCTCATGCTC 360
GTGAAGCTCA ATAGCCAGGC CAGGCTGTCA TCCATGGTGA AGAAAGTCAG GCTGCCCTCC 420
CGCTGCGAAC CCCCTGGAAC CACCTGTACT GTCTCCGGCT GGGGCACTAC CACGAGCCCA 480
GATGTGACCT TTCCCTCTGA CCTCATGTGC GTGGATGTCA AGCTCATCTC CCCCCAGGAC 540
TGCACGAAGG TTTACAAGGA CTTACTGGAA AATTCCATGC TGTGCGCTGG CATCCCCGAC 600
TCCAAGAAAA ACGCCTGCAA TGGTGACTCA GGGGGACCGT TGGTGTGCAG AGGTACCCTG 660
CAAGGTCTGG TGTCCTGGGG AACTTTCCCT TGCGGCCAAC CCAATGACCC AGGAGTCTAC 720
ACTCAAGTGT GCAAGTTCAC CAAGTGGATA AATGACACCA TGAAAAAGCA TCGCTAACGC 780
CACACTGAGT TAATTAACTG TGTGCTTCCA ACAGAAAATG CACAGGAGTG AGGACGCCGA 840
TGACCTATGA AGTCAAATTT GACTTTACCT TTCCTCAAAG ATATATTTAA ACCTCATGCC 900
CTGTTGATAA ACCAATCAAA TTGGTAAAGA CCTAAAACCA AAACAAATAA AGAAACACAA 960
AACCCTCAA

Seq ID NO: 48 Protein sequence
Protein Accession #: NP_005037

1 11 21 31 41 51
MARSLLLPLQ ILLLSLALET AGEEAQGDKI IDGAPCARGS HPWQVALLSG NQLHCGGVLV 60
NERWVLTAAH CKMNEYTVHL GSDTLGDRRA QRIKASKSFR HPGYSTQTHV NDLMLVKLNS 120
QARLSSMVKK VRLPSRCEPP GTTCTVSGWG TTTSPDVTFP SDLMCVDVKL ISPQDCTKVY 180
KDLLENSMLC AGIPDSKKNA CNGDSGGPLV CRGTLQGLVS WGTFPCGQPN DPGVYTQVCK 240
FTKWINDTMK KHR

Seq ID NO: 49 DNA sequence
Nucleic Acid Accession #: NM_003466.1
Coding sequence: 11..1363

1 11 21 31 41 51
GAATTCGGCG ATGCCTCACA ACTCCATCAG ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG 60
AGGGGCCTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT 120
GGCCCACCAG GGTGTAAGGC CCTGCGACAT CTCTCGCCAG CTCCGCGTCA GCCATGGTTG 180
CGTCAGCAAG ATCCTTGGCA GGTACTACGA GACTGGCAGC ATCCGGCCTG GAGTGATAGG 240
GGGCTCCAAG CCCAAGGTGG CCACCCCCAA GGTGGTGGAG AAGATTGGGG ACTACAAACG 300
CCAGAACCCT ACCATGTTTG CCTGGGAGAT CCGAGACCGG CTCCTGGCTG AGGGCGTCTG 360
TGACAATGAC ACTGTGCCCA GTGTCAGCTC CATTAATAGA ATCATCCGGA CCAAAGTGCA 420
GCAACCATTC AACCTCCCTA TGGACAGCTG CGTGGCCACC AAGTCCCTGA GTCCCGGACA 480
CACGCTGATC CCCAGCTCAG CTGTAACTCC CCCGGAGTCA CCCCAGTCGG ATTCCCTGGG 540
CTCCACCTAC TCCATCAATG GGCTCCTGGG CATCGCTCAG CCTGGCAGCG ACAAGAGGAA 600
AATGGATGAC AGTGATCAGG ATAGCTGCCG ACTAAGCATT GACTCACAGA GCAGCAGCAG 660
CGGACCCCGA AAGCACCTTC GCACGGATGC CTTCAGCCAG CACCACCTCG AGCCGCTCGA 720
GTGCCCATTT GAGCGGCAGC ACTACCCAGA GGCCTATGCC TCCCCCAGCC ACACCAAAGG 780
CGAGCAGGGC CTCTACCCGC TGCCCTTGCT CAACAGCACC CTGGACGACG GGAAGGCCAC 840
CCTGACCCCT TCCAACACGC CACTGGGGCG CAACCTCTCG ACTCACCAGA CCTACCCCGT 900
GGTGGCAGAT CCTCACTCAC CCTTCGCCAT AAAGCAGGAA ACCCCCGAGG TGTCCAGTTC 960
TAGCTCCACC CCTTCCTCTT TATCTAGCTC CGCCTTTTTG GATCTGCAGC AAGTCGGCTC 1020
CGGGGTCCCG CCCTTCAATG CCTTTCCCCA TGCTGCCTCC GTGTACGGGC AGTTCACGGG 1080
CCAGGCCCTC CTCTCAGGGC GAGAGATGGT GGGGCCCACG CTGCCCGGAT ACCCACCCCA 1140
CATCCCCACC AGCGGACAGG GCAGCTATGC CTCCTCTGCC ATCGCAGGCA TGGTGGCAGG 1200
AAGTGAATAC TCTGGCAATG CCTATGGCCA CACCCCCTAC TCCTCCTACA GCGAGGCCTG 1260
GCGCTTCCCC AACTCCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC 1320
GAGTGCACCG CCCACCACTG CCACGGCCTT TGACCATCTG TAGTTGAAGC TT

Seq ID NO: 50 Protein sequence
Protein Accession #: NP_003457

1 11 21 31 41 51
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
ERQHYPEAYA SPSHTKGEQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAD 300
PHSPFAIKQE TPEVSSSSST PSSLSSSAFL DLQQVGSGVP PFNAFPHAAS VYGQFTGQAL 360
LSGREMVGPT LPGYPPHIPT SGQGSYASSA IAGMVAGSEY SGNAYGHTPY SSYSEAWRFP 420
NSSLLSSPYY YSSTSRPSAP PTTATAFDHL

Seq ID NO: 51 DNA sequence
Nucleic Acid Accession #: NM_013952
Coding sequence: 161..1357

```
1          11         21         31         41         51
|          |          |          |          |          |
TTCAGAAGGA GGAGAGACAC CGGGCCCAGG GCACCCTCGC GGGCGGGCGG ACCCAAGCAG     60
TGAGGGCCTG CAGCCGGCCG GCCAGGGCAG CGGCAGGCGC GGCCCGGACC TACGGGAGGA    120
AGCCCCGAGC CCTCGGCGGG CTGCGAGCGA CTCCCCGGCG ATGCCTCACA ACTCCATCAG    180
ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG AGGGGCCTTT GTGAATGGCA GACCTCTGCC    240
GGAAGTGGTC CGCCAGCGCA TCGTAGACCT GGCCCACCAG GGTGTAAGGC CCTGCGACAT    300
CTCTCGCCAG CTCCGCGTCA GCCATGGCTG CGTCAGCAAG ATCCTTGGCA GGTACTACGA    360
GACTGGCAGC ATCCGGCCTG GAGTGATAGG GGGCTCCAAG CCCAAGGTGG CCACCCCCAA    420
GGTGGTGGAG AAGATTGGGG ACTACAAACG CCAGAACCCT ACCATGTTTG CCTGGGAGAT    480
CCGAGACCGG CTCCTGGCTG AGGGCGTCTG TGACAATGAC ACTGTGCCCA GTGTCAGCTC    540
CATTAATAGA ATCATCCGGA CCAAAGTGCA GCAACCATTC AACCTCCCTA TGGACAGCTG    600
CGTGGCCACC AAGTCCCTGA GTCCCGGACA CACGCTGATC CCCAGCTCAG CTGTAACTCC    660
CCCGGAGTCA CCCCAGTCGG ATTCCCTGGG CTCCACCTAC TCCATCAATG GGCTCCTGGG    720
CATCGCTCAG CCTGGCAGCG ACAAGAGGAA AATGGATGAC AGTGATCAGG ATAGCTGCCG    780
ACTAAGCATT GACTCACAGA GCAGCAGCAG CGGACCCCGA AAGCACCTTC GCACGGATGC    840
CTTCAGCCAG CACCACCTCG AGCCGCTCGA GTGCCCATTT GAGCGGCAGC ACTACCCAGA    900
GGCCTATGCC TCCCCCAGCC ACACCAAAGG CGAGCAGGGC CTCTACCCGC TGCCCTTGCT    960
CAACAGCACC CTGGACGACG GGAAGGCCAC CCTGACCCCT TCCAACACGC CACTGGGGCG   1020
CAACCTCTCG ACTCACCAGA CCTACCCCGT GGTGGCAGCT CCGCCCTTTT GGATCTGCAG   1080
CAAGTCGGCT CCGGGGTCCC GCCCTTCAAT GCCTTTCCCC ATGCTGCCTC CGTGTACGGG   1140
CAGTTCACGG GCCAGGCCCT CCTCTCAGGG CGAGAGATGG TGGGGCCCAC GCTGCCCGGA   1200
TACCCACCCC ACATCCCCAC CAGCGGACAG GGCAGCTATG CCTCCTCTGC CATCGCAGGC   1260
ATGGTGGCAG GAAGTGAATA CTCTGGCAAT GCCTATGGCC ACACCCCCTA CTCCTCCTAC   1320
AGCGAGGCCT GGGGCTTCCC CAACTCCAGC TTGCTGAGTT CCCCATATTA TTACAGTTCC   1380
ACATCAAGGC CGAGTGCACC GCCCACCACT GCCACGGCCT TTGACCATCT GTAGTTGCCA   1440
TGGGGACAGT G
```

Seq ID NO: 52 Protein sequence
Protein Accession #: NP_039246

```
1          11         21         31         41         51
|          |          |          |          |          |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK     60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND    120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY    180
SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF    240
ERQHYPEAYA SPSHTKGEQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAA    300
PPFWICSKSA PGSRPSMPPP MLPPCTGSSR ARPSSQGERW WGPRCPDTHP TSPPADRAAM    360
PPLPSQAWWQ EVNTLAMPMA TPPTPPTARP GASPTPAC
```

Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_012427
Coding sequence: 43..924

```
1          11         21         31         41         51
|          |          |          |          |          |
CTTGTGGTTC CTCTCTACTT GGGGAAATCA GGTGCAGCGG CCATGGCTAC AGCAAGACCC     60
CCCTGGATGT GGGTGCTCTG TGCTCTGATC ACAGCCTTGC TTCTGGGGGT CACAGAGCAT    120
GTTCTCGCCA ACAATGATGT TTCCTGTGAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC    180
AACCAGGACC TGGGAGCTGG GGCCGGGGAA GACGCCCGGT CGGATGACAG CAGCAGCCGC    240
ATCATCAATG GATCCGACTG CGATATGCAC ACCCAGCCGT GGCAGGCCGC GCTGTTGCTA    300
AGGCCCAACC AGCTCTACTG CGGGGCGGTG TTGGTGCATC CACAGTGGCT GCTCACGGCC    360
GCCCACTGCA GGAAGAAAGT TTTCAGAGTC CGTCTCGGCC ACTACTCCCT GTCACCAGTT    420
TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAATCCA TCCCCCACCC TGGCTACTCC    480
CACCCTGGCC ACTCTAACGA CCTCATGCTC ATCAAACTGA ACAGAAGAAT TCGTCCCACT    540
AAAGATGTCA GACCCATCAA CGTCTCCTCT CATTGTCCCT CTGCTGGGAC AAAGTGCTTG    600
GTGTCTGGCT GGGGGACAAC CAAGAGCCCC CAAGTGCACT TCCCTAAGGT CCTCCAGTGC    660
TTGAATATCA GCGTGCTAAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT    720
GACACCATGT TCTGCGCCGG TGACAAAGCA GGTAGAGACT CCTGCCAGGG TGATTCTGGG    780
GGGCCTGTGG TCTGCAATGG CTCCCTGCAG GGACTCGTGT CCTGGGGAGA TTACCCTTGT    840
GCCCGGCCCA ACAGACCGGG TGTCTACACG AACCTCTGCA AGTTCACCAA GTGGATCCAG    900
GAAACCATCC AGGCCAACTC CTGAGTCATC CCAGGACTCA GCACACCGGC ATCCCCACCT    960
GCTGCAGGGA CAGCCCTGAC ACTCCTTTCA GACCCTCATT CCTTCCCAGA GATGTTGAGA   1020
ATGTTCATCT CTCCAGCCCC TGACCCCATG TCTCCTGGAC TCAGGGTCTG CTTCCCCCAC   1080
ATTGGGCTGA CCGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAAA CTGTCCAGGG   1140
CGGGGGTTGC GTCTCAATCT CCCTGGGGCA CTTTCATCCT CAAGCTCAGG GCCCATCCCT   1200
TCTCTGCAGC TCTGACCCAA ATTTAGTCCC AGAAATAAAC TGAGAAGTGG AAAAAAAAAA
```

Seq ID NO: 54 Protein sequence
Protein Accession #: NP_036559

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1          11         21         31         41         51
|          |          |          |          |          |
MATARPPWMW VLCALITALL LGVTEHVLAN NDVSCDHPSN TVPSGSNQDL GAGAGEDARS     60
DDSSSRIING SDCDMHTQPW QAALLLRPNQ LYCGAVLVHP QWLLTAAHCR KKVFRVRLGH    120
YSLSPVYESG QQMFQGVKSI PHPGYSHPGH SNDLMLIKLN RRIRPTKDVR PINVSSHCPS    180
AGTKCLVSGW GTTKSPQVHF PKVLQCLNIS VLSQKRCEDA YPRQIDDTMF CAGDKAGRDS    240
CQGDSGGPVV CNGSLQGLVS WGDYPCARPN RPGVYTNLCK FTKWIQETIQ ANS
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Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: NM_002214
Coding sequence: 681..2990

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1          11         21         31         41         51
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CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGACG     60
CTGCCGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT    120
GTTGGCCTCC CTGCCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT    180
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TCCCCTCGAC CTCGCCGGCG TACCCTCCCA CAGATCCAGC ATCACCCAGT GAATGTACAT   240
TAGGGTGGTT TCCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG   300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT   360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT   420
TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCCGGGAG   480
GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT   540
CCGAGCCGCG GGGTCCGCCT GCTAGGCCTG CGGAAAACGT CCTAGCGACA CTCGCCCGCG   600
GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGCGC   660
GGGGCGGGCT GTTTTGCATT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCATTTG   720
TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTCGTTCCT CTGGGCAGCC TGGGTGTTTT   780
CACTTGTTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT   840
CCTGTGCCAG GTGCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA   900
TTTCAGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT   960
GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAATGAAA  1020
TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA  1080
ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTTG  1140
ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTTAT  1200
CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTCGTCTTGG ATTTGGCTCA TACGTTGATA  1260
AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT  1320
ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA  1380
TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG  1440
AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA  1500
AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA  1560
GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACGTCT  1620
ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG  1680
ACAACAACAT TAATGTCATC TTTGCAGTTC AAGGAAAACA ATTTCATTGG TATAAGGATC  1740
TTCTACCCCT CTTGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA  1800
ATAATTTGGT AGTGGAAGCC TATCAGAAGC TCATTTCAGA AGTGAAAGTT CAGGTGGAAA  1860
ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC  1920
CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG  1980
TTACAATGAA AAAATGTGAT GTCACAGGAG GAAAAAACTA TGCAATAATC AAACCTATTG  2040
GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCAG TGTGAGGACA  2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACTTTTCT AGATTCCAAG TGTTTCCAGT  2160
GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC  2220
ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC  2280
ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC  2340
CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT  2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG  2460
TCAATTCAAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT  2520
GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT  2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCCTCA CAATTTGTCT CAGGCTATAC  2640
TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAACAACA GCATTATGTC GACCAAACTT  2700
CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTTT CATCATTTTC ATAGTTACAT  2760
TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGGAATAGTA  2820
ATAAAATTAA GTCCTCATCA GATTACAGAG TGTCAGCCTC AAAAAAGGAT AAGTTGATTC  2880
TGCAAAGTGT TTGCACAAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA  2940
TGGATATCAG CAAATTAAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATTT  3000
TTAAACACTT AATGGGAAAC TGGAATTGTT AATAATTGCT CCTAAAGATT ATAATTTTAA  3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACTCGAAC  3120
GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA  3180
AAAATGTGTC TTACTACTGT TTGAGACTAG TGTCGTTGTA GCACTTTACT GTAATATATA  3240
ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG  3300
TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT  3360
CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAAATA ATCTGGCAAG  3420
TATATTCTAA GGTTGCCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG  3480
ATGAATAAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA  3540
AAAGATTATT GCTTTTTAAA GTGTGTAGTT TTATGCATGT GTGTTTATGG TTTGCTTATT  3600
TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCCTCTTT GCCTTTATGT TTTGTTTTCT  3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC  3720
TACTGCCATA AAAAACTAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT  3780
GAATGTTAA
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Seq ID NO: 56 Protein sequence
Protein Accession #: NP_002205

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1          11         21         31         41         51
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MCGSALAFFT AAFVCLQNDR RGPASFLWAA WVFSLVLGLG QGEDNRCASS NAASCARCLA    60
LGPECGWCVQ EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP   120
GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAFF   180
SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA   240
VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRLL LVMTDQTSHL ALDSKLAGIV   300
VPNDGNCHLK NNVYVKSTTM EHPSLGQLSE KLIDNNINVI FAVQGKQFHW YKDLLPLLPG   360
TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR   420
NVTSNDEVLF NVTVTMKKCD VTGGKNYAII KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK   480
CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKDQPVC SGRGVCVCGK CSCHKIKLGK   540
VYGKYCEKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRCQCPSAAA QHCVNSKGQV   600
CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNLS QAILDQCKTS   660
CALMEQQHYV DQTSECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNKIKSSS   720
DYRVSASKKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF
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Seq ID NO: 57 DNA sequence
Nucleic Acid Accession #: NM_001719
Coding sequence: 123..1418

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CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG    120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC    180
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA    240
GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT    300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC    360
CCATGTTCAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG    420
GCCAGGGCTT CTCCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA    480
GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG    540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC    600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT    660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG    720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG    780
AGGAGGGCTG GCTGGTGTTT GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC    840
GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA    900
AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT    960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA   1020
GCCAGAACCG CTCCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG   1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC   1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG   1200
AGGGGGAGTG TGCCTTCCCT CTGAACTCCT ACATGAACGC CACCAACCAC GCCATCGTGC   1260
AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCACGC   1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT   1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCCT   1440
TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA   1500
CTGCCTTTTG TGAGACCTTC CCCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG   1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA   1620
TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAAAA ACAACGCATA AAGAAAAATG   1680
GCCGGGCCAG GTCATTGGCT GGGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA   1740
TTATGAGCGC CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT   1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA   1860
CAATAAAACG AATGAATG
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Seq ID NO: 58 Protein sequence
Protein Accession #: NP_001710

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1          11         21         31         41         51
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MHVRSLRAAA PHSFVALWAP LFLLRSALAD FSLDNEVHSS FIHRRLRSQE RREMQREILS    60
ILGLPHRPRP HLQGKHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS   120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY   180
IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVFDITA TSNHWVVNPR   240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS   300
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE   360
GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY   420
RNMVVRACGC H
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Seq ID NO: 59 DNA sequence
Nucleic Acid Accession #: NM_002821
Coding sequence: 150..3362

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1          11         21         31         41         51
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GCGCTCCGGT GCGTCCGCCT CCTGTGCCCG CCGCGGAGCA GTCTGCGGCC CGCCGTGCGC    120
CCTCAGCTCC TTTTCCTGAG CCCGCCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC    180
CCCGCCGGTT GCCTCTGCTC AGCGTCCTGC TGCTGCCGCT GCTGGGCGGT ACCCAGACAG    240
CCATTGTCTT CATCAAGCAG CCGTCCTCCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC    300
TTCGCTGTGA GGTTGAGGCT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC    360
CTGTCCAGGA CACGGAGCGG CGTTTCGCCC AGGGCAGCAG CCTGAGCTTT GCAGCTGTGG    420
ACCGGCTGCA GGACTCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG    480
AAGCCCGCAG TGCCAACGCC TCCTTCAACA TCAAATGGAT TGAGGCAGGT CCTGTGGTCC    540
TGAAGCATCC AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGGTCACA CTTCGTTGCC    600
ACATTGATGG GCACCCTCGG CCCACCTACC AATGGTTCCG AGATGGGACC CCCCTTTCTG    660
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GTCCTGAGCA TAGTGGGCTG TATTCCTGCT GCGCCCACAG TGCTTTTGGC CAGGCTTGCA    780
GCAGCCAGAA CTTCACCTTG AGCATTGCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC    840
CCCAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC    900
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GCCCCCCACA CCTCCGCAGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG   1020
TCCGGCCACG CAATGCAGGG ATCTACCGCT GCATTGGCCA GGGGCAGAGG GGCCCACCCA   1080
TCATCCTGGA AGCCACACTT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTTGAGCCAC   1140
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AGCCCAGCGT GTGGTGGGAG CACGCGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC   1260
AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGGT GTCTACACCT   1320
GCCACGCGGC CAACCTGGCT GGTCAGCGGA GACAGGATGT CAACATCACT GTGGCCACTG   1380
TGCCCTCCTG GCTGAAGAAG CCCCAAGACA GCCAGCTGGA GGAGGGCAAA CCCGGCTACT   1440
TGGATTGCCT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGGTACAGA AACCAGATGC   1500
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ACGCTGGGAC CCTGCATTTT GCCCGGGTGA CTCGAGATGA CGCTGGCAAC TACACTTGCA   1860
TTGCCTCCAA CGGGCCGCAG GGCCAGATTC GTGCCCATGT CCAGCTCACT GTGGCAGTTT   1920
TTATCACCTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC   1980
TGCAGTGCGA GGCCCAGGGG GACCCCAAGC CGCTGATTCA GTGGAAAGGC AAGGACCGCA   2040
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TCCTGGACCC CACCAAGCTG GGACCCAGGA TGCACATCTT CCAGAATGGC TCCCTGGTGA  2100
TCCATGACGT GGCCCCTGAG GACTCAGGCC GCTACACCTG CATTGCAGGC AACAGCTGCA  2160
ACATCAAGCA CACGGAGGCC CCCCTCTATG TCGTGGACAA GCCTGTGCCG GAGGAGTCGG  2220
AGGGCCCTGG CAGCCCTCCC CCCTACAAGA TGATCCAGAC CATTGGGTTG TCGGTGGGTG  2280
CCGCTGTGGC CTACATCATT GCCGTGCTGG GCCTCATGTT CTACTGCAAG AAGCGCTGCA  2340
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TCCCACGGTC TAGCCTGCAG CCCATCACCA CGCTGGGGAA GAGTGAGTTT GGGGAGGTGT  2580
TCCTGGCAAA GGCTCAGGGC TTGGAGGAGG GAGTGGCAGA GACCCTGGTA CTTGTGAAGA  2640
GCCTGCAGAC GAAGGATGAG CAGCAGCAGC TGGACTTCCG GAGGGAGTTG GAGATGTTTG  2700
GGAAGCTGAA CCACGCCAAC GTGGTGCGGC TCCTGGGGCT GTGCCGGGAG GCTGAGCCCC  2760
ACTACATGGT GCTGGAATAT GTGGATCTGG GAGACCTCAA GCAGTTCCTG AGGATTTCCA  2820
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GCACCCAGGT AGCCCTGGGC ATGGAGCACC TGTCCAACAA CCGCTTTGTG CATAAGGACT  2940
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GCTGGATGTC CCCCGAGGCC ATCCTGGAGG GTGACTTCTC TACCAAGTCT GATGTCTGGG  3120
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CAGATGATGA AGTACTGGCA GATTTGCAGG CTGGGAAGGC TAGACTTCCT CAGCCCGAGG  3240
GCTGCCCTTC CAAACTCTAT CGGCTGATGC AGCGCTGCTG GGCCCTCAGC CCCAAGGACC  3300
GGCCCTCCTT CAGTGAGATT GCCAGCGCCC TGGGAGACAG CACCGTGGAC AGCAAGCCGT  3360
GAGGAGGGAG CCCGCTCAGG ATGGCCTGGG CAGGGGAGGA CATCTCTAGA GGGAAGCTCA  3420
CAGCATGATG GGCAAGATCC CTGTCCTCCT GGGCCCTGAG GTGCCCTAGT GCAACAGGCA  3480
TTGCTGAGGT CTGAGCAGGG CCTGGCCTTT CCTCCTCTTC CTCACCCTCA TCCTTTGGGA  3540
GGCTGACTTG GACCCAAACT GGGCGACTAG GGCTTTGAGC TGGGCAGTTT CCCCTGCCAC  3600
CTCTTCCTCT ATCAGGGACA GTGTGGGTGC CACAGGTAAC CCCAATTTCT GGCCTTCAAC  3660
TTCTCCCCTT GACCGGGTCC AACTCTGCCA CTCATCTGCC AACTTTGCCT GGGGAGGGCT  3720
AGGCTTGGGA TGAGCTGGGT TTGTGGGGAG TTCCTTAATA TTCTCAAGTT CTGGGCACAC  3780
AGGGTTAATG AGTCTCTTGC CCACTGGTCC ACTTGGGGGT CTAGACCAGG ATTATAGAGG  3840
ACACAGCAAG TGAGTCCTCC CCACTCTGGG CTTGTGCACA CTGACCCAGA CCCACGTCTT  3900
CCCCACCCTT CTCTCCTTTC CTCATCCTAA GTGCCTGGCA GATGAAGGAG TTTTCAGGAG  3960
CTTTTGACAC TATATAAACC GCCCTTTTTG TATGCACCAC GGGCGGCTTT TATATGTAAT  4020
TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CCTGGAGATG AGGAGGGTGG  4080
GCCATCCTTA CCCCACACTT TTATTGTTGT CGTTTTTTGT TTGTTTTGTT TTTTTGTTTT  4140
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Seq ID NO: 60 Protein sequence
Protein Accession #: NP_002812

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IKWIEAGPVV LKHPASEAEI QPQTQVTLRC HIDGHPRPTY QWFRDGTPLS DGQSNHTVSS   180
KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SSQNFTLSIA DESFARVVLA PQDVVVARYE   240
EAMFHCQFSA QPPPSLQWLF EDETPITNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR   300
CIGQGQRGPP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG   360
VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD   420
SQLEEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVYDGTWYR   480
CMSSTPAGSI EAQARVQVLE KLKFTPPPQP QQCMEFDKEA TVPCSATGRE KPTIKWERAD   540
GSSLPEWVTD NAGTLHFARV TRDDAGNYTC IASNGPQGQI RAHVQLTVAV FITFKVEPER   600
TTVYQGHTAL LQCEAQGDPK PLIQWKGKDR ILDPTKLGPR MHIFQNGSLV IHDVAPEDSG   660
RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGPGSPPPYK MIQTIGLSVG AAVAYIIAVL   720
GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN   780
KRHSTSDKMH FPRSSLQPIT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ   840
LDFRRELEMF GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ   900
PLSTKQKVAL CTQVALGMEH LSNNRFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY   960
YHFRQAWVPL RWMSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVLADLQ  1020
AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP
```

Seq ID NO: 61 DNA sequence
Nucleic Acid Accession #: NM_006103
Coding sequence: 29..406

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1          11         21         31         41         51
|          |          |          |          |          |
CACCTGCACC CCGCCCGGGC ATAGCACCAT GCCTGCTTGT CGCCTAGGCC CGCTAGCCGC    60
CGCCCTCCTC CTCAGCCTGC TGCTGTTCGG CTTCACCCTA GTCTCAGGCA CAGGAGCAGA   120
GAAGACTGGC GTGTGCCCCG AGCTCCAGGC TGACCAGAAC TGCACGCAAG AGTGCGTCTC   180
GGACAGCGAA TGCGCCGACA ACCTCAAGTG CTGCAGCGCG GGCTGTGCCA CCTTCTGCCT   240
TCTCTGCCCA AATGATAAGG AGGGTTCCTG CCCCCAGGTG AACATTAACT TTCCCCAGCT   300
CGGCCTCTGT CGGGACCAGT GCCAGGTGGA CAGCCAGTGT CCTGGCCAGA TGAAATGCTG   360
CCGCAATGGC TGTGGGAAGG TGTCCTGTGT CACTCCCAAT TTCTGAGGTC CAGCCACCAC   420
CAGGCTGAGC AGTGAGGAGA GAAAGTTTCT GCCTGGCCCT GCATCTGGTT CCAGCCCACC   480
TGCCCTCCCC TTTTTCGGGA CTCTGTATTC CCTCTTGGGC TGACCACAGC TTCTCCCTTT   540
CCCAACCAAT AAAGTAACCA CTTTCAGCAA AAAAAAAAAA AAAA
```

Seq ID NO: 62 Protein sequence
Protein Accession #: NP_006094

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1          11         21         31         41         51
|          |          |          |          |          |
MPACRLGPLA AALLLSLLLF GFTLVSGTGA EKTGVCPELQ ADQNCTQECV SDSECADNLK    60
CCSAGCATFC LLCPNDKEGS CPQVNINFPQ LGLCRDQCQV DSQCPGQMKC CRNGCGKVSC   120
VTPNF
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Seq ID NO: 63 DNA sequence

```
Nucleic Acid Accession #: NM_001203
Coding sequence: 274..1782
1          11         21         31         41         51
|          |          |          |          |          |
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTGCGGAGA CCGCGGCGCT     60
GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT    120
GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTTGATAAA GGTTCAGACT TCTGCTGATT    180
CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC    240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA    300
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC    360
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA    420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTGCCTGT GGTCACTTCT    480
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTCGGG ACACTCCCAT TCCTCATCAA    540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCTACA    600
CTGCCTCCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGCTTTACTT    660
ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG    720
TATAAAAGAC AAGAAACCAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC    780
ATTCCTCCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA    840
TCAGGCCTCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAAACAG    900
ATTGGAAAAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT    960
GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG   1020
ACAGTGTTGA TGAGGCATGA AAACATTTTG GGTTTCATTG CTGCAGATAT CAAAGGGACA   1080
GGGTCCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT   1140
TATCTGAAGT CCACCACCCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC   1200
AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAACC AGCAATTGCC   1260
CATCGAGATC TGAAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACTTG CTGTATTGCT   1320
GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC   1380
ACTCGAGTTG GCACCAAACG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA   1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG   1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC   1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA   1620
CGCCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAAACTC   1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA   1740
ACACTTGCCA AAATGTCAGA GTCCCAGGAC ATTAAACTCT GATAGGAGAG GAAAAGTAAG   1800
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA   1860
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC   1920
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG   1980
TCTGTTTGTA GGCGGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT
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Seq ID NO: 64 Protein sequence
Protein Accession #: NP_001194
1          11         21         31         41         51
|          |          |          |          |          |
MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED     60
DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD    120
GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPRYS IGLEQDETYI PPGESLRDLI    180
EQSQSSGSGS GLPLLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTEEAS    240
WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS    300
MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNILV KKNGTCCIAD LGLAVKFISD    360
TNEVDIPPNT RVGTKRYMPP EVLDESLNRN HFQSYIMADM YSFGLILWEV ARRCVSGGIV    420
EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS    480
RLTALRVKKT LAKMSESQDI KL
```

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Seq ID NO: 65 DNA sequence
Nucleic Acid Accession #: NM_006475.1
Coding sequence: 28..2538
1          11         21         31         41         51
|          |          |          |          |          |
AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCCATGTT TTCTCTACTA     60
TTGCTGCTTA TTGTTAACCC TATAAACGCC AACAATCATT ATGACAAGAT CTTGGCTCAT    120
AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC    180
ACCAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG    240
AAAACGACTG TTTTATATGA ATGTTGCCCT GGTTATATGA GAATGGAAGG AATGAAAGGC    300
TGCCCAGCAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC    360
ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC    420
TTCACTTACT TTGCACCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCCGTAGA    480
GGTTTGGAGA GCAACGTGAA TGTTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT    540
AAGAGAATGT TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAT    600
TTGGGGCTTT TCATTAACCA TTATCCTAAT GGGGTTGTCA CTGTTAATTG TGCTCGAATC    660
ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA    720
CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA    780
GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACACTC    840
TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGTCCTAGA AAGGTTCATG    900
GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT    960
TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA   1020
GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT   1080
GTGACAAATA ATGGTGTGAT CCATTTGATT GATCAGGTCC TAATTCCTGA TTCTGCCAAA   1140
CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA   1200
GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT   1260
GCATTTTCTG ATGATACTCT CAGCATGGTT CAGCGCCTCC TTAAATTAAT TCTGCAGAAT   1320
CACATATTGA AAGTAAAAGT TGGCCTTAAT GAGCTTTACA ACGGGCAAAT ACTGGAAACC   1380
ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGTCTGCAT TGAAAATTCA   1440
TGCATGGAGA AAGGGAGTAA GCAAGGGAGA AACGGTGCGA TTCACATATT CCGCGAGATC   1500
ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAAAC AAGATAAGCG CTTTAGCACC   1560
TTCCTCAGCC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAACC TGGAGACTGG   1620
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ACATTATTTG TGCCAACCAA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT  1680
CTGATACGGG ACAAAAATGC TCTTCAAAAC ATCATTCTTT ATCACCTGAC ACCAGGAGTT  1740
TTCATTGGAA AAGGATTTGA ACCTGGTGTT ACTAACATTT TAAAGACCAC ACAAGGAAGC  1800
AAAATCTTTC TGAAAGAAGT AAATGATACA CTTCTGGTGA ATGAATTGAA ATCAAAAGAA  1860
TCTGACATCA TGACAACAAA TGGTGTAATT CATGTTGTAG ATAAACTCCT CTATCCAGCA  1920
GACACACCTG TTGGAAATGA TCAACTGCTG GAAATACTTA ATAAATTAAT CAAATACATC  1980
CAAATTAAGT TTGTTCGTGG TAGCACCTTC AAAGAAATCC CCGTGACTGT CTATACAACT  2040
AAAATTATAA CCAAAGTTGT GGAACCAAAA ATTAAAGTGA TTGAAGGCAG TCTTCAGCCT  2100
ATTATCAAAA CTGAAGGACC CACACTAACA AAAGTCAAAA TTGAAGGTGA ACCTGAATTC  2160
AGACTGATTA AAGAAGGTGA AACAATAACT GAAGTGATCC ATGGAGAGCC AATTATTAAA  2220
AAATACACCA AAATCATTGA TGGAGTGCCT GTGGAAATAA CTGAAAAAGA GACACGAGAA  2280
GAACGAATCA TTACAGGTCC TGAAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA  2340
ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTCAC CAAATTCATT  2400
GAAGGTGGTG ATGGTCATTT ATTTGAAGAT GAAGAAATTA AAAGACTGCT TCAGGGAGAC  2460
ACACCCGTGA GGAAGTTGCA AGCCAACAAA AAAGTTCAAG GTTCTAGAAG ACGATTAAGG  2520
GAAGGTCGTT CTCAGTGAAA ATCCAAAAAC CAGAAAAAAA TGTTTATACA ACCCTAAGTC  2580
AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAACTG AAACATCAGC  2640
ACAAAGAAGC AATCATCAAA TAATTCTGAA CACAAATTTA ATATTTTTTT TTCTGAATGA  2700
GAAACATGAG GGAAATTGTG GAGTTAGCCT CCTGTGGTAA AGGAATTGAA GAAAATATAA  2760
CACCTTACAC CCTTTTTCAT CTTGACATTA AAAGTTCTGG CTAACTTTGG AATCCATTAG  2820
AGAAAAATCC TTGTCACCAG ATTCATTACA ATTCAAATCG AAGAGTTGTG AACTGTTATC  2880
CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAAATGCA CGCAAGCCAT  2940
TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA  3000
TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTTA  3060
CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA  3120
TCTCAAACGT TTCAATAAAA CCATTTTTCA GATATAAAGA GAATTACTTC AAATTGAGTA  3180
ATTCAGAAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA
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Seq ID NO: 66 protein sequence
Protein Accession #: NP_006466.1

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1          11         21         31         41         51
|          |          |          |          |          |
MIPFLPMFSL LLLLIVNPIN ANNHYDKILA HSRIRGRDQG PNVCALQQIL GTKKKYFSTC   60
KNWYKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTLGIVGA TTTQRYSDAS  120
KLREEIEGKG SFTYFAPSNE AWDNLDSDIR RGLESNVNVE LLNALHSHMI NKRMLTKDLK  180
NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IIHGNQIATN GVVHVIDRVL TQIGTSIQDF  240
IEAEDDLSSF RAAAITSDIL EALGRDGHFT LFAPTNEAFE KLPRGVLERF MGDKVASEAL  300
MKYHILNTLQ CSESIMGGAV FETLEGNTIE IGCDGDSITV NGIKMVNKKD IVTNNGVIHL  360
IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLLAPVN NAFSDDTLSM  420
VQRLLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG  480
RNGAIHIFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA  540
FKGMTSEEKE ILIRDKNALQ NIILYHLTPG VFIGKGFEPG VTNILKTTQG SKIFLKEVND  600
TLLVNELKSK ESDIMTTNGV IHVVDKLLYP ADTPVGNDQL LEILNKLIKY IQIKFVRGST  660
FKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIIKTEGPTL TKVKIEGEPE FRLIKEGETI  720
TEVIHGEPII KKYTKIIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEETLKKLL  780
QEEVTKVTKF IEGGDGHLFE DEEIKRLLQG DTPVRKLQAN KKVQGSRRRL REGRSQ
```

Seq ID NO: 67 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 1-927

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCTGGGG GGTGCTCCCG GGGCCCCGCC GCCGGGGACG GGCGTCTGCG GCTGGCGCGA   60
CTAGCGCTGG TACTCCTGGG CTGGGTCTCC TCGTCTTCTC CCACCTCCTC GGCATCCTCC  120
TTCTCCTCCT CGGCGCCGTT CCTGGCTTCC GCCGTGTCCG CCCAGCCCCC GCTGCCGGAC  180
CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC  240
AATCTGACCG AGGTGCCCAC GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC  300
AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC  360
AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCCTTC  420
CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCCTTCAC  480
AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCCACATTA GGGTTTTCCT GGACAACAAT  540
CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA  600
GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAA AAATGAGGAA TCGGGTCCTC  660
TTGGAACTCA ACAGTGCTGA CCTGGACTGT GACCCGATTC TTCCCCCATC CCTGCAAACC  720
TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCCT CCTGGTTTTG  780
TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT  840
CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC  900
AGTTCTAACT CGGATGTCCT CGAGTGA
```

Seq ID NO: 68 Protein sequence
Protein Accession #: EOS sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPGGCSRGPA AGDGRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD   60
QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLASNHFLY LPRDVLAQLP  120
SLRHLDLSNN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAELQGL PHIRVFLDNN  180
PWVCDCHMAD MVTWLKETEV VQGKDRLTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT  240
SYVFLGIVLA LIGAIFLLVL YLNRKGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL  300
SSNSDVLE
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Seq ID NO: 69 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

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1          11         21         31         41         51
|          |          |          |          |          |
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CAGCACCCAG CTCCCCGCCA CCGCCATGGT CCCCGACACC GCCTGCGTTC TTCTGCTCAC   60
CCTGGCTGCC CTCGGCGCGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC  120
GCAGATGCTT CGGGAACTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT  180
GCGGCAGCAG GTCAGGGAGA TCACGTTCCT GAAAAACACG GTGATGGAGT GTGACGCGTG  240
CGGGATGCAG CAGTCAGTAC GCACCGGCCT ACCCAGCGTG CGGCCCCTGC TCCACTGCGC  300
GCCCGGCTTC TGCTTCCCCG GCGTGGCCTG CATCCAGACG GAGAGCGGCG GCCGCTGCGG  360
CCCCTGCCCC GCGGGCTTCA CGGGCAACGG CTCGCACTGC ACCGACGTCA ACGAGTGCAA  420
CGCCCACCCC TGCTTCCCCC GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA  480
GGCTTGCCCG CCGGGGTACA GCGGCCCCAC CCACCAGGGC GTGGGGCTGG CTTTCGCCAA  540
GGCCAACAAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACTGCGT  600
CCCCAACTCC GTGTGCATCA ACACCCGGGG CTCCTTCCAG TGCGGCCCGT GCCAGCCCGG  660
CTTCGTGGGC GACCAGGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCCGACGG  720
CTCGCCCAGC GAGTGCCACG AGCATGCAGA CTGCGTCCTA GAGCGCGATG GCTCGCGGTC  780
GTGCGTGTGT CGCGTTGGCT GGGCCGGCAA CGGGATCCTC TGTGGTCGCG ACACTGACCT  840
AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCCGGAGCCG CAGTGCCGTA AGGACAACTG  900
CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCCTG  960
CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGCG 1020
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCCG 1080
GTCCCAGAAG AACGACGACC AAAAGGACAC AGACCAGGAC GGCCGGGGCG ATGCGTGCGA 1140
CGACGACATC GACGGCGACC GGATCCGCAA CCAGGCCGAC AACTGCCCTA GGGTACCCAA 1200
CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260
GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACTGTC CCACGGTGCC 1380
TAACAGTGCC CAGGAGGACT CAGACCACGA TGGCCAGGGT GATGCCTGCG ACGACGACGA 1440
CGACAATGAC GGAGTCCCTG ACAGTCGGGA CAACTGCCGC CTGGTGCCTA ACCCCGGCCA 1500
GGAGGACGCG GACAGGGACG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620
GGCCTTCCAG ACAGTCGTGC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740
GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCACG TTCCATGTGA ACACGGTCAC 1800
GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860
CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920
GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA 1980
CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
AAACGTGGGT TGGAAGGACA AGAAGTCCTA TCGTTGGTTC CTGCAGCACC GGCCCCAAGT 2100
GGGCTACATC AGGGTGCGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
CTTGGACACA ACCATGCGGG GTGGCCGCCT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
TCAGCTGCGG CAAGCCTAGG GACCAGGGTG AGGACCCGCC GGATGACAGC CACCCTCACC 2340
GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCCTGAGG GGGAAGTGAG 2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG
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Seq ID NO: 70 Protein sequence
Protein Accession #: NP_000086.1

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1          11         21         31         41         51
|          |          |          |          |          |
MVPDTACVLL LTLAALGASG QGQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQQVREIT   60
FLKNTVMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG  120
NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD  180
INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH  240
ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSGQ  300
EDVDRDGIGD ACDPDADGDG VPNEKDNCPL VRNPDQRNTD EDKWGDACDN CRSQKNDDQK  360
DTDQDGRGDA CDDDIDGDRI RNQADNCPRV PNSDQKDSDG DGIGDACDNC PQKSNPDQAD  420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPDS  480
RDNCRLVPNP GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD  540
PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI  600
FGYQDSSSFY VVMWKQMEQT YWQANPFRAV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT  660
ESQVRLLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG  720
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA
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Seq ID NO: 71 DNA sequence
Nucleic Acid Accession #: NM_024626
Coding sequence: 71..919

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1          11         21         31         41         51
|          |          |          |          |          |
GAGTCACCAA GGAAGGCAGC GGCAGCTCCA CTCAGCCAGT ACCCAGATAC GCTGGGAACC   60
TTCCCCAGCC ATGGCTTCCC TGGGGCAGAT CCTCTTCTGG AGCATAATTA GCATCATCAT  120
TATTCTGGCT GGAGCAATTG CACTCATCAT TGGCTTTGGT ATTTCAGGGA GACACTCCAT  180
CACAGTCACT ACTGTCGCCT CAGCTGGGAA CATTGGGGAG GATGGAATCC TGAGCTGCAC  240
TTTTGAACCT GACATCAAAC TTTCTGATAT CGTGATACAA TGGCTGAAGG AAGGTGTTTT  300
AGGCTTGGTC CATGAGTTCA AAGAAGGCAA AGATGAGCTG TCGGAGCAGG ATGAAATGTT  360
CAGAGGCCGG ACAGCAGTGT TTGCTGATCA AGTGATAGTT GGCAATGCCT CTTTGCGGCT  420
GAAAAACGTG CAACTCACAG ATGCTGGCAC CTACAAATGT TATATCATCA CTTCTAAAGG  480
CAAGGGGAAT GCTAACCTTG AGTATAAAAC TGGAGCCTTC AGCATGCCGG AAGTGAATGT  540
GGACTATAAT GCCAGCTCAG AGACCTTGCG GTGTGAGGCT CCCCGATGGT TCCCCCAGCC  600
CACAGTGGTC TGGGCATCCC AAGTTGACCA GGGAGCCAAC TTCTCGGAAG TCTCCAATAC  660
CAGCTTTGAG CTGAACTCTG AGAATGTGAC CATGAAGGTT GTGTCTGTGC TCTACAATGT  720
TACGATCAAC AACACATACT CCTGTATGAT TGAAAATGAC ATTGCCAAAG CAACAGGGGA  780
TATCAAAGTG ACAGAATCGG AGATCAAAAG GCGGAGTCAC CTACAGCTGC TAAACTCAAA  840
GGCTTCTCTG TGTGTCTCTT CTTTCTTTGC CATCAGCTGG GCACTTCTGC CTCTCAGCCC  900
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AAAAAAAAAA A

Seq ID NO: 72 Protein sequence
Protein Accession #: NP_078902
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DIKLSDIVIQ WLKEGVLGLV HEFKEGKDEL SEQDEMFRGR TAVFADQVIV GNASLRLKNV 120
QLTDAGTYKC YIITSKGKGN ANLEYKTGAF SMPEVNVDYN ASSETLRCEA PRWFPQPTVV 180
WASQVDQGAN FSEVSNTSFE LNSENVTMKV VSVLYNVTIN NTYSCMIEND IAKATGDIKV 240
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Seq ID NO: 73 DNA sequence
Nucleic Acid Accession #: XM_057014
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Seq ID NO: 74 Protein sequence
Protein Accession #: XP_057014
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GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIIYLDQ 180
GSPEMNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIIEE 240
LPK

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TCTGCAGCCG GCTCCCAGGG AGATCTCGGT GGAACTTCAG AAACGCTGGG CAGTCTGCCT 240
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CGTGGTAACT GTGGTGCTGG GCCAGGACGC AAAACTGCCC TGCTTCTACC GAGGGGACTC 420
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GGCGCGGCTG CGGCTCCGAG TGCTGGTGCC TCCCCTGCCC TCACTGAATC CTGGTCCAGC 720
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CTCCCGCTCT GCTGCCGTCA CCTCAGAGTT CCACTTGGTG CCTAGCCGCA GCATGAATGG 900
GCAGCCACTG ACTTGTGTGG TGTCCCATCC TGGCCTGCTC CAGGACCAAA GGATCACCCA 960
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Seq ID NO: 76 Protein sequence
Protein Accession #: AAH10423

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DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS   180
VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL   240
HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL   300
GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL   360
FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA   420
EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ   480
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Seq ID NO: 77 DNA sequence
Nucleic Acid Accession #: NM_003474.2
Coding sequence: 37..3036

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CCGGAGCTGA CTCGCCGAGG CAGGAAATCC CTCCGGTCGC GACGCCCGGC CCCGCTCGGC   240
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GCCGGTGCTC TGCTCGCGCC CTGCGAGGCC CGAGGGGTGA GCTTATGGAA CGAAGGAAGA   420
GCTGATGAAG TTGTCAGTGC CTCTGTTCGG AGTGGGGACC TCTGGATCCC AGTGAAGAGC   480
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CTGATCATAA ATCTGGAAAG AAATGAAGGT CTCATTGCCA GCAGTTTCAC GGAAACCCAC   600
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CAGACATGGG CAAGAAGGCA TAAAAGAGAG ACCCTCAAGG CAACTAAGTA TGTGGAGCTG   960
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GAGTGTGCAA TGCAGTGCCA CGGCAGAGGG GTGTGCAACA ACAGGAAGAA CTGCCACTGC  2340
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Seq ID NO: 78 Protein sequence
Protein Accession #: NP_003465

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SHHNTPNLAA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR   240
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Seq ID NO: 79 DNA sequence
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Coding sequence: 135..1043

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ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGGAG ATCCAGCACT   300
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AGGGGGTGCT TGGTGCCAAA CTGAAATTCA GTTTCTTGTG TGGGGCCTTG CGGTTCAGAG  1620
CTCTTGGCGA GGGTGGAGGG AGGAGTGTCA TTTCTATGTG TAATTTCTGA GCCATTGTAC  1680
TGTCTGGGCT GGGGGGGACA CTGTCCAAGG GAGTGGCCCC TATGAGTTTA TATTTTAACC  1740
ACTGCTTCAA ATCTCGATTT CACTTTTTTT ATTTATCCAG TTATATCTAC ATATCTGTCA  1800
TCTAAATAAA TGGCTTTCAA ACAAAGCAAC TGGGTCATTA AAACCAGCTC AAAGGGGGTT  1860
TAAAAAAAAA AAAACCAGCC CATCCTTTGA GGCTGATTTT TCTTTTTTTT AAGTTCTATT  1920
TTAAAAGCTA TCAAACAGCG ACATAGCCAT ACATCTGACT GCCTGACATG GACTCCTGCC  1980
CACTTGGGGG AAACCTTATA CCCAGAGGAA AATACACACC TGGGGAGTAC ATTTGACAAA  2040
TTTCCCTTAG GATTTCGTTA TCTCACCTTG ACCCTCAGCC AAGATTGGTA AAGCTGCGTC  2100
CTGGCGATTC CAGGAGACCC AGCTGGAAAC CTGGCTTCTC CATGTGAGGG GATGGGAAAG  2160
GAAAGAAGAG AATGAAGACT ACTTAGTAAT TCCCATCAGG AAATGCTGAC CTTTTACATA  2220
AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAA  2280
TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA  2340
GGGAGAGGAA GAAAAGAGAG AGAGAAAAGA GCCTCGTGCC
```

Seq ID NO: 80 Protein sequence
Protein Accession #: NP_003705

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1          11         21         31         41         51
|          |          |          |          |          |
MCAERLGQFM TLALVLATFD PARGTDATNP PEGPQDRSSQ QKGRLSLQNT AEIQHCLVNA    60
GDVGCGVFEC FENNSCEIRG LHGICMTFLH NAGKFDAQGK SFIKDALKCK AHALRHRFGC   120
ISRKCPAIRE MVSQLQRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT   180
CGEEVKEAIT HSVQVQCEQN WGSLCSILSF CTSAIQKPPT APPERQPQVD RTKLSRAHHG   240
EAGHHLPEPS SRETGRGAKG ERGSKSHPNA HARGRVGGLG AQGPSGSSEW EDEQSEYSDI   300
RR
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Seq ID NO: 81 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
AATCATGTTT TTGGAATAAA AATGGTAAAT GTTTTTTTTT TTTTTTTTTT GTTAGTAATG    60
GAAGTATTCT ATTATTTTTA ATTTTATGTA TGTACAGACA AGAGCTATAT GGGAAAGTAG   120
CTATTACAGA CCCATTATAG TTTCATCATT TATAACCAGG GTTGGTAGTA AAGCAACAGA   180
AATACATCTT CAATGCAGAC TTGCTCCCAG CATCTCTTTC CTTTCATCCT TGACCATATT   240
GCATCCTGGA CAGGAAGAAG ACATCCTCAG CCCACCACCC CTTCCCCTCC AATGTGGACT   300
GAGTGTTGGG TCAACTGATA AGCAGTGCAG ACTCTTCATT TTGCTTTGTT GGTGCCTTGG   360
AGGCATGTGA GGGCACAGCC TCAAATTCCA GAGACCTTGC CTTCAGGATT TGAGGTGGGC   420
AAAGATGTGA AAGAAGACCT TTAGCCACTC AGTGTTATCA AAAGCAATCA CCAAAGAAGT   480
TTTTGCATCT GGCATTGTGT TGGGACGTCC ATCAGCAGTA CCGTACGGTC TCTTTACTGG   540
ACAAGTATTT ACACCTTGTT AACAGCAGTG TACACCCGGT GGAAAACTCC TATCTAATGG   600
CATGGCAGAA TTGTAAACAT TTCCTCCTTC ACCAAATTTG TGGATGGAAT AAACATGTAG   660
CCTTAAACTT TATTGGCTTC TCCGGTCTTG CCACTGCGGG GCCCAAAAAC TTTCAGAAGT   720
AGGAATCCTG TGGCATCTGC TAATGGTGAT TGGAAGAAAG AGTAGAGGTG ACAGTATCTA   780
TGGGTGCAGT ACCAGAACTA TTACGAAATG TTCCAGCTGC GATTTCAGAG GAATCCCCCC   840
TGACCCCTGG ACGTGGTTCT CCTATTTCAG TCACCCTGTG CCG
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Seq ID NO: 82 DNA sequence
Nucleic Acid Accession #: XM_061091.1
Coding sequence: 1..2481

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1          11         21         31         41         51
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ATGCCAAATA CTTCAGGAAC AACCAGGATT GAAATTTGGC TTCTCCAAGA GCCGCCCGGG    60
CACCGAGCGC TGGTCGCCGC TCTCCTTCCG GTGAGTCCCA GCCCCGAGTT GGCTCTGGCG   120
CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT   180
CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTTA   240
GTTGGGAAGC CTCCTTTTGA GGCAAACGAA GTCCATGTAA GCAAAGAAAC CATCGGGAAG   300
ATTTCAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTTCTGTTA   360
GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA   420
GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT   480
TCCACTCCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA   540
AGAATCAAGA GGATGGTTTT CAAAGGAGGG CGCACGGAGA CGGAACTTGC TCTGAAATAC   600
CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC   660
GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG   720
GGTGTCACTG TGTTTGCTGT GGGGGTCAGG TTTCCCAGGT GGGAGGAGCT GCATGCACTG   780
GCCAGCGAGC CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC   840
GGCCTCTTCA GCACCCTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC   900
CCCGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG   960
CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCTC  1020
TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG  1080
GTCGACCTCC TCTTCCTGCT GGACAGCTCT GCGGGCACCA CTCTGGACGG CTTCCTGCGG  1140
GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCCGTGCTGA GCGAGGACTC TCGGGCCCGA  1200
GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCCTGTGGG GGAGTACCAG  1260
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GATGTGCCTG ACCTGGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGGTGG CCCCACCCTG  1320
ACGGGCAGTG CCTTGCGGCA GGCGGCAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC  1380
CAGGACCGGC CACGTAGAGT GGTGGTTTTG CTCACTGAGT CACACTCCGA GGATGAGGTT  1440
GCGGGCCCAG CGCGTCACGC AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG  1500
GCCGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG  1560
GATCCTCAGG ATCTGTTCAA CCAAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG  1620
CGGCCAGGGT GCCGGACACA AGCCCTGGAC CTCGTCTTCA TGTTGGACAC CTCTGCCTCA  1680
GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT  1740
GAGGTGAACC CTGACGTGAC ACAGGTCGGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT  1800
GCCTTCGGGC TGGACACCAA ACCCACCCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC  1860
CCCTACCTAG GTGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGCACATCTA TGACAAAGTG  1920
ATGACCGTCC AGAGGGGTGC CCGGCCTGGT GTCCCCAAAG CTGTGGTGGT GCTCACAGGC  1980
GGGAGAGGCG CAGAGGATGC AGCCGTTCCT GCCCAGAAGC TGAGGAACAA TGGCATCTCT  2040
GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC  2100
CGGGATTCCC TGATCCACGT GGCAGCTTAC GCCGACCTGC GGTACCACCA GGACGTGCTC  2160
ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAAACC CAGCCCGTGC  2220
ATGAATGAGG GCAGCTGCGT CCTGCAGAAT GGGAGCTACC GCTGCAAGTG TCGGGATGGC  2280
TGGGAGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG  2340
GGATGGATTC TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT  2400
ACCCCTCCCA GCAACTACAG AGAAGGCCTG GGCACTGAAA TGGTGCCTAC CTTCTGGAAT  2460
GTCTGTGCCC CAGGTCCTTA G
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Seq ID NO: 83 Protein sequence
Protein Accession #: XP_061091.1 .

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1          11         21         31         41         51
|          |          |          |          |          |
MPNTSGTTRI EIWLLQEPPG HRALVAALLP VSPSPELALA PGYPPVPAAD DRFTLPMIGG    60
QMHGEKVDLW SLGVLCYEFL VGKPPFEANE VHVSKETIGK ISAASKMMWC SAAVDIMFLL   120
DGSNSVGKGS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQQEVKA   180
RIKRMVFKGG RTETELALKY LLHRGLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER   240
GVTVFAVGVR FPRWEELHAL ASEPRGQHVL LAEQVEDATN GLFSTLSSSA ICSSATPAGS   300
PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR   360
VDLLFLLDSS AGTTLDGFLR AKVFVKRFVR AVLSEDSRAR VGVATYSREL LVAVPVGEYQ   420
DVPDLVWSLD GIPFRGGPTL TGSALRQAAE RGFGSATRTG QDRPRRVVVL LTESHSEDEV   480
AGPARHARAR ELLLLGVGSE AVRAELEEIT GSPKHVMVYS DPQDLFNQIP ELQGKLCSRQ   540
RPGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSCALQF EVNPDVTQVG LVVYGSQVQT   600
AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG   660
GRGAEDAAVP AQKLRNNGIS VLVVGVGPVL SEGLRRLAGP RDSLIHVAAY ADLRYHQDVL   720
IEWLCGEAKQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ   780
GWILETPLRH MAPVQEGSSR TPPSNYREGL GTEMVPTFWN VCAPGP
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Seq ID NO: 84 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

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1          11         21         31         41         51
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TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC   120
AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC   180
AGCGTCGGGA AAGGGAGCTT TGAAAGGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT   240
CTGGACATCA GCCCCGAGAG GGTCAGAGTG GGAGCATTCC AGTTCAGTTC CACTCCTCAT   300
CTGGAATTCC CCTTGGATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG   360
ATGGTTTTCA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAAATACCT TCTGCACAGA   420
GGGTTGCCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG   480
AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG   540
TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT   600
AGAGGGCAGC ACGTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC   660
ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC   720
CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTCG CTGGCAATGC CCCATGCTGG   780
AGAGGATCGC GGCGGACCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG   840
AGAGTGTTCC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCCTGTGAC   900
TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAGTGC   960
CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCTGGAATGC  1020
AGGGTCGACC TCCTCTTCCT GCTGGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCCTG  1080
CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC  1140
CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCCTGT GGGGGAGTAC  1200
CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATTC CCTTCCGTGG TGGCCCCACC  1260
CTGACGGGCA GTGCCTTGCG GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA  1320
GGCCAGGACC GGCCACGTAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG  1380
GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT  1440
GAGGCCGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC  1500
TCGGATCCTC AGGATCTGTT CAACCAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG  1560
CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC  1620
TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG  1680
TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG  1740
ACTGCCTTCG GGCTGGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG  1800
GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA  1860
GTGATGACCG TCCAGAGGGG TGCCCGGCCT GGTGTCCCCA AAGCTGTGGT GGTGCTCACA  1920
GGCGGGAGAG GCGCAGAGGA TGCAGCCGTT CCTGCCCAGA AGCTGAGGAA CAATGGCATC  1980
TCTGTCTTGG TCGTGGGCGT GGGGCCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT  2040
CCCCGGGATT CCCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG  2100
CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG  2160
TGCATGAATG AGGGCAGCTG CGTCCTGCAG AATGGGAGCT ACCGCTGCAA GTGTCGGGAT  2220
GGCTGGGAGG GCCCCCACTG CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC  2280
CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC  2340
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CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG  2400
AATGTCTGTG CCCCAGGTCC TTAG
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Seq ID NO: 85 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN    60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEPPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL   360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS   780
RTPPSNYREG LGTEMVPTFW NVCAPGP
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Seq ID NO: 86 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 89..2356

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1          11         21         31         41         51
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GCCCCCTGGC CCGAGCCGCG CCCGGGTCTG TGAGTAGAGC CGCCCGGGCA CCGAGCGCTG    60
GTCGCCGCTC TCCTTCCGTT ATATCAACAT GCCCCCTTTC CTGTTGCTGG AAGCCGTCTG   120
TGTTTTCCTG TTTTCCAGAG TGCCCCCATC TCTCCCTCTC CAGGAAGTCC ATGTAAGCAA   180
AGAAACCATC GGGAAGATTT CAGCTGCCAG CAAAATGATG TGGTGCTCGG CTGCAGTGGA   240
CATCATGTTT CTGTTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGGTCCAA   300
GCACTTTGCC ATCACAGTCT GTGACGGTCT GGACATCAGC CCCGAGAGGG TCAGAGTGGG   360
AGCATTCCAG TTCAGTTCCA CTCCTCATCT GGAATTCCCC TTGGATTCAT TTTCAACCCA   420
ACAGGAAGTG AAGGCAAGAA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CGGAGACGGA   480
ACTTGCTCTG AAATACCTTC TGCACAGAGG GTTGCCTGGA GGCAGAAATG CTTCTGTGCC   540
CCAGATCCTC ATCATCGTCA CTGATGGGAA GTCCCAGGGG GATGTGGCAC TGCCATCCAA   600
GCAGCTGAAG GAAAGGGGTG TCACTGTGTT TGCTGTGGGG GTCAGGTTTC CCAGGTGGGA   660
GGAGCTGCAT GCACTGGCCA GCGAGCCTAG AGGGCAGCAC GTGCTGTTGG CTGAGCAGGT   720
GGAGGATGCC ACCAACGGCC TCTTCAGCAC CCTCAGCAGC TCGGCCATCT GCTCCAGCGC   780
CACGCCAGAC TGCAGGGTCG AGGCTCACCC CTGTGAGCAC AGGACGCTGG AGATGGTCCG   840
GGAGTTCGCT GGCAATGCCC CATGCTGGAG AGGATCGCGG CGGACCCTTG CGGTGCTGGC   900
TGCACACTGT CCCTTCTACA GCTGGAAGAG AGTGTTCCTA ACCCACCCTG CCACCTGCTA   960
CAGGACCACC TGCCCAGGCC CCTGTGACTC GCAGCCCTGC CAGAATGGAG GCACATGTGT  1020
TCCAGAAGGA CTGGACGGCT ACCAGTGCCT CTGCCCGCTG GCCTTTGGAG GGGAGGCTAA  1080
CTGTGCCCTG AAGCTGAGCC TGGAATGCAG GGTCGACCTC CTCTTCCTGC TGGACAGCTC  1140
TGCGGGCACC ACTCTGGACG GCTTCCTGCG GGCCAAAGTC TTCGTGAAGC GGTTTGTGCG  1200
GGCCGTGCTG AGCGAGGACT CTCGGGCCCG AGTGGGTGTG GCCACATACA GCAGGGAGCT  1260
GCTGGTGGCG GTGCCTGTGG GGGAGTACCA GGATGTGCCT GACCTGGTCT GGAGCCTCGA  1320
TGGCATTCCC TTCCGTGGTG GCCCCACCCT GACGGGCAGT GCCTTGCGGC AGGCGGCAGA  1380
GCGTGGCTTC GGGAGCGCCA CCAGGACAGG CCAGGACCGG CCACGTAGAG TGGTGGTTTT  1440
GCTCACTGAG TCACACTCCG AGGATGAGGT TGCGGGCCCA GCGCGTCACG CAAGGGCGCG  1500
AGAGCTGCTC CTGCTGGGTG TAGGCAGTGA GGCCGTGCGG GCAGAGCTGG AGGAGATCAC  1560
AGGCAGCCCA AAGCATGTGA TGGTCTACTC GGATCCTCAG GATCTGTTCA ACCAAATCCC  1620
TGAGCTGCAG GGGAAGCTGT GCAGCCGGCA GCGGCCAGGG TGCCGGACAC AAGCCCTGGA  1680
CCTCGTCTTC ATGTTGGACA CCTCTGCCTC AGTAGGGCCC GAGAATTTTG CTCAGATGCA  1740
GAGCTTTGTG AGAAGCTGTG CCCTCCAGTT TGAGGTGAAC CCTGACGTGA CACAGGTCGG  1800
CCTGGTGGTG TATGGCAGCC AGGTGCAGAC TGCCTTCGGG CTGGACACCA AACCCACCCG  1860
GGCTGCGATG CTGCGGGCCA TTAGCCAGGC CCCCTACCTA GGTGGGGTGG GCTCAGCCGG  1920
CACCGCCCTG CTGCACATCT ATGACAAAGT GATGACCGTC CAGAGGGGTG CCCGGCCTGG  1980
TGTCCCCAAA GCTGTGGTGG TGCTCACAGG CGGGAGAGGC GCAGAGGATG CAGCCGTTCC  2040
TGCCCAGAAG CTGAGGAACA ATGGCATCTC TGTCTTGGTC GTGGGCGTGG GGCCTGTCCT  2100
AAGTGAGGGT CTGCGGAGGC TTGCAGGTCC CCGGGATTCC CTGATCCACG TGGCAGCTTA  2160
CGCCGACCTG CGGTACCACC AGGACGTGCT CATTGAGTGG CTGTGTGGAG AAGCCAAGCA  2220
GCCAGTCAAC CTCTGCAAAC CCAGCCCGTG CATGAATGAG GGCAGCTGCG TCCTGCAGAA  2280
TGGGAGCTAC CGCTGCAAGT GTCGGGATGG CTGGGAGGGC CCCCACTGCG AGAACCGATT  2340
CTTGAGACGC CCCTGAGGCA CATGGCTCCC GTGCAGGAGG GCAGCAGCCG TACCCCTCCC  2400
AGCAACTACA GAGAAGGCCT GGGCACTGAA ATGGTGCCTA CCTTCTGGAA TGTCTGTGCC  2460
CCAGGTCCTT AGAATGTCTG CTTCCCGCCG TGGCCAGGAC CACTATTCTC ACTGAGGGAG  2520
GAGGATGTCC CAACTGCAGC CATGCTGCTT AGAGACAAGA AAGCAGCTGA TGTCACCCAC  2580
AAACGATGTT GTTGAAAAGT TTTGATGTGT AAGTAAATAC CCACTTTCTG TACCTGCTGT  2640
GCCTTGTTGA GGCTATGTCA TCTGCCACCT TTCCCTTGAG GATAAACAAG GGGTCCTGAA  2700
GACTTAAATT TAGCGGCCTG ACGTTCCTTT GCACACAATC AATGCTCGCC AGAATGTTGT  2760
TGACACAGTA ATGCCCAGCA GAGGCCTTTA CTAGAGCATC CTTTGGACGG
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Seq ID NO: 87 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN    60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEPPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL   360
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RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP
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Seq ID NO: 88 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

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AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA    120
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC    180
TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG    240
CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT    300
GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA    360
GGGAACTGGT TCTCTGCCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT    420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG    480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT    540
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG    600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC    660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC    720
CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA    780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA    840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC    900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA    960
GCCACCCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT   1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT   1080
GCGTACCAGG GGGAAGTCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG   1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG   1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCCAGG AGTATACACC   1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
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Seq ID NO: 89 Protein sequence:
Protein Accession #: NP_063947.1

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1          11         21         31         41         51
|          |          |          |          |          |
MLQDPDSDQP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY     60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT    120
GNWFSACFDN FTEALAETAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELRMRNSS    180
GPCLSGSLVS LHCLACGKSL KTPRVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHWV    240
LTAAHCFRKH TDVFNWKVRA GSDKLGSFPS LAVAKIIIIE FNPMYPKDND IALMKLQFPL    300
TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD    360
AYQGEVTEKM MCAGIPEGGV DTCQGDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT    420
KVSAYLNWIY NVWKAEL
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Seq ID NO: 90 DNA sequence
Nucleic Acid Accession #: NM_002776.1
Coding sequence: 82..912

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1          11         21         31         41         51
|          |          |          |          |          |
ACCAGCGGCA GACCACAGGC AGGGCAGAGG CACGTCTGGG TCCCCTCCCT CCTTCCTATC     60
GGCGACTCCC AGATCCTGGC CATGAGAGCT CCGCACCTCC ACCTCTCCGC CGCCTCTGGC    120
GCCCGGGCTC TGGCGAAGCT GCTGCCGCTG CTGATGGCGC AACTCTGGGC CGCAGAGGCG    180
GCGCTGCTCC CCCAAAACGA CACGCGCTTG GACCCCGAAG CCTATGGCGC CCCGTGCGCG    240
CGCGGCTCGC AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGCGCGGGT    300
GTCCTGGTGG ACCAGAGTTG GGTGCTGACG GCCGCGCACT GCGGAAACAA GCCACTGTGG    360
GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTCAGGGCG AGCAGCTCCG CCGGACGACT    420
CGCTCTGTTG TCCATCCCAA GTACCACCAG GGCTCAGGCC CCATCCTGCC AAGGCGAACG    480
GATGAGCACG ATCTCATGTT GCTAAAGCTG GCCAGGCCCG TAGTGCCGGG GCCCCGCGTC    540
CGGGCCCTGC AGCTTCCCTA CCGCTGTGCT CAGCCCGGAG ACCAGTGCCA GGTTGCTGGC    600
TGGGGCACCA CGGCCGCCCG GAGAGTGAAG TACAACAAGG GCCTGACCTG CTCCAGCATC    660
ACTATCCTGA GCCCTAAAGA GTGTGAGGTC TTCTACCCTG GCGTGGTCAC CAACAACATG    720
ATATGTGCTG GACTGGACCG GGGCCAGGAC CCTTGCCAGA GTGACTCTGG AGGCCCCCTG    780
GTCTGTGACG AGACCCTCCA AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC    840
CAGCATCCAG CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA    900
CGCTCCAACT GATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT CCTGCTGATC    960
CAGATGCCCA GAGGCTCCAT CGTCCATCCT CTTCCTCCCC AGTCGGCTGA ACTCTCCCCT   1020
TGTCTGCACT GTTCAAACCT CTGCCGCCCT CCACACCTCT AAACATCTCC CCTCTCACCT   1080
CATTCCCCCA CCTATCCCCA TTCTCTGCCT GTACTGAAGC TGAAATGCAG GAAGTGGTGG   1140
CAAAGGTTTA TTCCAGAGAA GCCAGGAAGC CGGTCATCAC CCAGCCTCTG AGAGCAGTTA   1200
CTGGGGTCAC CCAACCTGAC TTCCTCTGCC ACTCCCCGCT GTGTGACTTT GGGCAAGCCA   1260
AGTGCCCTCT CTGAACCTCA GTTTCCTCAT CTGCAAAATG GGAACAATGA CGTGCCTACC   1320
TCTTAGACAT GTTGTGAGGA GACTATGATA TAACATGTGT ATGTAAATCT TCATGTGATT   1380
GTCATGTAAG GCTTAACACA GTGGGTGGTG AGTTCTGACT AAAGGTTACC TGTTGTCGTG   1440
AAAAAAAAAA AAAA
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Seq ID NO: 91 Protein sequence
Protein Accession #: NP_002767.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRAPHLHLSA ASGARALAKL LPLLMAQLWA AEAALLPQND TRLDPEAYGA PCARGSQPWQ     60
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VSLFNGLSFH CAGVLVDQSW VLTAAHCGNK PLWARVGDDH LLLLQGEQLR RTTRSVVHPK   120
YHQGSGPILP RRTDEHDLML LKLARPVVPG PRVRALQLPY RCAQPGDQCQ VAGWGTTAAR   180
RVKYNKGLTC SSITILSPKE CEVFYPGVVT NNMICAGLDR GQDPCQSDSG GPLVCDETLQ   240
GILSWGVYPC GSAQHPAVYT QICKYMSWIN KVIRSN
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Seq ID NO: 92 DNA sequence
Nucleic Acid Accession #: NM_032044.1
Coding sequence: 182-658

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1          11         21         31         41         51
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AAGATATAAA AGCTCCAGAA ACGTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG     60
GCCCTTAGAG TCTTGGTTGC CAAACAGATT TGCAGATCAA GGAGAACCCA GGAGTTTCAA    120
AGAAGCGCTA GTAAGGTCTC TGAGATCCTT GCACTAGCTA CATCCTCAGG GTAGGAGGAA    180
GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCTGGCCA AAACAGGAGT    240
CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTTACC ACAAGTCCAA    300
TTGCTATGGT TACTTCAGGA AGCTGAGGAA CTGGTCTGAT GCCGAGCTCG AGTGTCAGTC    360
TTACGGAAAC GGAGCCCACC TGGCATCTAT CCTGAGTTTA AAGGAAGCCA GCACCATAGC    420
AGAGTACATA AGTGGCTATC AGAGAAGCCA GCCGATATGG ATTGGCCTGC ACGACCCACA    480
GAAGAGGCAG CAGTGGCAGT GGATTGATGG GGCCATGTAT CTGTACAGAT CCTGGTCTGG    540
CAAGTCCATG GGTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTTAAC    600
TTGGAGCAGC AACGAATGCA ACAAGCGCCA ACACTTCCTG TGCAAGTACC GACCATAGAG    660
CAAGAATCAA GATTCTGCTA ACTCCTGCAC AGCCCCGTCC TCTTCCTTTC TGCTAGCCTG    720
GCTAAATCTG CTCATTATTT CAGAGGGGAA ACCTAGCAAA CTAAGAGTGA TAAGGGCCCT    780
ACTACACTGG CTTTTTTAGG CTTAGAGACA GAAACTTTAG CATTGGCCCA GTAGTGGCTT    840
CTAGCTCTAA ATGTTTGCCC CGCCATCCCT TTCCACAGTA TCCTTCTTCC CTCCTCCCCT    900
GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT    960
CTTTGGCCAT AAGAAGTAAA GATTTGAAGA CAGAAGGAAG AAACTCAGGA GTAAGCTTCT   1020
AGACCCCTTC AGCTTCTACA CCCTTCTGCC CTCTCTCCAT TGCCTGCACC CCACCCCAGC   1080
CACTCAACTC CTGCTTGTTT TTCCTTTGGC CATAGGAAGG TTTACCAGTA GAATCCTTGC   1140
TAGGTTGATG TGGGCCATAC ATTCCTTTAA TAAACCATTG TGTACATAAG AAAAAAAAAA
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Seq ID NO: 93 Protein sequence
Protein Accession #: NP_114433.1

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1          11         21         31         41         51
|          |          |          |          |          |
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKSN CYGYFRKLRN WSDAELECQS     60
YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG    120
KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP
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Seq ID NO: 94 DNA sequence
Nucleic Acid Accession #: XM_051860
Coding sequence: 1..4086

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1          11         21         31         41         51
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GAGCTAGCGC TCAAGCAGAG CCCAGCGCGG TGCTATCGGA CAGAGCCTGG CGAGCGCAAG     60
CGGCGCGGGG AGCCAGCGGG GCTGAGCGCG GCCAGGGTCT GAACCCAGAT TTCCCAGACT    120
AGCTACCACT CCGCTTGCCC ACGCCCCGGG AGCTCGCGGC GCCTGGCGGT CAGCGACCAG    180
ACGTCCGGGG CCGCTGCGCT CCTGGCCCGC GAGGCGTGAC ACTGTCTCGG CTACAGACCC    240
AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCCTC TTCAAGGCCA    300
TGCTGACCAT CAGCTGGCTC ACTCTGACCT GCTTCCCTGG GGCCACATCC ACAGTGGCTG    360
CTGGGTGCCC TGACCAGAGC CCTGAGTTGC AACCCTGGAA CCCTGGCCAT GACCAAGACC    420
ACCATGTGCA TATCGGCCAG GGCAAGACAC TGCTGCTCAC CTCTTCTGCC ACGGTCTATT    480
CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT    540
TGCGAACCCG GCACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGCCCTCT    600
GCCCTTTCCA GGGCAATTTC ACCATCATTT TGTATGGAAG GGCTGATGAA GGTATTCAGC    660
CGGATCCTTA CTATGGTCTG AAGTACATTG GGGTTGGTAA AGGAGGCGCT CTTGAGTTGC    720
ATGGACAGAA AAAGCTCTCC TGGACATTTC TGAACAAGAC CCTTCACCCA GGTGGCATGG    780
CAGAAGGAGG CTATTTTTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA    840
TCGACCCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA    900
AAGAGAGTGA ACGTCTGGTC CAGTATTTGA ACGCGGTGCC CGATGGCAGG ATCCTTTCTG    960
TTGCAGTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA   1020
AATTGGGAAG CAAACACTTC CTGCACCTTG GATTTAGACA CCCTTGGAGT TTTCTAACTG   1080
TGAAAGGAAA TCCATCATCT TCAGTGGAAG ACCATATTGA ATATCATGGA CATCGAGGCT   1140
CTGCTGCTGC CCGGGTATTC AAATTGTTCC AGACAGAGCA TGGCGAATAT TTCAATGTTT   1200
CTTTGTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTCGAT CATGATAAAG   1260
TATCTCAGAC TAAAGGTGGG GAGAAAATTT CAGACCTCTG GAAAGCTCAC CCAGGAAAAA   1320
TATGCAATCG TCCCATTGAT ATACAGGCCA CTACAATGGA TGGAGTTAAC CTCAGCACCG   1380
AGGTTGTCTA CAAAAAAGGC CAGGATTATA GGTTTGCTTG CTACGACCGG GGCAGAGCCT   1440
GCCGGAGCTA CCGTGTACGG TTCCTCTGTG GGAAGCCTGT GAGGCCCAAA CTCACAGTCA   1500
CCATTGACAC CAATGTGAAC AGCACCATTC TGAACTTGGA GGATAATGTA CAGTCATGGA   1560
AACCTGGAGA TACCCTGGTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAGAGT   1620
TCCAGGTGCT TCCCTGCAGA TCCTGCGCCC CCAACCAGGT CAAAGTGGCA GGGAAACCAA   1680
TGTACCTGCA CATCGGGGAG GAGATAGACG GCGTGGACAT GCGGGCGGAG GTTGGGCTTC   1740
TGAGCCGGAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC   1800
ACATCTGCAA TTTCTTTGAC TTCGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT   1860
TTAAGGCAGC ACACTTGGAG GGCACGGAGC TGAAGCATAT GGGACAGCAG CTGGTGGGTC   1920
AGTACCCGAT TCACTTCCAC CTGGCCGGTG ATGTAGACGA AAGGGGAGGT TATGACCCAC   1980
CCACATACAT CAGGGACCTC TCCATCCATC ATACATTCTC TCGCTGCGTC ACAGTCCATG   2040
GCTCCAATGG CTTGTTGATC AAGGACGTTG TGGGCTATAA CTCTTTGGGC CACTGCTTCT   2100
TCACGGAAGA TGGGCCGGAG GAACGCAACA CTTTTGACCA CTGTCTTGGC CTCCTTGTCA   2160
AGTCTGGAAC CCTCCTCCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCACAGAGG   2220
ACTCCTACCC GGGGTACATC CCCAAGCCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT   2280
GGATGGCCAA TCCCAACAAC AACCTCATCA ACTGTGCCGC TGCAGGATCT GAGGAAACTG   2340
GATTTTGGTT TATTTTTCAC CACGTACCAA CGGGCCCCTC CGTGGGAATG TACTCCCCAG   2400
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GTTATTCAGA GCACATTCCA CTGGGAAAAT TCTATAACAA CCGAGCACAT TCCAACTACC 2460
GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCACCGA GGCCTCTGCC AAGGACAAGC 2520
GGCCGTTCCT CTCAATCATC TCTGCCAGAT ACAGCCCTCA CCAGGACGCC GACCCGCTGA 2580
AGCCCCGGGA GCCGGCCATC ATCAGACACT TCATTGCCTA CAAGAACCAG GACCACGGGG 2640
CCTGGCTGCG CGGCGGGGAT GTGTGGCTGG ACAGCTGCCG GTTTGCTGAC AATGGCATTG 2700
GCCTGACCCT GGCCAGTGGT GGAACCTTCC CGTATGACGA CGGCTCCAAG CAAGAGATAA 2760
AGAACAGCTT GTTTGTTGGC GAGAGTGGCA ACGTGGGGAC GGAAATGATG GACAATAGGA 2820
TCTGGGGCCC TGGCGGCTTG GACCATAGCG GAAGGACCCT CCCTATAGGC CAGAATTTTC 2880
CAATTAGAGG AATTCAGTTA TATGATGGCC CCATCAACAT CCAAAACTGC ACTTTCCGAA 2940
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GGCAGAGCTG CCCCCATAAC AACGTGACCG GCATTGCCTT TGAGGACGTT CCGATTACTT 3060
CCAGAGTGTT CTTCGGAGAG CCTGGGCCCT GGTTCAACCA GCTGGACATG GATGGGGATA 3120
AGACATCTGT GTTCCATGAC GTCGACGGCT CCGTGTCCGA GTACCCTGGC TCCTACCTCA 3180
CGAAGAATGA CAACTGGCTG GTCCGGCACC CAGACTGCAT CAATGTTCCC GACTGGAGAG 3240
GGGCCATTTG CAGTGGGTGC TATGCACAGA TGTACATTCA AGCCTACAAG ACCAGTAACC 3300
TGCGAATGAA GATCATCAAG AATGACTTCC CCAGCCACCC TCTTTACCTG GAGGGGGCGC 3360
TCACCAGGAG CACCCATTAC CAGCAATACC AACCGGTTGT CACCCTGCAG AAGGGCTACA 3420
CCATCCACTG GGACCAGACG GCCCCCGCCG AACTCGCCAT CTGGCTCATC AACTTCAACA 3480
AGGGCGACTG GATCCGAGTG GGGCTCTGCT ACCCGCGAGG CACCACATTC TCCATCCTCT 3540
CGGATGTTCA CAATCGCCTG CTGAAGCAAA CGTCCAAGAC GGGCGTCTTC GTGAGGACCT 3600
TGCAGATGGA CAAAGTGGAG CAGAGCTACC CTGGCAGGAG CCACTACTAC TGGGACGAGG 3660
ACTCAGGGCT GTTGTTCCTG AAGCTGAAAG CTCAGAACGA GAGAGAGAAG TTTGCTTTCT 3720
GCTCCATGAA AGGCTGTGAG AGGATAAAGA TTAAAGCTCT GATTCCAAAG AACGCAGGCG 3780
TCAGTGACTG CACAGCCACA GCTTACCCCA AGTTCACCGA GAGGGCTGTC GTAGACGTGC 3840
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AGATGGAGAG TTCCAAGCAG CACTTCTTCC ACCTCTGGAA CGACTTCGCT TACATTGAAG 3960
TGGATGGGAA GAAGTACCCC AGTTCGGAGG ATGGCATCCA GGTGGTGGTG ATTGACGGGA 4020
ACCAAGGGCG CGTGGTGAGC CACACGAGCT TCAGGAACTC CATTCTGCAA GGCATACCAT 4080
GGCAGCTTTT CAACTATGTG GCGACCATCC CTGACAATTC CATAGTGCTT ATGGCATCAA 4140
AGGGAAGATA CGTCTCCAGA GGCCCATGGA CCAGAGTGCT GGAAAAGCTT GGGGCAGACA 4200
GGGGTCTCAA GTTGAAAGAG CAAATGGCAT TCGTTGGCTT CAAAGGCAGC TTCCGGCCCA 4260
TCTGGGTGAC ACTGGACACT GAGGATCACA AAGCCAAAAT CTTCCAAGTT GTGCCCATCC 4320
CTGTGGTGAA GAAGAAGAAG TTGTGAGGAC AGCTGCCGCC CGGTGCCACC TCGTGGTAGA 4380
CTATGACGGT GACTCTTGGC AGCAGACCAG TGGGGGATGG CTGGGTCCCC CAGCCCCTGC 4440
CAGCAGCTGC CTGGGAAGGC CGTGTTTCAG CCCTGATGGG CCAAGGGAAG GCTATCAGAG 4500
ACCCTGGTGC TGCCACCTGC CCCTACTCAA GTGTCTACCT GGAGCCCCTG GGGCGGTGCT 4560
GGCCAATGCT GGAAACATTC ACTTTCCTGC AGCCTCTTGG GTGCTTCTCT CCTATCTGTG 4620
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CTTAAGGAAA TCTTTACTCC TGTAAGCAAG AGCCAACCTC ACAGGATTAG GAGCTGGGGT 4860
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GAGGGCCTGG GGAGCCCCAC CCTAGCCCTT GCTGCCACAC CACATTGCCT CAACAACCGG 5760
CCCCAGAGTG CCCAGGCACT CCTGAGGTAG CTTCTGGAAA TGGGGACAAG TCCCCTCGAA 5820
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GCACACAAAC CCGCCCTCCC CTTGGTGTTG GCGGTCCCTG TGGCCTTCAC TTTGTTCACT 5940
ACCTGTCAGC CCAGCCTGGG TGCACAGTAG CTGCAACTCC CCATTGGTGC TACCTGGCTC 6000
TCCTGTCTCT GCAGCTCTAC AGGTGAGGCC CAGCAGAGGG AGTAGGGCTC GCCATGTTTC 6060
TGGTGAGCCA ATTTGGCTGA TCTTGGGTGT CTGAACAGCT ATTGGGTCCA CCCCAGTCCC 6120
TTTCAGCTGC TGCTTAATGC CCTGCTCTCT CCCTGGCCCA CCTTATAGAG AGCCCAAAGA 6180
GCTCCTGTAA GAGGGAGAAC TCTATCTGTG GTTTATAATC TTGCACGAGG CACCAGAGTC 6240
TCCCTGGGTC TTGTGATGAA CTACATTTAT CCCCTTTCCT GCCCCAACCA CAAACTCTTT 6300
CCTTCAAAGA GGGCCTGCCT GGCTCCCTCC ACCCAACTGC ACCCATGAGA CTCGGTCCAA 6360
GAGTCCATTC CCCAGGTGGG AGCCAACTGT CAGGGAGGTC TTTCCCACCA AACATCTTTC 6420
AGCTGCTGGG AGGTGACCAT AGGGCTCTGC TTTTAAAGAT ATGGCTGCTT CAAAGGCCAG 6480
AGTCACAGGA AGGACTTCTT CCAGGGAGAT TAGTGGTGAT GGAGAGGAGA GTTAAAATGA 6540
CCTCATGTCC TTCTTGTCCA CGGTTTTGTT GAGTTTTCAC TCTTCTAATG CAAGGGTCTC 6600
ACACTGTGAA CCACTTAGGA TGTGATCACT TTCAGGTGGC CAGGAATGTT GAATGTCTTT 6660
GGCTCAGTTC ATTTAAAAAA GATATCTATT TGAAAGTTCT CAGAGTTGTA CATATGTTTC 6720
ACAGTACAGG ATCTGTACAT AAAAGTTTCT TTCCTAAACC ATTCACCAAG AGCCAATATC 6780
TAGGCATTTT CTTGGTAGCA CAAATTTTCT TATTGCTTAG AAAATTGTCC TCCTTGTTAT 6840
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CTTGTCTTTT TTCTGTTGCC GAAATAGCTG GTCCTTTTTC GGGAGTTAGA TGTATAGAGT 6960
GTTTGTATGT AAACATTTCT TGTAGGCATC ACCATGAACA AAGATATATT TTCTATTTAT 7020
TTATTATATG TGCACTTCAA GAAGTCACTG TCAGAGAAAT AAAGAATTGT CTTAAATGTC

Seq ID NO: 95 Protein sequence
Protein Accession #: XP_051860.2

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1          11         21         31         41         51
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MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPWNPGH DQDHHVHIGQ    60
GKTLLLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFQGNF   120
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TIILYGRADE GIQPDPYYGL KYIGVGKGGA LELHGQKKLS WTFLNKTLHP GGMAEGGYFF   180
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SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTVKGNPSS SVEDHIEYHG HRGSAAARVF   300
KLFQTEHGEY FNVSLSSEWV QDVEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID   360
IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVRPK LTVTIDTNVN   420
STILNLEDNV QSWKPGDTLV IASTDYSMYQ AEEFQVLPCR SCAPNQVKVA GKPMYLHIGE   480
EIDGVDMRAE VGLLSRNIIV MGEMEDKCYP YRNHICNFFD FDTFGGHIKF ALGFKAAHLE   540
GTELKHMGQQ LVGQYPIHFH LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI   600
KDVVGYNSLG HCFFTEDGPE ERNTFDHCLG LLVKSGTLLP SDRDSKMCKM ITEDSYPGYI   660
PKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP   720
LGKFYNNRAH SNYRAGMIID NGVKTTEASA KDKRPFLSII SARYSPHQDA DPLKPREPAI   780
IRHFIAYKNQ DHGAWLRGGD VWLDSCRFAD NGIGLTLASG GTFPYDDGSK QEIKNSLFVG   840
ESGNVGTEMM DNRIWGPGGL DHSGRTLPIG QNFPIRGIQL YDGPINIQNC TFRKFVALEG   900
RHTSALAFRL NNAWQSCPHN NVTGIAFEDV PITSRVFFGE PGPWFNQLDM DGDKTSVFHD   960
VDGSVSEYPG SYLTKNDNWL VRHPDCINVP DWRGAICSGC YAQMYIQAYK TSNLRMKIIK  1020
NDFPSHPLYL EGALTRSTHY QQYQPVVTLQ KGYTIHWDQT APAELAIWLI NFNKGDWIRV  1080
GLCYPRGTTF SILSDVHNRL LKQTSKTGVF VRTLQMDKVE QSYPGRSHYY WDEDSGLLFL  1140
KLKAQNEREK FAFCSMKGCE RIKIKALIPK NAGVSDCTAT AYPKFTERAV VDVPMPKKLF  1200
GSQLKTKDHF LEVKMESSKQ HFFHLWNDFA YIEVDGKKYP SSEDGIQVVV IDGNQGRVVS  1260
HTSFRNSILQ GIPWQLFNYV ATIPDNSIVL MASKGRYVSR GPWTRVLEKL GADRGLKLKE  1320
QMAFVGFKGS FRPIWVTLDT EDHKAKIFQV VPIPVVKKKK L
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Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: NM_020436 and AK001666
Coding sequence: 63-3224

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CCATGTCGAG GCGCAAGCAG GCGAAACCCC AGCACATCAA CTCGGAGGAG GACCAGGGCG    120
AGCAGCAGCC GCAGCAGCAG ACCCCGGAGT TTGCAGATGC GGCCCCAGCG GCGCCCGCGG    180
CGGGGGAGCT GGGTGCTCCA GTGAACCACC CAGGGAATGA CGAGGTGGCG AGTGAGGATG    240
AAGCCACAGT AAAGCGGCTT CGTCGGGAGG AGACGCACGT CTGTGAGAAA TGCTGTGCGG    300
AGTTCTTCAG CATCTCTGAG TTCCTGGAAC ATAAGAAAAA TTGCACTAAA AATCCACCTG    360
TCCTCATCAT GAATGACAGC GAGGGGCCTG TGCCTTCAGA AGACTTCTCC GGAGCTGTAC    420
TGAGCCACCA GCCCACCAGT CCCGGCAGTA AGGACTGTCA CAGGGAGAAT GGCGGCAGCT    480
CAGAGGACAT GAAGGAGAAG CCGGATGCGG AGTCTGTGGT GTACCTAAAG ACAGAGACAG    540
CCCTGCCACC CACCCCCCAG GACATAAGCT ATTTAGCCAA AGGCAAAGTG GCCAACACTA    600
ATGTGACCTT GCAGGCACTA CGGGGCACCA AGGTGGCGGT GAATCAGCGG AGCGCGGATG    660
CACTCCCTGC CCCCGTGCCT GGTGCCAACA GCATCCCGTG GGTCCTCGAG CAGATCTTGT    720
GTCTGCAGCA GCAGCAGCTA CAGCAGATCC AGCTCACCGA GCAGATCCGC ATCCAGGTGA    780
ACATGTGGGC CTCCCACGCC CTCCACTCAA GCGGGGCAGG GGCCGACACT CTGAAGACCT    840
TGGGCAGCCA CATGTCTCAG CAGGTTTCTG CAGCTGTGGC TTTGCTCAGC CAGAAAGCTG    900
GAAGCCAAGG TCTGTCTCTG GATGCCTTGA AACAAGCCAA GCTACCTCAC GCCAACATCC    960
CTTCTGCCAC CAGCTCCCTG TCCCCAGGGC TGGCACCCTT CACTCTGAAG CCGGATGGGA   1020
CCCGGGTGCT CCCGAACGTC ATGTCCCGCC TCCCGAGCGC TTTGCTTCCT CAGGCCCCGG   1080
GCTCGGTGCT CTTCCAGAGC CCTTTCTCCA CTGTGGCGCT AGACACATCC AAGAAAGGGA   1140
AGGGGAAGCC ACCGAACATC TCCGCGGTGG ATGTCAAACC CAAAGACGAG GCGGCCCTCT   1200
ACAAGCACAA GTGTAAGTAC TGTAGCAAGG TTTTTGGGAC TGATAGCTCC TTGCAGATCC   1260
ACCTCCGCTC CCACACTGGA GAGAGACCCT TCGTGTGCTC TGTCTGTGGT CATCGCTTCA   1320
CCACCAAGGG CAACCTCAAG GTGCACTTTC ACCGACATCC CCAGGTGAAG GCAAACCCCC   1380
AGCTGTTTGC CGAGTTCCAG GACAAAGTGG CGGCCGGCAA TGGCATCCCC TATGCACTCT   1440
CTGTACCTGA CCCCATAGAT GAACCGAGTC TTTCTTTAGA CAGCAAACCT GTCCTTGTAA   1500
CCACCTCTGT AGGGCTACCT CAGAATCTTT CTTCGGGGAC TAATCCCAAG GACCTCACGG   1560
GTGGCTCCTT GCCCGGTGAC CTGCAGCCTG GGCCTTCTCC AGAAAGTGAG GGTGGACCCA   1620
CACTCCCTGG GGTGGGACCA AACTATAATT CCCCAAGGGC TGGTGGCTTC CAAGGGAGTG   1680
GGACCCCTGA GCCAGGGTCA GAGACCCTGA AATTGCAGCA GTTGGTGGAG AACATTGACA   1740
AGGCCACCAC TGATCCCAAC GAATGTCTCA TTTGCCACCG AGTCTTAAGC TGTCAGAGCT   1800
CCCTCAAGAT GCATTATCGC ACCCACACCG GGGAGAGACC GTTCCAGTGT AAGATCTGTG   1860
GCCGAGCCTT TTCTACCAAA GGTAACCTGA AGACACACCT TGGGGTTCAC CGAACCAACA   1920
CATCCATTAA GACGCAGCAT TCGTGCCCCA TCTGCCAGAA GAAGTTCACT AATGCCGTGA   1980
TGCTGCAGCA ACATATTCGG ATGCACATGG GCGGTCAGAT TCCCAACACG CCCCTGCCAG   2040
AGAATCCCTG TGACTTTACG GGTTCTGAGC CAATGACCGT GGGTGAGAAC GGCAGCACCG   2100
GCGCTATCTG CCATGATGAT GTCATCGAAA GCATCGATGT AGAGGAAGTC AGCTCCCAGG   2160
AGGCTCCCAG CAGCTCCTCC AAGGTCCCCA CGCCTCTTCC CAGCATCCAC TCGGCATCAC   2220
CCACGCTAGG GTTTGCCATG ATGGCTTCCT TAGATGCCCC AGGGAAAGTG GGTCCTGCCC   2280
CTTTTAACCT GCAGCGCCAG GGCAGCAGAG AAAACGGTTC CGTGGAGAGC GATGGCTTGA   2340
CCAACGACTC ATCCTCGCTG ATGGGAGACC AGGAGTATCA GAGCCGAAGC CCAGATATCC   2400
TGGAAACCAC ATCCTTCCAG GCACTCTCCC CGGCCAATAG TCAAGCCGAA AGCATCAAGT   2460
CAAAGTCTCC CGATGCTGGG AGCAAAGCAG AGAGCTCCGA GAACAGCCGC ACTGAGATGG   2520
AAGGTCGGAG CAGTCTCCCT TCCACGTTTA TCCGAGCCCC GCCGACCTAT GTCAAGGTTG   2580
AAGTTCCTGG CACATTTGTG GGACCCTCGA CATTGTCCCC AGGGATGACC CCTTTGTTAG   2640
CAGCCCAGCC ACGCCGACAG GCCAAGCAAC ATGGCTGCAC ACGGTGTGGG AAGAACTTCT   2700
CGTCTGCTAG CGCTCTTCAG ATCCACGAGC GGACTCACAC TGGAGAGAAG CCTTTTGTGT   2760
GCAACATTTG TGGGCGAGCT TTTACCACCA AAGGCAACTT AAAGGTTCAC TACATGACAC   2820
ACGGGGCGAA CAATAACTCA GCCCGCCGTG GAAGGAAGTT GGCCATCGAG AACACCATGG   2880
CTCTGTTAGG TACGGACGGA AAAAGAGTCT CAGAAATCTT TCCCAAGGAA ATCCTGGCCC   2940
CTTCAGTGAA TGTGGACCCT GTTGTGTGGA ACCAGTACAC CAGCATGCTC AATGGCGGTC   3000
TGGCCGTGAA GACCAATGAG ATCTCTGTGA TCCAGAGTGG GGGGGTTCCT ACCCTCCCGG   3060
TTTCCTTGGG GGCCACCTCC GTTGTGAATA ACGCCACTGT CTCCAAGATG GATGGCTCCC   3120
AGTCGGGTAT CAGTGCAGAT GTGGAAAAAC CAAGTGCTAC TGACGGCGTT CCCAAACACC   3180
AGTTTCCTCA CTTCCTGGAA GAAAACAAGA TTGCGGTCAG CTAAGGGAGA ACTTGCGTGG   3240
AAGGAGCAAT GCAGACACAG TGAAATCTCT AGAATCTGCT TTGTTTTGTA AGAACTCATC   3300
TCCTCCTGTT TTCTTTTTCT TACTGATATG CAAATGATGT TTACTACGTT GGTTGTGACC   3360
ACAACCTCAG GCAAGTGCTA CAATCACGAT TGTTGCTATG CTGCTTTGCA AAAAGTTG
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Seq ID NO: 97  Protein sequence:
Protein Accession #: NP_065169.1
1          11         21         31         41         51
|          |          |          |          |          |
MSRRKQAKPQ HINSEEDQGE QQPQQQTPEF ADAAPAAPAA GELGAPVNHP GNDEVASEDE    60
ATVKRLRREE THVCEKCCAE FFSISEFLEH KKNCTKNPPV LIMNDSEGPV PSEDFSGAVL   120
SHQPTSPGSK DCHRENGGSS EDMKEKPDAE SVVYLKTETA LPPTPQDISY LAKGKVANTN   180
VTLQALRGTK VAVNQRSADA LPAPVPGANS IPWVLEQILC LQQQQLQQIQ LTEQIRIQVN   240
MWASHALHSS GAGADTLKTL GSHMSQQVSA AVALLSQKAG SQGLSLDALK QAKLPHANIP   300
SATSSLSPGL APFTLKPDGT RVLPNVMSRL PSALLPQAPG SVLFQSPFST VALDTSKKGK   360
GKPPNISAVD VKPKDEAALY KHKCKYCSKV FGTDSSLQIH LRSHTGERPF VCSVCGHRFT   420
TKGNLKVHFH RHPQVKANPQ LFAEFQDKVA AGNGIPYALS VPDPIDEPSL SLDSKPVLVT   480
TSVGLPQNLS SGTNPKDLTG GSLPGDLQPG PSPESEGGPT LPGVGPNYNS PRAGGFQGSG   540
TPEPGSETLK LQQLVENIDK ATTDPNECLI CHRVLSCQSS LKMHYRTHTG ERPFQCKICG   600
RAFSTKGNLK THLGVHRTNT SIKTQHSCPI CQKKFTNAVM LQQHIRMHMG GQIPNTPLPE   660
NPCDFTGSEP MTVGENGSTG AICHDDVIES IDVEEVSSQE APSSSSKVPT PLPSIHSASP   720
TLGFAMMASL DAPGKVGPAP FNLQRQGSRE NGSVESDGLT NDSSSLMGDQ EYQSRSPDIL   780
ETTSFQALSP ANSQAESIKS KSPDAGSKAE SSENSRTEME GRSSLPSTFI RAPPTYVKVE   840
VPGTFVGPST LSPGMTPLLA AQPRRQAKQH GCTRCGKNFS SASALQIHER THTGEKPFVC   900
NICGRAFTTK GNLKVHYMTH GANNNSARRG RKLAIENTMA LLGTDGKRVS EIFPKEILAP   960
SVNVDPVVWN QYTSMLNGGL AVKTNEISVI QSGGVPTLPV SLGATSVVNN ATVSKMDGSQ  1020
SGISADVEKP SATDGVPKHQ FPHFLEENKI AVS

Seq ID NO: 98 DNA sequence
Nucleic Acid Accession #: NM_000612.2
Coding sequence: 553..1095
1          11         21         31         41         51
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CTCCCCCCCT CACGCCCGCC CTCTCGCCTT CGCCGAACCA AAGTGGATTA ATTACACGCT   120
TTCTGTTTCT CTCCGTGCTG TTCTCTCCCG CTGTGCGCCT GCCCGCCTCT CGCTGTCCTC   180
TCTCCCCCTC GCCCTCTCTT CGGCCCCCCC CTTTCACGTT CACTCTGTCT CTCCCACTAT   240
CTCTGCCCCC CTCTATCCTT GATACAACAG CTGACCTCAT TTCCCGATAC CTTTTCCCCC   300
CCGAAAAGTA CAACATCTGG CCCGCCCCAG CCCGAAGACA GCCCGTCCTC CCTGGACAAT   360
CAGACGAATT CTCCCCCCCC CCCCAAAAAA AAAAGCCATC CCCCCGCTCT GCCCCGTCGC   420
ACATTCGGCC CCCGCGACTC GGCCAGAGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGGG   480
CCAACGCCCG CTGTTCGGTT TGCGACACGC AGCAGGGAGG TGGGCGGCAG CGTCGCCGGC   540
TTCCAGACAC CAATGGGAAT CCCAATGGGG AAGTCGATGC TGGTGCTTCT CACCTTCTTG   600
GCCTTCGCCT CGTGCTGCAT TGCTGCTTAC CGCCCCAGTG AGACCCTGTG CGGCGGGGAG   660
CTGGTGGACA CCCTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTCAG CAGGCCCGCA   720
AGCCGTGTGA GCCGTCGCAG CCGTGGCATC GTTGAGGAGT GCTGTTTCCG CAGCTGTGAC   780
CTGGCCCTCC TGGAGACGTA CTGTGCTACC CCCGCCAAGT CCGAGAGGGA CGTGTCGACC   840
CCTCCGACCG TGCTTCCGGA CAACTTCCCC AGATACCCCG TGGGCAAGTT CTTCCAATAT   900
GACACCTGGA AGCAGTCCAC CCAGCGCCTG CGCAGGGGCC TGCCTGCCCT CCTGCGTGCC   960
CGCCGGGGTC ACGTGCTCGC CAAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACGTCACCGT  1020
CCCCTGATTG CTCTACCCAC CCAAGACCCC GCCCACGGGG GCGCCCCCCC AGAGATGGCC  1080
AGCAATCGGA AGTGAGCAAA ACTGCCGCAA GTCTGCAGCC CGGCGCCACC ATCCTGCAGC  1140
CTCCTCCTGA CCACGGACGT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCCACGT  1200
CCCCCTGGGG CTTCTCCTGA CCCAGTCCCC GTGCCCCGCC TCCCCGAAAC AGGCTACTCT  1260
CCTCGGCCCC CTCCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAAACAT GTACAAAATC  1320
GATTGGCTTT AAACACCCTT CACATACCCT CCCCCC

Seq ID NO: 99 Protein sequence
Protein Accession #: NP_000603.1
1          11         21         31         41         51
|          |          |          |          |          |
MGIPMGKSML VLLTFLAFAS CCIAAYRPSE TLCGGELVDT LQFVCGDRGF YFSRPASRVS    60
RRSRGIVEEC CFRSCDLALL ETYCATPAKS ERDVSTPPTV LPDNFPRYPV GKFFQYDTWK   120
QSTQRLRRGL PALLRARRGH VLAKELEAFR EAKRHRPLIA LPTQDPAHGG APPEMASNRK

Seq ID NO: 100 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092
1          11         21         31         41         51
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GCCCAGAAGG AGAACTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG   120
AGCACCCTGC CCCAGCGAGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCCTC   180
ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCCTGGCC AGAAGGTGAT GGAGAATAGC   240
AGTGGGACAC CCGACATCTT AACGCGGCAC TTCACAATTG ATGACTTTGA GATTGGGCGT   300
CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC   360
ATCGTGGCGC TCAAGGTCCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG   420
CTGCGCAGAG AGATCGAAAT CCAGGCCCAC CTGCACCATC CCAACATCCT GCGTCTCTAC   480
AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG   540
CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CACGATCATG   600
GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA   660
AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTCGGCTGG   720
TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCCTGGA CTACCTGCCC   780
CCAGAGATGA TTGAGGGGCG CATGCACAAT GAGAAGGTGG ATCTGTGGTG CATTGGAGTG   840
CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC   900
TATCGCCGCA TCGTCAAGGT GGACCTAAAG TTCCCCGCTT CTGTGCCCAC GGGAGCCCAG   960
GACCTCATCT CCAAACTGCT CAGGCATAAC CCCTCGGAAC GGCTGCCCCT GGCCCAGGTC  1020
TCAGCCCACC CTTGGGTCCG GGCCAACTCT CGGAGGGTGC TGCCTCCCTC TGCCCTTCAA  1080
TCTGTCGCCT GATGGTCCCT GTCATTCACT CGGGTGCGTG TGTTTGTATG TCTGTGTATG  1140
TATAGGGGAA AGAAGGGATC CCTAACTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT  1200
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TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 101 Protein sequence
Protein Accession #: NP_004208

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1          11         21         31         41         51
|          |          |          |          |          |
MAQKENSYPW PYGRQTAPSG LSTLPQRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN    60
SSGTPDILTR HFTIDDFEIG RPLGKGKFGN VYLAREKKSH FIVALKVLFK SQIEKEGVEH   120
QLRREIEIQA HLHHPNILRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI   180
MEELADALMY CHGKKVIHRD IKPENLLLGL KGELKIADFG WSVHAPSLRR KTMCGTLDYL   240
PPEMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA   300
QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSVA
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Seq ID NO: 102 DNA sequence
Nucleic Acid Accession #: AK025790
Coding sequence: 56..1642

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1          11         21         31         41         51
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GCAAGGGATC CTTTCTCCGC CAGCGGGCTT GCTGTCCGAT GACGATGTCG TAGTTTCTCC   120
CATGTTTGAG TCCACAGCTG CAGATTTGGG GTCTGTGGTA CGCAAGAACC TGCTATCAGA   180
CTGCTCTGTC GTCTCTACCT CCCTAGAGGA CAAGCAGCAG GTTCCATCTG AGGACAGTAT   240
GGAGAAGGTG AAAGTATACT TGAGGGTTAG GCCCTTGTTA CCTTCAGAGT TGGAACGACA   300
GGAAGATCAG GGTTGTGTCC GTATTGAGAA TGTGGAGACC CTTGTTCTAC AAGCACCCAA   360
GGACTCTTTT GCCCTGAAGA GCAATGAACG GGGAATTGGC CAAGCCACAC ACAGGTTCAC   420
CTTTTCCCAG ATCTTTGGGC CAGAAGTGGG ACAGGCATCC TTCTTCAACC TAACTGTGAA   480
GGAGATGGTA AAGGATGTAC TCAAAGGGCA GAACTGGCTC ATCTATACAT ATGGAGTCAC   540
TAACTCAGGG AAAACCCACA CGATTCAAGG TACCATCAAG GATGGAGGGA TTCTCCCCCG   600
GTCCCTGGCG CTGATCTTCA ATAGCCTCCA AGGCCAACTT CATCCAACAC CTGATCTGAA   660
GCCCTTGCTC TCCAATGAGG TAATCTGGCT AGACAGCAAG CAGATCCGAC AGGAGGAAAT   720
GAAGAAGCTG TCCCTGCTAA ATGGAGGCCT CCAAGAGGAG GAGCTGTCCA CTTCCTTGAA   780
GAGGAGTGTC TACATCGAAA GTCGGATAGG TACCAGCACC AGCTTCGACA GTGGCATTGC   840
TGGGCTCTCT TCTATCAGTC AGTGTACCAG CAGTAGCCAG CTGGATGAAA CAAGTCATCG   900
ATGGGCACAG CCAGACACTG CCCCACTACC TGTCCCGGCA AACATTCGCT TCTCCATCTG   960
GATCTCATTC TTTGAGATCT ACAACGAACT GCTTTATGAC CTATTAGAAC CGCCTAGCCA  1020
ACAGCGCAAG AGGCAGACTT TGCGGCTATG CGAGGATCAA AATGGCAATC CCTATGTGAA  1080
AGATCTCAAC TGGATTCATG TGCAAGATGC TGAGGAGGCC TGGAAGCTCC TAAAAGTGGG  1140
TCGTAAGAAC CAGAGCTTTG CCAGCACCCA CCTCAACCAG AACTCCAGCC GCAGTCACAG  1200
CATCTTCTCA ATCAGGATCC TACACCTTCA GGGGGAAGGA GATATAGTCC CCAAGATCAG  1260
CGAGCTGTCA CTCTGTGATC TGGCTGGCTC AGAGCGCTGC AAAGATCAGA AGAGTGGTGA  1320
ACGGTTGAAG GAAGCAGGAA ACATTAACAC CTCTCTACAC ACCCTGGGCC GCTGTATTGC  1380
TGCCCTTCGT CAAAACCAGC AGAACCGGTC AAAGCAGAAC CTGGTTCCCT TCCGTGACAG  1440
CAAGTTGACT CGAGTGTTCC AAGGTTTCTT CACAGGCCGA GGCCGTTCCT GCATGATTGT  1500
CAATGTGAAT CCCTGTGCAT CTACCTATGA TGAAACTCTT CATGTGGCCA AGTTCTCAGC  1560
CATTGCTAGC CAGGTGACTT GTGCATGCCC CACCTATGCA ACTGGGATTC CCATCCCTGC  1620
ACTCGTTCAT CAAGGAACAT AGTCTTCAGG TATCCCCCAG CTTAGAGAAA GGGGCTAAGG  1680
CAGACACAGG CCTTGATGAT GATATTGAAA ATGAAGCTGA CATCTCCATG TATGGCAAAG  1740
AGGAGCTCCT ACAAGTTGTG GAAGCCATGA AGACACTGCT TTTGAAGGAA CGACAGGAAA  1800
AGCTACAGCT GGAGATGCAT CTCCGAGATG AAATTTGCAA TGAGATGGTA GAACAGATGC  1860
AACAGCGGGA ACAGTGGTGC AGTGAACATT TGGACACCCA AAAGGAACTA TTGGAGGAAA  1920
TGTATGAAGA AAAACTAAAT ATCCTCAAGG AGTCACTGAC AAGTTTTTAC CAAGAAGAGA  1980
TTCAGGAGCG GGATGAAAAG ATTGAAGAGC TAGAAGCTCT CTTGCAGGAA GCCAGACAAC  2040
AGTCAGTGGC CCATCAGCAA TCAGGGTCTG AATTGGCCCT ACGGCGGTCA CAAAGGTTGG  2100
CAGCTTCTGC CTCCACCCAG CAGCTTCAGG AGGTTAAAGC TAAATTACAG CAGTGCAAAG  2160
CAGAGCTAAA CTCTACCACT GAAGAGTTGC ATAAGTATCA GAAAATGTTA GAACCACCAC  2220
CCTCAGCCAA GCCCTTCACC ATTGATGTGG ACAAGAAGTT AGAAGAGGGC CAGAAGAATA  2280
TAAGGCTGTT GCGGACAGAG CTTCAGAAAC TTGGTGAGTC TCTCCAATCA GCAGAGAGAG  2340
CTTGTTGCCA CAGCACTGGG GCAGGAAAAC TTCGTCAAGC CTTGACCACT TGTGATGACA  2400
TCTTAATCAA ACAGGACCAG ACTCTGGCTG AACTGCAGAA CAACATGGTG CTAGTGAAAC  2460
TGGACCTTCG GAAGAAGGCA GCATGTATTG CTGAGCAGTA TCATACTGTG TTGAAACTCC  2520
AAGGCCAGGT TTCTGCCAAA AAGCGCCTTG GTACCAACCA GGAAAATCAG CAACCAAACC  2580
AACAACCACC AGGGAAGAAA CCATTCCTTC GAAATTTACT TCCCCGAACA CCAACCTGCC  2640
AAAGCTCAAC AGACTGCAGC CCTTATGCCC GGATCCTACG CTCACGGCGT TCCCCTTTAC  2700
TCAAATCTGG GCCTTTTGGC AAAAAGTACT AAGGCTGTGG GGAAAGAGAA GAGCAGTCAT  2760
GGCCCTGAGG TGGGTCAGCT ACTCTCCTGA AGAAATAGGT CTCTTTTATG CTTTACCATA  2820
TATCAGGAAT TATATCCAGG ATGCAATACT CAGACACTAG CTTTTTTCTC ACTTTTGTAT  2880
TATAACCACC TATGTAATCT CATGTTGTTG TTTTTTTTTA TTTACTTATA TGATTTCTAT  2940
GCACACAAAA ACAGTTATAT TAAAGATATT ATTGTTCACA TTTTTTATTG AATTCCAAAT  3000
GTAGCAAAAT CATTAAAACA AATTATAAAA GGGACAGAAA AA
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Seq ID NO: 103 Protein sequence
Protein Accession #: NP_005724.1

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1          11         21         31         41         51
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MSQGILSPPA GLLSDDDVVV SPMFESTAAD LGSVVRKNLL SDCSVVSTSL EDKQQVPSED    60
SMEKVKVYLR VRPLLPSELE RQEDQGCVRI ENVETLVLQA PKDSFALKSN ERGIGQATHR   120
FTFSQIFGPE VGQASFFNLT VKEMVKDVLK GQNWLIYTYG VTNSGKTHTI QGTIKDGGIL   180
PRSLALIFNS LQGQLHPTPD LKPLLSNEVI WLDSKQIRQE EMKKLSLLNG GLQEEELSTS   240
LKRSVYIESR IGTSTSFDSG IAGLSSISQC TSSSQLDETS HRWAQPDTAP LPVPANIRFS   300
IWISFFEIYN ELLYDLLEPP SQQRKRQTLR LCEDQNGNPY VKDLNWIHVQ DAEEAWKLLK   360
VGRKNQSFAS THLNQNSSRS HSIFSIRILH LQGEGDIVPK ISELSLCDLA GSERCKDQKS   420
GERLKEAGNI NTSLHTLGRC IAALRQNQQN RSKQNLVPFR DSKLTRVFQG FFTGRGRSCM   480
IVNVNPCAST YDETLHVAKF SAIASQVTCA CPTYATGIPI PALVHQGT
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Seq ID NO: 104 DNA sequence

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Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793
1          11         21         31         41         51
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TGGAAATGTG ATTATTGGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT   120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG   180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCTGTCTG TTCTAGGCAT   240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT   300
AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC   360
ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACAACAGCC CTCCAAACAA   420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA   480
CAATTGCTGT GGCGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC   540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA   600
AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTTATC ACAATCAGGG   660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG   720
ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG   780
AATTGAATAT TAAGAA
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Seq ID NO: 105 Protein sequence
Protein Accession #: NP_008883.1
1          11         21         31         41         51
|          |          |          |          |          |
MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW    60
IGIFVGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL   120
FLKQMLERYQ NNSPPNNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN   180
DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI   240
LCWTFWVLLG TMFYWSRIEY
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Seq ID NO: 106 DNA sequence
Nucleic Acid Accession #: NM_002740.1
Coding sequence: 178..1968
1          11         21         31         41         51
|          |          |          |          |          |
CCGCGGTTCC GGCTGCTCCG GCGAGGCGAC CCTTGGGTCG GCGCTGCGGG CGAGGTGGGC    60
AGGTAGGTGG GCGGACGGCC GCGGTTCTCC GGCAAGCGCA GGCGGCGGAG TCCCCCACGG   120
CGCCCGAAGC GCCCCCCGCA CCCCCGGCCT CCAGCGTTGA GGCGGGGGAG TGAGGAGATG   180
CCGACCCAGA GGGACAGCAG CACCATGTCC CACACGGTCG CAGGCGGCGG CAGCGGGGAC   240
CATTCCCACC AGGTCCGGGT GAAAGCCTAC TACCGCGGGG ATATCATGAT AACACATTTT   300
GAACCTTCCA TCTCCTTTGA GGGCCTTTGC AATGAGGTTC GAGACATGTG TTCTTTTGAC   360
AACGAACAGC TCTTCACCAT GAAATGGATA GATGAGGAAG GAGACCCGTG TACAGTATCA   420
TCTCAGTTGG AGTTAGAAGA AGCCTTTAGA CTTTATGAGC TAAACAAGGA TTCTGAACTC   480
TTGATTCATG TGTTCCCTTG TGTACCAGAA CGTCCTGGGA TGCCTTGTCC AGGAGAAGAT   540
AAATCCATCT ACCGTAGAGG TGCACGCCGC TGGAGAAAGC TTTATTGTGC CAATGGCCAC   600
ACTTTCCAAG CCAAGCGTTT CAACAGGCGT GCTCACTGTG CCATCTGCAC AGACCGAATA   660
TGGGGACTTG GACGCCAAGG ATATAAGTGC ATCAACTGCA AACTCTTGGT TCATAAGAAG   720
TGCCATAAAC TCGTCACAAT TGAATGTGGG CGGCATTCTT TGCCACAGGA ACCAGTGATG   780
CCCATGGATC AGTCATCCAT GCATTCTGAC CATGCACAGA CAGTAATTCC ATATAATCCT   840
TCAAGTCATG AGAGTTTGGA TCAAGTTGGT GAAGAAAAAG AGGCAATGAA CACCAGGGAA   900
AGTGGCAAAG CTTCATCCAG TCTAGGTCTT CAGGATTTTG ATTTGCTCCG GGTAATAGGA   960
AGAGGAAGTT ATGCCAAAGT ACTGTTGGTT CGATTAAAAA AAACAGATCG TATTTATGCA  1020
ATGAAAGTTG TGAAAAAAGA GCTTGTTAAT GATGATGAGG ATATTGATTG GGTACAGACA  1080
GAGAAGCATG TGTTTGAGCA GGCATCCAAT CATCCTTTCC TTGTTGGGCT GCATTCTTGC  1140
TTTCAGACAG AAAGCAGATT GTTCTTTGTT ATAGAGTATG TAAATGGAGG AGACCTAATG  1200
TTTCATATGC AGCGACAAAG AAAACTTCCT GAAGAACATG CCAGATTTTA CTCTGCAGAA  1260
ATCAGTCTAG CATTAAATTA TCTTCATGAG CGAGGGATAA TTTATAGAGA TTTGAAACTG  1320
GACAATGTAT TACTGGACTC TGAAGGCCAC ATTAAACTCA CTGACTACGG CATGTGTAAG  1380
GAAGGATTAC GGCCAGGAGA TACAACCAGC ACTTTCTGTG GTACTCCTAA TTACATTGCT  1440
CCTGAAATTT TAAGAGGAGA AGATTATGGT TTCAGTGTTG ACTGGTGGGC TCTTGGAGTG  1500
CTCATGTTTG AGATGATGGC AGGAAGGTCT CCATTTGATA TTGTTGGGAG CTCCGATAAC  1560
CCTGACCAGA ACACAGAGGA TTATCTCTTC CAAGTTATTT TGGAAAAACA AATTCGCATA  1620
CCACGTTCTC TGTCTGTAAA AGCTGCAAGT GTTCTGAAGA GTTTTCTTAA TAAGGACCCT  1680
AAGGAACGAT TGGGTTGTCA TCCTCAAACA GGATTTGCTG ATATTCAGGG ACACCCGTTC  1740
TTCCGAAATG TTGATTGGGA TATGATGGAG CAAAAACAGG TGGTACCTCC CTTTAAACCA  1800
AATATTTCTG GGGAATTTGG TTTGGACAAC TTTGATTCTC AGTTTACTAA TGAACCTGTC  1860
CAGCTCACTC CAGATGACGA TGACATTGTG AGGAAGATTG ATCAGTCTGA ATTTGAAGGT  1920
TTTGAGTATA TCAATCCTCT TTTGATGTCT GCAGAAGAAT GTGTCTGATC CTCATTTTTC  1980
AACCATGTAT TCTACTCATG TTGCCATTTA ATGCATGGAT AAACTTGCTG CAAGCCTGGA  2040
TACAATTAAC CATTTTATAT TTGCCACCTA CAAAAAAACA CCCAATATCT TCTCTTGTAG  2100
ACTATATGAA TCAATTATTA CATCTGTTTT ACTATGAAAA AAAAATTAAT ACTACTAGCT  2160
TCCAGACAAT CATGTCAAAA TTTAGTTGAA CTGGTTTTTC AGTTTTTAAA AGGCCTACAG  2220
ATGAGTAATG AAGTTACCTT TTTTGTTTAA AAAAAAAAAA G
```

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Seq ID NO: 107 Protein sequence
Protein Accession #: NP_002731.1
1          11         21         31         41         51
|          |          |          |          |          |
MSHTVAGGGS GDHSHQVRVK AYYRGDIMIT HFEPSISFEG LCNEVRDMCS FDNEQLFTMK    60
WIDEEGDPCT VSSQLELEEA FRLYELNKDS ELLIHVFPCV PERPGMPCPG EDKSIYRRGA   120
RRWRKLYCAN GHTFQAKRFN RRAHCAICTD RIWGLGRQGY KCINCKLLVH KKCHKLVTIE   180
CGRHSLPQEP VMPMDQSSMH SDHAQTVIPY NPSSHESLDQ VGEEKEAMNT RESGKASSSL   240
GLQDFDLLRV IGRGSYAKVL LVRLKKTDRI YAMKVVKKEL VNDDEDIDWV QTEKHVFEQA   300
SNHPFLVGLH SCFQTESRLF FVIEYVNGGD LMFHMQRQRK LPEEHARFYS AEISLALNYL   360
HERGIIYRDL KLDNVLLDSE GHIKLTDYGM CKEGLRPGDT TSTFCGTPNY IAPEILRGED   420
YGFSVDWWAL GVLMFEMMAG RSPFDIVGSS DNPDQNTEDY LFQVILEKQI RIPRSLSVKA   480
```

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ASVLKSFLNK DPKERLGCHP QTGPADIQGH PFFRNVDWDM MEQKQVVPPF KPNISGEFGL   540
DNFDSQFTNE PVQLTPDDDD IVRKIDQSEF EGFEYINPLL MSAEECV
```

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: NM_000349.1
Coding sequence: 127..984

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1          11         21         31         41         51
|          |          |          |          |          |
GGGACTCAGA GGCGAAGCTT GAGGGGCTCA GGAAGGACGA AGAACCACCC TTGAGAGAAG     60
AGGCAGCAGC AGCGGCGGCA GCAGCAGCGG CAGCGACCCC ACCACTGCCA CATTTGCCAG    120
GAAACAATGC TGCTAGCGAC ATTCAAGCTG TGCGCTGGGA GCTCCTACAG ACACATGCGC    180
AACATGAAGG GGCTGAGGCA ACAGGCTGTG ATGGCCATCA GCCAGGAGCT GAACCGGAGG    240
GCCCTGGGGG GCCCCACCCC TAGCACGTGG ATTAACCAGG TTCGGCGGCG GAGCTCTCTA    300
CTCGGTTCTC GGCTGGAAGA GACTCTCTAC AGTGACCAGG AGCTGGCCTA TCTCCAGCAG    360
GGGGAGGAGG CCATGCAGAA GGCCTTGGGC ATCCTTAGCA ACCAAGAGGG CTGGAAGAAG    420
GAGAGTCAGC AGGACAATGG GGACAAAGTG ATGAGTAAAG TGGTCCCAGA TGTGGGCAAG    480
GTGTTCCGGC TGGAGGTCGT GGTGGACCAG CCCATGGAGA GGCTCTATGA AGAGCTCGTG    540
GAGCGCATGG AAGCAATGGG GGAGTGGAAC CCCAATGTCA AGGAGATCAA GGTCCTGCAG    600
AAGATCGGAA AAGATACATT CATTACTCAC GAGCTGGCTG CCGAGGCAGC AGGAAACCTG    660
GTGGGGCCCC GTGACTTTGT GAGCGTGCGC TGTGCCAAGC GCCGAGGCTC CACCTGTGTG    720
CTGGCTGGCA TGGACACAGA CTTCGGGAAC ATGCCTGAGC AGAAGGGTGT CATCAGGGCG    780
GAGCACGGTC CCACTTGCAT GGTGCTTCAC CCGTTGGCTG GAAGTCCCTC TAAGACCAAA    840
CTTACGTGGC TACTCAGCAT CGACCTCAAG GGGTGGCTGC CCAAGAGCAT CATCAACCAG    900
GTCCTGTCCC AGACCCAGGT GGATTTTGCC AACCACCTGC GCAAGCGCCT GGAGTCCCAC    960
CCTGCCTCTG AAGCCAGGTG TTGAAGACCA GCCTGCTGTT CCCAACTGTG CCCAGCTGCA   1020
CTGGTACACA CGCTCATCAG GAGAATCCCT ACTGGAAGCC TGCAAGTCTA AGATCTCCAT   1080
CTGGTGACAG TGGGATGGGT GGGGTTCGTG TTTAGAGTAT GACACTAGGA TTCAGATTGG   1140
TGAAGTTTTT AGTACCAAGA AAACAGGGAT GAGGCTCTTG GATTAAAAGG TAACTTCATT   1200
CACTGATTAG CTATGACATG AGGGTTCAGG CCCCTAAAAT AATTGTAAAA CTTTTTTTCT   1260
GGGCCCTTAT GTACCCACCT AAAACCATCT TTAAAATGCT AGTGGCTGAT ATGGGTGTGG   1320
GGGATGCTAA CCACAGGGCC TGAGAAGTCT TGCTTTATGG GCTCAAGAAT GCCATGCGCT   1380
GGCAGTACAT GTGCACAAAG CAGAATCTCA GAGGGTCTCC TGCAGCCCTC TGCTCCTCCC   1440
GGCCGCTGCA CAGCAACACC ACAGAACAAG CAGCACCCCA CAGTGGGTGC CTTCCAGAAA   1500
TATAGTCCAA GCTTTCTCTG TGGAAAAAGA CAAAACTCAT TAGTAGACAT GTTTCCCTAT   1560
TGCTTTCATA GGCACCAGTC AGAATAAAGA ATCATAATTC ACACC
```

Seq ID NO: 109 Protein sequence
Protein Accession #: NP_000340.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLLATFKLCA GSSYRHMRNM KGLRQQAVMA ISQELNRRAL GGPTPSTWIN QVRRRSSLLG     60
SRLEETLYSD QELAYLQQGE EAMQKALGIL SNQEGWKKES QQDNGDKVMS KVVPDVGKVF    120
RLEVVVDQPM ERLYEELVER MEAMGEWNPN VKEIKVLQKI GKDTFITHEL AAEAAGNLVG    180
PRDFVSVRCA KRRGSTCVLA GMDTDFGNMP EQKGVIRAEH GPTCMVLHPL AGSPSKTKLT    240
WLLSIDLKGW LPKSIINQVL SQTQVDFANH LRKRLESHPA SEARC
```

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 131-682

```
1          11         21         31         41         51
|          |          |          |          |          |
GCTGGGAGCC TGGGCCGGGA GCCGGGTGAG GGCGCCGAGA GGCTCGGTGG GCGCGGGCGG     60
CGAGATATGC CACACTTCTG CCTGCTGTTG GCAACCCTCC TGGACTAGGC TGCTCTTGTT    120
AATCACATGG ATGTTATATA AGAGTTCGGA CCGCCCAGCA CACAAGGTCA GCATGCTGCT    180
CCTCTGTCAC GCTCTCGCTA TAGCTGTTGT CCAGATCGTT ATCTTCTCAG AAAGCTGGGC    240
ATTTGCCAAG AACATCAACT TCTATAATGT GAGGCCTCCT CTCGACCCTA CACCATTTCC    300
AAATAGCTTC AAGTGCTTTA CTTGTGAAAA CGCAGGGGAT AATTATAACT GCAATCGATG    360
GGCAGAAGAC AAATGGTGTC CACAAAATAC ACAGTACTGT TTGACAGTTC ATCACTTCAC    420
CAGCCACGGA AGAAGCACAT CCATCACCAA AAAGTGTGCC TCCAGAAGTG AATGTCATTT    480
TGTCGGTTGC CACCACAGCC GAGATTCTGA ACATACGGAG TGTAGGTCTT GCTGTGAAGG    540
AATGATCTGC AATGTAGAAT TACCCACCAA TCACACTAAT GCAGTGTTTG CCGTAATGCA    600
CGCTCAGAGA ACATCTGGCA GCAGTGCCCC CACACTCTAC CTACCAGTGC TTGCCTGGGT    660
CTTTGTGCTT CCATTGCTGT GATGCCACCA TTCCTAGGAG AGGCAGAGAC CAGCCTCTAA    720
AGCACAAGCC AAAAACTGTG TGAACGGTGA ACTTTGGAGT GAAGATCAAT CTTGCACTTG    780
GTGAAGAGTG CACATTGGAC CTCAAGGCGA AAGCCAGTGG TTTGCTTGGA TAAAATGTTC    840
CCGCATGAGG CCACAGGACT GAGGATGGGA ATTTGGCAGG GCCTGAGAAG ATGGTCTGAC    900
TTCCAGGCTT CCTGGTCAAA GAGAGCTACG TTTGGGCAGT TCTGCAGAGA GGATCCTGGC    960
AACTAGTCCC ACCTGACTAG GCCTTTAGCT GAAAGGATTT CTTGACCTCC TTGACTGCCT   1020
CAGAGGCTGC CAGGTCAAAC CCTCTTGTTT ATGTGATTAG CTCAGAGCAT CTCTATGAAA   1080
TCTAACCCTT CCCCTCATGA GAAAGCAGTT TTCCCCACCA ACAGCATAGT CAATGAGAAA   1140
GGCAACTGTA CGAAGAAAAC TTCCAGTGGA ACTAATATGA AATCTATTTG CAAATTATGG   1200
GGGGAAATAA AGCTTTTAAA TTATACAATG T
```

Seq ID NO: 111 Protein sequence
Protein Accession #: AAM20908.1

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1          11         21         31         41         51
|          |          |          |          |          |
MLYKSSDRPA HKVSMLLLCH ALAIAVVQIV IFSESWAFAK NINFYNVRPP LDPTPFPNSF     60
KCFTCENAGD NYNCNRWAED KWCPQNTQYC LTVHHFTSHG RSTSITKKCA SRSECHFVGC    120
HHSRDSEHTE CRSCCEGMIC NVELPTNHTN AVFAVMHAQR TSGSSAPTLY LPVLAWVFVL    180
PLL
```

Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 228-884

```
1          11         21         31         41         51
|          |          |          |          |          |
CGCCCGCCGG CCCCAGGCGG GTGCGCTGGG AGCCTGGGCC GGGAGCCGGG TGAGGGCGCC    60
GAGAGGCTCG GTGGGCGCGG GCGGCGAGGA CTCTGCTGGA GCAGGACTTC AGAGTGTTTG   120
TTTTCAGCCT GCTTTTAAAG TGATTTGAAG AGAGCGGCTT TGAAGATATG CCACACTTCT   180
GCCTGCTGTT GGCAACCCTC CTGGACTAGG CTGCTCTTGT TAATCACATG GATGTTGCTG   240
ATTACTCTGA GTGCAAACCT TTTCACTGTT CCAGAGAGGA GCCTGACAAC CACATTCTCC   300
TTCTCAAGGT GTGGTGCTTA CTGCGCAGGC TGACCAGATA TAAGAGTTCG GACCGCCCAG   360
CACACAAGGT CAGCATGCTG CTCCTCTGTC ACGCTCTCGC TATAGCTGTT GTCCAGATCG   420
TTATCTTCTC AGAAAGCTGG GCATTTGCCA AGAACATCAA CTTCTATAAT GTGAGGCCTC   480
CTCTCGACCC TACACCATTT CCAAATAGCT TCAAGTGCTT TACTTGTGAA AACGCAGGGG   540
ATAATTATAA CTGCAATCGA TGGGCAGAAG ACAAATGGTG TCCACAAAAT ACACAGTACT   600
GTTTGACAGT TCATCACTTC ACCAGCCACG GAAGAAGCAC ATCCATCACC AAAAAGTGTG   660
CCTCCAGAAG TGAATGTCAT TTTGTCGGTT GCCACCACAG CCGAGATTCT GAACATACGG   720
AGTGTAGGTC TTGCTGTGAA GGAATGATCT GCAATGTAGA ATTACCCACC AATCACACTA   780
ATGCAGTGTT TGCCGTAATG CACGCTCAGA GAACATCTGG CAGCAGTGCC CCCACACTCT   840
ACCTACCAGT GCTTGCCTGG GTCTTTGTGC TTCCATTGCT GTGATGCCAC CATTCCTAGG   900
AGAGGCAGAG ACCAGCCTCT AAAGCACAAG CCAAAAACTG TGTGAACGGT GAACTTTGGA   960
GTGAAGATCA ATCTTGCACT TGGTGAAGAG TGCACATTGG ACCTCAAGGC GAAAGCCAGT  1020
GGTTTGCTTG GATAAAATGT TCCCGCATGA GGCCACAGGA CTGAGGATGG GAATTTGGCA  1080
GGGCCTGAGA AGATGGTCTG ACTTCCAGGC TTCCTGGTCA AAGAGAGCTA CGTTTGGGCA  1140
GTTCTGCAGA GAGGATCCTG GCAACTAGTC CCACCTGACT AGGCCTTTAG CTGAAAGGAT  1200
TTCTTGACCT CCTTGACTGC CTCAGAGGCT GCCAGGTCAA ACCCTCTTGT TTATGTGATT  1260
AGCTCAGAGC ATCTCTATGA AATCTAACCC TTCCCCTCAT GAGAAAGCAG TTTTCCCCAC  1320
CAACAGCATA GTCAATGAGA AAGGCAACTG TACGAAGAAA ACTTCCAGTG GAACTAATAT  1380
GAAATCTATT TGCAAATTAT GGGGGGAAAT AAAGCTTTTA AATTATAAA
```

Seq ID NO:, 113 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MDVADYSECK PFHCSREEPD NHILLLKVWC LLRRLTRYKS SDRPAHKVSM LLLCHALAIA    60
VVQIVIFSES WAFAKNINFY NVRPPLDPTP FPNSFKCFTC ENAGDNYNCN RWAEDKWCPQ   120
NTQYCLTVHH FTSHGRSTSI TKKCASRSEC HFVGCHHSRD SEHTECRSCC EGMICNVELP   180
TNHTNAVFAV MHAQRTSGSS APTLYLPVLA WVFVLPLL
```

Seq ID NO: 114 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 402-1025

```
1          11         21         31         41         51
|          |          |          |          |          |
ACTTCCTGAG CCGGGCTGGC TGGGTGGGAA CAGGCTCCTT GCCGCCTCCC CAGCGCTGGC    60
CACTACCACA CTGCCGCCCG CCTGGGCCTC CTTTCAACCT CGTGGTGGAG CCCTGCGGTT   120
TCCCAGCGGA GCCGGGCCCG GGGCTGCTCC CTCGCGGGCG AGGCTCACCT GTCCCGGCCC   180
GGCCCCCTCC CGCGCCCCAG GTGGTTCAGG GCAGGGAGGA GCCGCGCCCC GCCCCGCGCG   240
GTAGCAGCCA ACGCCGGCCC CAGGCGGGTG CGCTGGGAGC CTGGGCCGGG AGCCGGGTGA   300
GGGCGCCGAG AGGCTCGGTG GGCGCGGGCG GCGAGATATG CCACACTTCT GCCTGCTGTT   360
GGCAACCCTC CTGGACTAGG CTGCTCTTGT TAATCACATG GATGTTGCTG ATTACTCTGA   420
GTGCAAACCT TTTCACTGTT CCAGAGAGGA GCCTGACAAC CACATTCTCC TTCTCAAGAT   480
ATAAGAGTTC GGACCGCCCA GCACACAAGG TCAGCATGCT GCTCCTCTGT CACGCTCTCG   540
CTATAGCTGT TGTCCAGATC GTTATCTTCT CAGAAAGCTG GGCATTTGCC AAGAACATCA   600
ACTTCTATAA TGTGAGGCCT CCTCTCGACC CTACACCATT TCCAAATAGC TTCAAGTGCT   660
TTACTTGTGA AAACGCAGGG GATAATTATA ACTGCAATCG ATGGGCAGAA GACAAATGGT   720
GTCCACAAAA TACACAGTAC TGTTTGACAG TTCATCACTT CACCAGCCAC GGAAGAAGCA   780
CATCCATCAC CAAAAAGTGT GCCTCCAGAA GTGAATGTCA TTTTGTCGGT TGCCACCACA   840
GCCGAGATTC TGAACATACG GAGTGTAGGT CTTGCTGTGA AGGAATGATC TGCAATGTAG   900
AATTACCCAC CAATCACACT AATGCAGTGT TTGCCGTAAT GCACGCTCAG AGAACATCTG   960
GCAGCAGTGC CCCCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC  1020
TGTGATGCCA CCATTCCTAG GAGAGGCAGA GACCAGCCTC TAAAGCACAA GCCAAAAACT  1080
GTGTGAACGG TGAACTTTGG AGTGAAGATC AATCTTGCAC TTGGTGAAGA GTGCACATTG  1140
GACCTCAAGG CGAAAGCCAG TGGTTTGCTT GGATAAAATG TTCCCGCATG AGGCCACAGG  1200
ACTGAGGATG GGAATTTGGC AGGGCCTGAG AAGATGGTCT GACTTCCAGG CTTCCTGGTC  1260
AAAGAGAGCT ACGTTTGGGC AGTTCTGCAG AGAGGATCCT GGCAACTAGT CCCACCTGAC  1320
TAGGCCTTTA GCTGAAAGGA TTTCTTGACC TCCTTGACTG CCTCAGAGGC TGCCAGGTCA  1380
AACCCTCTTG TTTATGTGAT TAGCTCAGAG CATCTCTATG AAATCTAACC CTTCCCCTCA  1440
TGAGAAAGCA GTTTTCCCCA CCAACAGCAT AGTCAATGAG AAAGGCAACT GTACGAAGAA  1500
AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT  1560
AAATTATACA ATGT
```

Seq ID NO: 115 Protein sequence
Protein Accession #: EOS sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MLLITLSANL FTVPERSLTT TFSFSRYKSS DRPAHKVSML LLCHALAIAV VQIVIFSESW    60
AFAKNINFYN VRPPLDPTPF PNSFKCFTCE NAGDNYNCNR WAEDKWCPQN TQYCLTVHHF   120
TSHGRSTSIT KKCASRSECH FVGCHHSRDS EHTECRSCCE GMICNVELPT NHTNAVFAVM   180
HAQRTSGSSA PTLYLPVLAW VFVLP
```

Seq ID NO: 116 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1-1059

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGTATGGC AGCAAGATTA TGGAACCAGG AGAGAGCACC ATGGCTGCCG TCTGGAATTC    60
TGCCGTGTAT CTGCAGGGTG CCCTTGCCTA AGCCCCTTGA CCTCTTTGGT TATAGTTTCC   120
```

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TCATCTGCTG AGAGAGGTGA GGAAGCTGCA GAAGAAGACT TTGAAACTAG CAGAGGTGGG   180
TTCATGAGGA TGAAGGAAAG AAGCCATGCC CATAACATAA AAGTGCAAGG TGAAGCAGGA   240
GGTGCTGATG AAGAAGCTGC AGCAAGTGAT CCAGAAGATC TAGCTAAGAT CATTGATGAA   300
GATGTGAAAG GCATTGTACA GAAGAAGATG AGAATCACAG TAAACCAAAC AAAGGAAATG   360
CAGAAGAGAT ATTTTCAGCT GAATATTGGA AATGTAAAAT GCCACACGTT GGATGAGATG   420
ATTATCCGAG CTCAGACTTG GGAAATAGTC ATGCTTCTGG ACCAAGTGCC AGGTCCTGGC   480
CCTACACAAC AGGTAGATGG TTGGATATAT TTGGATAATG GAGCTTTCCA AACAGAAGCA   540
AAACACAAAC CCACTGATGT AAAATATAAA GAAACTGAAC CAGTGTGTCT TTTCACCATA   600
GATATAAGAG TTCGGACCGC CCAGCACACA AGAATAAAAC AGAAAGTCTC CATTACTTCT   660
ATGGCTACAC CATTTCCAAA TAGCTTCAAG TGCTTTACTT GTGAAAACGC AGGGGATAAT   720
TATAACTGCA ATCGATGGGC AGAAGACAAA TGGTGTCCAC AAAATACACA GTACTGTTTG   780
ACAGTTCATC ACTTCACCAG CCACGGAAGA AGCACATCCA TCACCAAAAA GTGTGCCTCC   840
AGAAGTGAAT GTCATTTTGT CGGTTGCCAC CACAGCCGAG ATTCTGAACA TACGGAGTGT   900
AGGTCTTGCT GTGAAGGAAT GATCTGCAAT GTAGAATTAC CCACCAATCA CACTAATGCA   960
GTGTTTGCCG TAATGCACGC TCAGAGAACA TCTGGCAGCA GTGCCCCCAC ACTCTACCTA  1020
CCAGTGCTTG CCTGGGTCTT TGTGCTTCCA TTGCTGTGAT GCCACCATTC CTAGGAGAGG  1080
CAGAGACCAG CCTCTAAAGC ACAAGCCAAA AACTGTGTGA ACGGTGAACT TTGGAGTGAA  1140
GATCAATCTT GCACTTGGTG AAGAGTGCAC ATTGGACCTC AAGGCGAAAG CCAGTGGTTT  1200
GCTTGGATAA AATGTTCCCG CATGAGGCCA CAGGACTGAG GATGGGAATT TGGCAGGGCC  1260
TGAGAAGATG GTCTGACTTC CAGGCTTCCT GGTCAAAGAG AGCTACGTTT GGGCAGTTCT  1320
GCAGAGAGGA TCCTGGCAAC TAGTCCCACC TGACTAGGCC TTTAGCTGAA AGGATTTCTT  1380
GACCTCCTTG ACTGCCTCAG AGGCTGCCAG GTCAAACCCT CTTGTTTATG TGATTAGCTC  1440
AGAGCATCTC TATGAAATCT AACCCTTCCC CTCATGAGAA AGCAGTTTTC CCCACCAACA  1500
GCATAGTCAA TGAGAAAGGC AACTGTACGA AGAAAACTTC CAGTGGAACT AATATGAAAT  1560
CTATTTGCAA ATTATGGGGG GAAATAAAGC TTTTAAATTA TACAATGTAA A
```

Seq ID NO: 117 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MVWQQDYGTR REHHGCRLEF CRVSAGCPCL SPLTSLVIVS SSAERGEEAA EEDFETSRGG    60
FMRMKERSHA HNIKVQGEAG GADEEAAASD PEDLAKIIDE DVKGIVQKKM RITVNQTKEM   120
QKRYFQLNIG NVKCHTLDEM IIRAQTWEIV MLLDQVPGPG PTQQVDGWIY LDNGAFQTEA   180
KHKPTDVKYK ETEPVCLFTI DIRVRTAQHT RIKQKVSITS MATPFPNSFK CFTCENAGDN   240
YNCNRWAEDK WCPQNTQYCL TVHHFTSHGR STSITKKCAS RSECHFVGCH HSRDSEHTEC   300
RSCCEGMICN VELPTNHTNA VFAVMHAQRT SGSSAPTLYL PVLAWVFVLP LL
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Seq ID NO: 118 DNA sequence
Nucleic Acid Accession #: XM_038659.6
Coding sequence: 528-1688

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1          11         21         31         41         51
|          |          |          |          |          |
AGTAGGGAGG TGGGCAGGAG CCAGTGATGA CGGAATGGCA ATCACATTTG ACCTCTGATC    60
TGTTTATTTC CTCCTCCTTG ACGTCTCCAT ATAAATGTTA CACGGGCATC CCCACACTCG   120
GATACGCACC CACAGTGGCT GATTCGGGGG TAACCGTGTC ATTTGCTTGC AACACTGGCA   180
CCTCTGCCCT GCACCCCGGG AGTGAGCAGT GAGTGAGGCT CGGGTCTGGG CGCTGGCTCC   240
GAATCTTCGG GCTGGGAGAG ACTCCACCAT CTGGGGGCGG CCTGGGGGAG CAGCCTTAGT   300
GTCTTCCTGC TGATGCAATC CGCTAGGTCG CGAGTCTCCG CCGCGAGAGG GCCGGTCTGC   360
AATCCAGCCC GCCACGTGTA CTCGCCGCCG CCTCGGGCAC TGCCCCAGGT CTTGCTGCAG   420
CCGGGACCGC GCTCTGCAGC CGCAGACCCG GTCCACACGG CCAGGGGCTA CGACCCTTGG   480
GATCTGCCCT CCGCTCAGCT CGAGCTTCCC TCGTGGCCGA CGGAACAATG AAGGATTGCA   540
GTAACGGATG CTCCGCAGAG TGTACCGGAG AAGGAGGATC AAAAGAGGTG GTGGGGACTT   600
TTAAGGCTAA AGACCTAATA GTCACACCAG CTACCATTTT AAAGGAAAAA CCAGACCCCA   660
ATAATCTGGT TTTTGGAACT GTGTTCACGG ATCATATGCT GACGGTGGAG TGGTCCTCAG   720
AGTTTGGATG GGAGAAACCT CATATCAAGC CTCTTCAGAA CCTGTCATTG CACCCTGGCT   780
CATCAGCTTT GCACTATGCA GTGGAATTAT TTGAAGGATT GAAGGCATTT CGAGGAGTAG   840
ATAATAAAAT TCGACTGTTT CAGCCAAACC TCAACATGGA TAGAATGTAT CGCTCTGCTG   900
TGAGGGCAAC TCTGCCGGTA TTTGACAAAG AAGAGCTCTT AGAGTGTATT CAACAGCTTG   960
TGAAATTGGA TCAAGAATGG GTCCCATATT CAACATCTGC TAGTCTGTAT ATTCGTCCTA  1020
CATTCATTGG AACTGAGCCT TCTCTTGGAG TCAAGAAGCC TACCAAAGCC CTGCTCTTTG  1080
TACTCTTGAG CCCAGTGGGA CCTTATTTTT CAAGTGGAAC CTTTAATCCA GTGTCCCTGT  1140
GGGCCAATCC CAAGTATGTA AGAGCCTGGA AAGGTGGAAC TGGGGACTGC AAGATGGGAG  1200
GGAATTACGG CTCATCTCTT TTTGCCCAAT GTGAAGCAGT AGATAATGGG TGTCAGCAGG  1260
TCCTGTGGCT CTATGGAGAG GACCATCAGA TCACTGAAGT GGGAACTATG AATCTTTTTC  1320
TTTACTGGAT AAATGAAGAT GGAGAAGAAG AACTGGCAAC TCCTCCACTA GATGGCATCA  1380
TTCTTCCAGG AGTGACAAGG CGGTGCATTC TGGACCTGGC ACATCAGTGG GGTGAATTTA  1440
AGGTGTCAGA GAGATACCTC ACCATGGATG ACTTGACAAC AGCCCTGGAG GGGAACAGAG  1500
TGAGAGAGAT GTTTGGCTCT GGTACAGCCT GTGTTGTTTG CCCAGTTTCT GATATACTGT  1560
ACAAAGGCGA GACAATACAC ATTCCAACTA TGGAGAATGG TCCTAAGCTG GCAAGCCGCA  1620
TCTTGAGCAA ATTAACTGAT ATCCAGTATG GAAGAGAAGA GAGCGACTGG ACAATTGTGC  1680
TATCCTGAAT GGAAAATAGA GGATACAATG GAAAATAGAG GATACCAACT GTATGCTACT  1740
GGGACAGACT GTTGCATTTG AATTGTGATA GATTTCTTTG GCTACCTGTG CATAATGTAG  1800
TTTGTAGTAT CAATGTGTTA CAAGAGTGAT TGTTTCTTCA TGCCAGAGAA AATGAATTGC  1860
AATCATCAAA TGGTGTTTCA TAACTTGGTA GTAGTAACTT ACCTTACCTT ACCTAGAAAA  1920
ACATTAATGT AAGCCATATA ACATGGGATT TTCCTCAATG ATTTTAGTGC CTCCTTTTGT  1980
ACTTCACTCA GATACTAAAT AGTAGTTTAT TCTTTAATAT AAGTTACATT CTGCTCCTCA  2040
AACAAATGCA ATTTTTTGTG TGTGTTTGAA AGCTAATTTG AGAAAATTTC ATAGGTTACA  2100
TTTCCTGCAG CCTATCTTTA TCCACAGAAA GTGTTTTCTT TTTTTTAAAT CAAGACTTTT  2160
AAAACTGGAT TTCCTCCCAT CACTGTTTTT TGAAGGTCCT CCAAGTCCGT GTTAAGGTAA  2220
ATATCTGTTT TCTTCCTGAT GTCACAGCCT GAGCATACTC TGTGCATTAG GAAGACCTGA  2280
GTGCATTTCC CACCATTGTC CTTTCCACAT TATGTTGTAG CTGGCTGGCT GTCAGGCGAC  2340
TACAAGACTG AGGGTCTTGT GCCTTATAGA TCTTTGTATC CCCCATGGCT GACATATAGT  2400
AGGTACTCAG TAAATGGTTT TATAATGAAT CAGTGAACAT TTTGCTTCTA TAGAAGTGTA  2460
CCTTCTTTGT TTCTATATTA TGAAACCTCT TTATTAGAAT TTGTGATTGA TTCTGACAGT  2520
GTATAGATTT ACCTTATATT GTCTTTATTT TCCATGAGCT ACTAAGTCAT TAGAGATACT  2580
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CTGAAGCATA GTTAGTTTAG GAAATCACTT CATATTGATT GTATTAGAAT TATCTTGGAA 2640
TTGAAGATAT ATCCCTAGAG CAGGGGACCC CAACCCCCAG GCCATGGGCC ACACAGCAGG 2700
AAGAGGTGAG TGGTGGGCCA TTGAGGAGCT TCATCTGTAT TTATGGCTAC TTCCCATCAC 2760
TCGAATTACC ACCTGAACTC CACCTCTTGT CAGCTCAGTG GCAGCATTAG ATTCTCATAG 2820
GAGCACAAAT CCTATTGTGA ACTCTGCATG CAAGGGATCT AGGCTATGCG CTCCTTATGA 2880
GAATCTAATG CTTGATGACC TGAGGTGTAA CAGTTTCATC CTGAAACCAC CCTTCACCCT 2940
GCAGTCTGTG GAAAAATTGT CTTCCACAAA ACTGGTCCCT GGTGCCAAAA ATGTTGGGGA 3000
CCACTGCTCT AGAGAGAGGT CATGATATCA TACCAACCAA ATGGAAATGA CAAATGTTTT 3060
ATGTCAAGTG TTAATTGCAG AAATAAATCT TTTTTTTTTT TTTTTGGTAG AAAACAAAGA 3120
GGCATACTCT GATTTTTATA CTCTGTTTTT GCAGGTGCTC TTTTCTTTGA ATGGAGATTT 3180
GATGAGCAAG TGGTTAGGAT GCAGGGAGAG CTACTATGGG TGATATTTTC CTTGTTTAGG 3240
AGCTGTGAGT TAAAATTGTA TCCTTTGTGG TTTATCTAAG GAAAGTCAAA TCTTGACAGA 3300
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Seq ID NO: 119 Protein sequence
Protein Accession #: XP_038659.2

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GCQQVLWLYG EDHQITEVGT MNLFLYWINE DGEEELATPP LDGIILPGVT RRCILDLAHQ  300
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Seq ID NO: 120 DNA sequence
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Coding sequence: 121..1194

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Seq ID NO: 121 Protein sequence
Protein Accession #: NP_005368

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IIAVRADLLD PRMNLFHISI HQQQHNYAAP FPPESCFQEG APKRMPPKEA LEREAPGGKD  240
DKEDEEIVSL PPVESEAAQS CQPKPIHYDT ENWTKKKYHS YLERKRRNDQ RSRFLALRDE  300
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Seq ID NO: 122 DNA sequence
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CACTCCAGGG CATCACATCC TGGGGCTCAG ACCCCTGTGG GAGGTCCGAC AAACCTGGCG   900
TCTATACCAA CATCTGCCGC TACCTGGACT GGATCAAGAA GATCATAGGC AGCAAGGGCT   960
GATTCTAGGA TAAGCACTAG ATCTCCCTTA ATAAACTCAC AACTCTC

Seq ID NO: 125 Protein sequence
Protein Accession #: NP_009127
1          11         21         31         41         51
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MGRPRPRAAK TWMFLLLLGG AWAGHSRAQE DKVLGGHECQ PHSQPWQAAL FQGQQLLCGG    60
VLVGGNWVLT AAHCKKPKYT VRLGDHSLQN KDGPEQEIPV VQSIPHPCYN SSDVEDHNHD   120
LMLLQLRDQA SLGSKVKPIS LADHCTQPGQ KCTVSGWGTV TSPRENFPDT LNCAEVKIFP   180
QKKCEDAYPG QITDGMVCAG SSKGADTCQG DSGGPLVCDG ALQGITSWGS DPCGRSDKPG   240
VYTNICRYLD WIKKIIGSKG

Seq ID NO: 126 DNA sequence
Nucleic Acid Accession #: NM_014791.1
Coding sequence: 171..2126
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TCCGCCCCTC AGGTTCTTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT   180
ATGATGAACT TCTCAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCTTTGCAA   240
AGGTCAAACT TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA   300
AAAACACACT AGGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC   360
TGAGACATCA GCATATATGT CAACTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA   420
TGGTTCTTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTTCC CAGGATCGCC   480
TGTCAGAAGA GGAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC   540
ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC   600
ATAAATTAAA GCTGATTGAC TTTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC   660
ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAAT   720
CATATCTTGG ATCAGAGGCA GATGTTTGGA GCATGGGCAT ACTGTTATAT GTTCTTATGT   780
GTGGATTTCT ACCATTTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG   840
GAAAATATGA TGTTCCCAAG TGGCTCTCTC CCAGTAGCAT TCTGCTTCTT CAACAAATGC   900
TGCAGGTGGA CCCAAAGAAA CGGATTTCTA TGAAAAATCT ATTGAACCAT CCCTGGATCA   960
TGCAAGATTA CAACTATCCT GTTGAGTGGC AAAGCAAGAA TCCTTTTATT CACCTCGATG  1020
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AAAATGTATA TACTCCTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCCTGAGC  1500
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TAAATTCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCAT TAGCCCTGAG AGGCGGTGCC  1680
GCTCAGTGGA ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG  1740
CCAAAGTGTT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA  1800
GCAAAAGGAA GGGTTCTGCC AGAGACGGGC CCAGAAGACT AAAGCTTCAC TATAATGTGA  1860
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GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGGAA  2220
CTACCAACTT GTTTCTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAAACAAAA  2280
GATATTATTT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTTT  2340
TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG  2400
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TTGTGAATAT

Seq ID NO: 127 Protein sequence
Protein Accession #: NP_055606.1
1          11         21         31         41         51
|          |          |          |          |          |
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AYVHSQGYAH RDLKPENLLF DEYHKLKLID FGLCAKPKGN KDYHLQTCCG SLAYAAPELI   180
QGKSYLGSEA DVWSMGILLY VLMCGFLPFD DDNVMALYKK IMRGKYDVPK WLSPSSILLL   240
QQMLQVDPKK RISMKNLLNH PWIMQDYNYP VEWQSKNPFI HLDDDCVTEL SVHHRNNRQT   300
MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSFSCG QASATPFTDI KSNNWSLEDV   360
TASDKNYVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL   420
KNKENVYTPK SAVKNEEYFM FPEPKTPVNK NQHKREILTT PNRYTTPSKA RNQCLKETPI   480
KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV   540
LTRSKRKGSA RDGPRRLKLH YNVTTTRLVN PDQLLNEIMS ILPKKHVDFV QKGYTLKCQT   600
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Seq ID NO: 128 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 169-1323

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GCCTCTCCGC AGCCACTCGC CACTGAGGAT GCCGATTCTG AGAATAGCAG CTTCTATTAC    240
TATGACTACC TGGATGAAGT GGCCTTCATG CTCTGCAGGA AGGATGCAGT GGTGTCCTTT    300
GGCAAAGTCT TCCTCCCAGT CTTCTATAGC CTGATTTTTG TGTTGGGCCT CAGCGGGAAC    360
CTCCTTCTTC TCATGGTCTT GCTCCGTTAC GTGCCTCGCA GGCGGATGGT TGAGATCTAT    420
CTGCTGAATC TGGCCATCTC CAACCTTCTG TTTCTGGTGA CACTGCCCTT CTGGGGCATC    480
TCCGTGGCCT GGCATTGGGT CTTCGGGAGT TTCTTGTGCA AGATGGTGAG CACTCTTTAT    540
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CCTGGCTAAT TTTTGTATTT TTTTTCTTTC TTTCTTTCTT TTCTTTTTTT TTTTTTTTTG   1860
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GGACCTAGTG CAGGAGGTTA GTCCAAAACA ATGGCCTTCC ATAGTTTTTA CTTAACAAGC   3180
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ACATTTCCCT GGTCACGGTG ATTTTTTTAG GGGTGGGCAC ATGACCTAGG TAGAGCCAAT  4320
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TGAGATCTGG AGCTACTCCT TCCTCCACCC AAACTTCAGA AGGTGAAGGA GATAGTGCAT  4440
GTGAGTGAGC AGATCCCGAG GGCACTGTTT GAGCCTCAGA ATCAAAGCAC TTCTGAAGCT  4500
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Seq ID NO: 129 Protein sequence
Protein Accession #: NP_001287.2
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LSGNLLLLMV LLRYVPRRRM VEIYLLNLAI SNLLFLVTLP FWGISVAWHW VFGSFLCKMV   120
STLYTINFYS GIFFISCMSL DKYLEIVHAQ PYHRLRTRAK SLLLATIVWA VSLAVSIPDM   180
VFVQTHENPK GVWNCHADFG GHGTIWKLFL RFQQNLLGFL LPLLAMIFFY SRIGCVLVRL   240
RPAGQGRALK IAAALVVAFF VLWFPYNLTL FLHTLLDLQV FGNCEVSQHL DYALQVTESI   300
AFLHCCFSPI LYAFSSHRFR QYLKAFLAAV LGWHLAPGTA QASLSSCSES SILTAQEEMT   360
GMNDLGERQS ENYPNKEDVG NKSA
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Seq ID NO: 130 DNA sequence
Nucleic Acid Accession #: NM_002774
Coding sequence: 246..980
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GCTGGCTCGC TCTCTCCTGG GGACACAGAG GTCGGCAGGC AGCACACAGA GGGACCTACG   180
GGCAGCTGTT CCTTCCCCCG ACTCAAGAAT CCCCGGAGGC CCGGAGGCCT GCAGCAGGAG   240
CGGCCATGAA GAAGCTGATG GTGGTGCTGA GTCTGATTGC TGCAGCCTGG GCAGAGGAGC   300
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ACATGTTGTG TGCTGGGGAT GAGAAGTACG GGAAGGATTC CTGCCAGGGT GATTCTGGGG   840
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GATCAAAGGA GAAGCCAGGA GTCTACACCA ACGTCTGCAG ATACACGAAC TGGATCCAAA   960
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Seq ID NO: 131 Protein sequence
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AHCKKPNLQV FLGKHNLRQR ESSQEQSSVV RAVIHPDYDA ASHDQDIMLL RLARPAKLSE   120
LIQPLPLERD CSANTTSCHI LGWGKTADGD FPDTIQCAYI HLVSREECEH AYPGQITQNM   180
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IQAK
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Seq ID NO: 132 DNA sequence
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TTCGGCAGGC TCTTTTCCAC AATGGCCCCC CTGACCAGCG CGTCGACCGC GGCCGCGCTC 1500
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Seq ID NO: 133 Protein sequence
Protein Accession #: AAK93901.1
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PFVPPPPALD ELGGPGGVTH PEERLGVAGG PGSAPAAGGG TGTEDDEEEL LEDEEDEDEE 240
EELLEDDEEE LLEEDDARALL KEPRRCPVAA TGAVAAAAAA AVATEGGELS PKEELLLHPE 300
DAEGKDGEDS VCLSAGSDSE EGLLKRKQRR YRTTFTSYQL EELERAFQKT HYPDVFTREE 360
LAMRLDLTEA RVQVWFQNRR AKWRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASPFP 420
PHHPALDSAW TAAAAAAAAA FPSLPPPPGS ASLPPSGAPL GLSTFLGAAV FRHPAFISPA 480
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EHAAQLTQLN ILPGTSTGKE VC

Seq ID NO: 134 DNA sequence
Nucleic Acid Accession #: CAT cluster
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CACGTAGCAC ACACATATTC AGCCATATCA TGCTGAATGG GAATACAGGA CTTTGTAGAA 180
ACAGAACTGA TTCCTGCAGA ATATCCTGAG ATACTTATCA AGCTGTTAAA GGAGACATCA 240
GTCTTTTGTC TGTATTGCCC TTGACACCTC CTCAAGGAAA GTATCTAGAA ATTCTTTGTC 300
TTCTGAAGAA CCCTCAGACC TCTTAGGTCT AATGTAGGTT AAGTGCCCTG CAGATCTCCC 360
TAGAATAGAA AAGCACCTTG AAAACTGTAG TCTGACTTAA TAGACACAAA TATAATGAAA 420
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Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_006799
Coding sequence: 19..963
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GCCGCGGGAG AGGAGGCCAT GGGCGCGCGC GGGGCGCTGC TGCTGGCGCT GCTGCTGGCT 60
CGGGCTGGAC TCAGGAAGCC GGAGTCGCAG GAGGCGGCGC CGTTATCAGG ACCATGCGGC 120
CGACGGGTCA TCACGTCGCG CATCGTGGGT GGAGAGGACG CCGAACTCGG GCGTTGGCCG 180
TGGCAGGGGA GCCTGCGCCT GTGGGATTCC CACGTATGCG GAGTGAGCCT GCTCAGCCAC 240
CGCTGGGCAC TCACGGCGGC GCACTGCTTT GAAACCTATA GTGACCTTAG TGATCCCTCC 300
GGGTGGATGG TCCAGTTTGG CCAGCTGACT TCCATGCCAT CCTTCTGGAG CCTGCAGGCC 360
TACTACACCC GTTACTTCGT ATCGAATATC TATCTGAGCC CTCGCTACCT GGGGAATTCA 420
CCCTATGACA TTGCCTTGGT GAAGCTGTCT GCACCTGTCA CCTACACTAA ACACATCCAG 480
CCCATCTGTC TCCAGGCCTC CACATTTGAG TTTGAGAACC GGACAGACTG CTGGGTGACT 540
GGCTGGGGGT ACATCAAAGA GGATGAGGCA CTGCCATCTC CCCACACCCT CCAGGAAGTT 600
CAGGTCGCCA TCATAAACAA CTCTATGTGC AACCACCTCT TCCTCAAGTA CAGTTTCCGC 660
AAGGACATCT TTGGAGACAT GGTTTGTGCT GGCAATGCCC AAGGCGGGAA GGATGCCTGC 720
TTCGGTGACT CAGGTGGACC CTTGGCCTGT AACAAGAATG GACTGTGGTA TCAGATTGGA 780
GTCGTGAGCT GGGGAGTGGG CTGTGGTCGG CCCAATCGGC CCGGTGTCTA CACCAATATC 840
AGCCACCACT TTGAGTGGAT CCAGAAGCTG ATGGCCCAGA GTGGCATGTC CCAGCCAGAC 900
CCCTCCTGGC CGCTACTCTT TTTCCCTCTT CTCTGGGCTC TCCCACTCCT GGGGCCGGTC 960
TGAGCCTACC TGAGCCCATG CAGCCTGGGG CCACTGCCAA GTCAGGCCCT GGTTCTCTTC 1020
TGTCTTGTTT GGTAATAAAC ACATTCCAGT TGATGCCTTG CAGGGCATTC TTCAAAA

Seq ID NO: 136 Protein sequence
Protein Accession #: NP_006790
1 11 21 31 41 51
| | | | | |
MGARGALLLA LLLARAGLRK PESQEAAPLS GPCGRRVITS RIVGGEDAEL GRWPWQGSLR 60
LWDSHVCGVS LLSHRWALTA AHCFETYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF 120
VSNIYLSPRY LGNSPYDIAL VKLSAPVTYT KHIQPICLQA STFEFENRTD CWVTGWGYIK 180
EDEALPSPHT LQEVQVAIIN NSMCNHLFLK YSFRKDIFGD MVCAGNAQGG KDACFGDSGG 240
PLACNKNGLW YQIGVVSWGV GCGRPNRPGV YTNISHHFEW IQKLMAQSGM SQPDPSWPLL 300
FFPLLWALPL LGPV

Seq ID NO: 137 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..939
1 11 21 31 41 51
| | | | | |
ATGGGCGCGC GCGGGGCGCT GCTGCTGGCG CTGCTGCTGG CTCGGGCTGG ACTCAGGAAG 60
CCGGAGTCGC AGGAGGCGGC GCCGTTATCA GGACCATGCG GCCGACGGGT CATCACGTCG 120
CGCATCGTGG GTGGAGAGGA CGCCGAACTC GGGCGTTGGC CGTGGCAGGG GAGCCTGCGC 180

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CTGTGGGATT CCCACGTATG CGGAGTGAGC CTGCTCAGCC ACCGCTGGGC ACTCACGGCG   240
GCGCACTGCT TTGAAACTGA CCTTAGTGAT CCCTCCGGGT GGATGGTCCA GTTTGGCCAG   300
CTGACTTCCA TGCCATCCTT CTGGAGCCTG CAGGCCTACT ACACCCGTTA CTTCGTATCG   360
AATATCTATC TGAGCCCTCG CTACCTGGGG AATTCACCCT ATGACATTGC CTTGGTGAAG   420
CTGTCTGCAC CTGTCACCTA CACTAAACAC ATCCAGCCCA TCTGTCTCCA GGCCTCCACA   480
TTTGAGTTTG AGAACCGGAC AGACTGCTGG GTGACTGGCT GGGGGTACAT CAAAGAGGAT   540
GAGGCACTGC CATCTCCCCA CACCCTCCAG GAAGTTCAGG TCGCCATCAT AAACAACTCT   600
ATGTGCAACC ACCTCTTCCT CAAGTACAGT TTCCGCAAGG ACATCTTTGG AGACATGGTT   660
TGTGCTGGCA ATGCCCAAGG CGGGAAGGAT GCCTGCTTCG GTGACTCAGG TGGACCCTTG   720
GCCTGTAACA AGAATGGACT GTGGTATCAG ATTGGAGTCG TGAGCTGGGG AGTGGGCTGT   780
GGTCGGCCCA ATCGGCCCGG TGTCTACACC AATATCAGCC ACCACTTTGA GTGGATCCAG   840
AAGCTGATGG CCCAGAGTGG CATGTCCCAG CCAGACCCCT CCTGGCCACT ACTCTTTTTC   900
CCTCTTCTCT GGGCTCTCCC ACTCCTGGGG CCGGTCTGA
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Seq ID NO: 138 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MGARGALLLA LLLARAGLRK PESQEAAPLS GPCGRRVITS RIVGGEDAEL GRWPWQGSLR    60
LWDSHVCGVS LLSHRWALTA AHCFETDLSD PSGWMVQFGQ LTSMPSFWSL QAYYTRYFVS   120
NIYLSPRYLG NSPYDIALVK LSAPVTYTKH IQPICLQAST PEFENRTDCW VTGWGYIKED   180
EALPSPHTLQ EVQVAIINNS MCNHLFLKYS FRKDIFGDMV CAGNAQGGKD ACFGDSGGPL   240
ACNKNGLWYQ IGVVSWGVGC GRPNRPGVYT NISHHFEWIQ KLMAQSGMSQ PDPSWPLLFF   300
PLLWALPLLG PV
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Seq ID NO: 139 DNA sequence
Nucleic Acid Accession #: NM_014344
Coding sequence: 131..1444

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1          11         21         31         41         51
|          |          |          |          |          |
GCGGCCGCGA TGGGGCCGAA GCGCCCGAAG CCCCGGAGCC CACAAACTGC CGGGCCCGCC    60
TCGCCGCCGG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG GCGGCGGCGC ACCGGCACAG   120
CCGCGGGAGC ATGGGCAGGA GGATGCGGGG CGCCGCCGCC ACCGCGGGGC TCTGGCTGCT   180
GGCGCTGGGC TCGCTGCTGG CGCTGTGGGG AGGGCTCCTG CCGCCGCGGA CCGAGCTGCC   240
CGCCTCCCGG CCGCCCGAAG ACCGACTCCC ACGGCGCCCG GCCCGGAGCG GCGGCCCCGC   300
GCCCGCGCCT CGCTTCCCTC TGCCCCCGCC CCTGGCGTGG GACGCCCGCG GCGGCTCCCT   360
GAAAACTTTC CGGGCGCTGC TCACCCTGGC GGCCGGCGCG GACGGCCCGC CCCGGCAGTC   420
CCGGAGCGAG CCCAGGTGGC ACGTGTCAGC CAGGCAGCCC CGGCCGGAGG AGAGCGCCGC   480
GGTGCACGGG GGCGTCTTCT GGAGCCGCGG CCTGGAGGAG CAGGTGCCCC CGGGCTTTTC   540
GGAGGCCCAG GCGGCGGCGT GGCTGGAGGC GGCTCGCGGC GCCCGGATGG TGGCCCTGGA   600
GCGCGGGGGT TGCGGGCGCA GCTCCAACCG ACTGGCCCGT TTTGCCGACG GCACCCGCGC   660
CTGCGTGCGC TACGGCATCA ACCCGGAGCA GATTCAGGGC GAGGCCCTGT CTTACTATCT   720
GGCGCGCCTG CTGGGCCTCC AGCGCCACGT GCCGCCGCTG GCACTGGCTC GGGTGGAGGC   780
TCGGGGCGCG CAGTGGGCGC AGGTGCAGGA GGAGCTGCGC GCTGCGCACT GGACCGAGGG   840
CAGCGTGGTG AGCCTGACAC GCTGGCTGCC CAACCTCACG GACGTGGTGG TGCCCGCGCC   900
CTGGCGCTCG GAGGACGGCC GTCTGCGCCC CCTCCGGGAT GCCGGGGGTG AGCTGGCCAA   960
CCTCAGCCAG GCGGAGCTGG TGGACCTAGT ACAATGGACC GACTTAATCC TTTTCGACTA  1020
CCTGACGGCC AACTTCGACC GGCTCGTAAG CAACCTCTTC AGCCTGCAGT GGGACCCGCG  1080
CGTCATGCAG CGTGCCACCA GCAACCTGCA CCGCGGTCCG GGCGGGGCGC TGGTCTTTCT  1140
GGACAATGAG GCGGGCTTGG TGCACGGCTA CCGGGTAGCA GGCATGTGGG ACAAGTATAA  1200
CGAGCCGCTG TTGCAGTCAG TGTGCGTGTT CCGCGAGCGG ACCGCGCGGC GCGTCCTGGA  1260
GCTGCACCGC GGACAGGACG CCGCGGCCCG GCTGCTGCGC CTCTACCGGC GCCACGAGCC  1320
TCGCTTCCCC GAGCTGGCCG CCCTTGCAGA CCCCCACGCT CAGCTGCTAC AGCGCCGCCT  1380
CGACTTCCTC GCCAAGCACA TTTTGCACTG TAAGGCCAAG TACGGCCGCC GGTCTGGGAC  1440
TTAGTGTCAC CGGGAGGAAA AGAGAGAGAT CTGGGGCTGG GGTATGGATG ATGGGGGGAA  1500
GGGCGGTCGC CTCTGCCACT GTCAGGGACC AGCCGGCCAA CGCCCACCCG CAAAGGTGTC  1560
TAAAAACTTC AGCTTTTCAC CCACCTGCCC CTTTCTTTCA ATCCCACGCT GTTTCCTTTC  1620
AAAGTTCTGG GAGGACGAAC TCACCGAGGC GAGAAGTGTA ACATTCTCTC CACCCAGCTT  1680
ATAAAAGGAT TCTTTACTGT GCCAGCACGG GGATTGGATC CGAAGAAACT GGCTACTGGG  1740
GTTTGGCCCC CGAGTGGCCG TCCCTGTGGG AGATGCACCC CATTCTTGGG CCCCCCTCAT  1800
TCCCTTTCCG AAAAAGGAAA ACTTGCGTTT GAGCCGTTGA GCTAATTCTG CAATTTTCTA  1860
CCAAACAGAG CGCTGGTGGC CCCGGAGCAG GGCTGTGACA TTGGCTGGTG GAGCCCCTTC  1920
CTGTGTTCTC CCTTTGTTCC AGCGCCGCGA TGGTGAGATC ACTGTTCCAA GCAGGGGGAC  1980
GGCTCGCGAT AGGACAAAGA GAGCAGGACC TCCAGACTCT GGGGAGCCCT GCAGACCTTG  2040
ACAATTTGCC TGACTCATTC CTGACCTCTT GTCATTTTGG CCTGAAGGCT ACAAATTCAG  2100
GGTCAGCTGT ATGCACTAAG TCAAATAATG AATTTCTTCC TCCCTCTCGC AACCGACCAA  2160
AATTTTGACA ACGATGATGT TCACCAGAAG GAAAAAAAAA TCAGTTTTAT GCACTTTATT  2220
TTGTTTTGAT TTTCATTTTT TATTAAGAAA AAATTTTATT TTACAGAATT TACCTTCTCT  2280
GTATATATGT GCATAAAGTG TGGTGTAAAT ATACTAAACA AACTTATATT TCAATAAAAG  2340
GGAGTTTAAA ATTTAAAAAA AAAAAAA
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Seq ID NO: 140 Protein sequence
Protein Accession #: NP_055159

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1          11         21         31         41         51
|          |          |          |          |          |
MGRRMRGAAA TAGLWLLALG SLLALWGGLL PPRTELPASR PPEDRLPRRP ARSGGPAPAP    60
RFPLPPPLAW DARGGSLKTF RALLTLAAGA DGPPRQSRSE PRWHVSARQP RPEESAAVHG   120
GVFWSRGLEE QVPPGPSEAQ AAAWLEAARG ARMVALERGG CGRSSNRLAR FADGTRACVR   180
YGINPEQIQG EALSYYLARL LGLQRHVPPL ALARVEARGA QWAQVQEELR AAHWTEGSVV   240
SLTRWLPNLT DVVVPAPWRS EDGRLRPLRD AGGELANLSQ AELVDLVQWT DLILFDYLTA   300
NFDRLVSNLF SLQWDPRVMQ RATSNLHRGP GGALVFLDNE AGLVHGYRVA GMWDKYNEPL   360
LQSVCVFRER TARRVLELHR GQDAAARLLR LYRRHEPRFP ELAALADPHA QLLQRRLDFL   420
AKHILHCKAK YGRRSGT
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Seq ID NO: 141 DNA sequence

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Nucleic Acid Accession #: Eos sequence
Coding sequence: 11..574
1          11         21         31         41         51
|          |          |          |          |          |
GTCCGCCAAG ATGCCTGCCC CAGTCCCTCT GCTGTCTGCA GCCCAGCCTT CACCCTCTTG    60
CATGGGGAAA TCGTCTACAG ACTTCTGCCC ATGGCTGTAT GTACGCACGG ACAGAGCTAG   120
CAATGACCCT GCTGGCAGGT ATGATAGGAA GCCTCTTCTG TCACAGGATT CATTCCCAGA   180
CAATGACCCC AAATGCCTGT CCCTGCTCCC CCCACCCCCC AACATCAAAA TAGCCGAGAA   240
AAATGCCCTT CTCGGAGCCA AATGTGTGGT GATGCCTTAC AATCAGAAAT TCCTACAGTG   300
GCCTGAGGCT TCCACCACTA AACGCAAAGC TGTAGATACC TATTGCTTGG ATTATAAGCC   360
TTCCAAGGGA AGAAGGTGGG CTGCAAGAGC ACCAAGCACC AGAATCACAT ATGGGACTAT   420
CACCAAAGAG AGAGACTACT GCGCGGAAGA CCAGACTATC GAGAGCTGGA GAGAAGAAGG   480
TTTCCCAGTG GGCTTGAAGC TTGCTGTGCT TGGTATTTTC ATCATTGTGG TGTTTGTCTA   540
CCTGACTGTG GAAAATAAGT CGCTGTTTGG TTAAGTAATT TAGG
```

```
Seq ID NO: 142 Protein sequence
Protein Accession #: Eos sequence
1          11         21         31         41         51
|          |          |          |          |          |
MPAPVPLLSA AQPSPSCMGK SSTDFCPWLY VRTDRASNDP AGRYDRKPLL SQDSFPDNDP    60
KCLSLLPPPP NIKIAEKNAL LGAKCVVMPY NQKFLQWPEA STTKRKAVDT YCLDYKPSKG   120
RRWAARAPST RITYGTITKE RDYCAEDQTI ESWREEGFPV GLKLAVLGIF IIVVFVYLTV   180
ENKSLFG
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Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: XM_050184.6
Coding sequence: 39..365
1          11         21         31         41         51
|          |          |          |          |          |
GATTCTACCA TCAGAAAAGA GGCCAAACTT CTATCATCAT GGTGGATGTG AAGTGTCTGA    60
GTGACTGTAA ATTGCAGAAC CAACTTGAGA AGCTTGGATT TTCACCTGGC CCAATACTAC   120
CTTCCACCAG AAAGTTGTAT GAAAAAAAGT TAGTACAGTT GTTGGTCTCA CCTCCCTGTG   180
CACCACCTGT GATGAATGGA CCCAGAGAGC TGGATGGAGC GCAGGACAGT GATGACAGCG   240
AAGGTGGGCT GCAAGAGCAC CAAGCACCAG AATCACATAT GGGACTATCA CCAAAGAGAG   300
AGACTACTGC GCGGAAGACC AGACTATCGA GAGCTGGAGA GAAGAAGGTT TCCCAGTGGG   360
CTTGAAGCTT GCTGTGCTTG GTATTTTCAT CATTGTGGTG TTTGTCTACC TGACTGTGGA   420
AAATAAGTCG CTGTTTGGTT AAGTAATTTA GGAGCAAAGC AATGCTCCAA GCGAGGCCTC   480
CTGCTTCAGG AAAGAACCAA AACACTACCC TGAAGGGCCA GCCTAGCCTG CAGCCCTCCC   540
TTGCAGGGAG CCTTCCCTTG CACTGTGCTG CTCTCACAGA TCGGTGTCTG GGCTCAGCCA   600
GGTGGAAGGA ACCTGCCTAA CCAGGCACCT GTGTTAAGAG CATGATGGTT AGGAAATCCC   660
CCAAGTCATG TCAACTCTCA TTAAAGGTGC TTCCATATTT GAGCAGGCGT CAAAC
```

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Seq ID NO: 144 Protein sequence
Protein Accession #: XP_050184.1
1          11         21         31         41         51
|          |          |          |          |          |
MVDVKCLSDC KLQNQLEKLG FSPGPILPST RKLYEKKLVQ LLVSPPCAPP VMNGPRELDG    60
AQDSDDSEGG LQEHQAPESH MGLSPKRETT ARKTRLSRAG EKKVSQWA
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Seq ID NO: 145 DNA sequence
Nucleic Acid Accession #: NM_002204.1
Coding sequence: 74..3229
1          11         21         31         41         51
|          |          |          |          |          |
AGGTGAACAG GTCCTCACGC CCAGCTCCGC CCCCTCACGC GCTCTCGCCG GGACCCCGCT    60
TCCGCTGGCA GCCATGGGCC CCGGCCCCAG CCGCGCGCCC CGCGCCCCAC GCCTGATGCT   120
CTGTGCGCTC GCCTTGATGG TGGCGGCCGG CGGCTGCGTC GTCTCCGCCT TCAACCTGGA   180
TACCCGATTC CTGGTAGTGA AGGAGGCCGG GAACCCGGGC AGCCTCTTCG GCTACTCGGT   240
CGCCCTCCAT CGGCAGACAG AGCGGCAGCA GCGCTACCTG CTCCTGGCTG GTGCCCCCCG   300
GGAGCTCGCT GTGCCCGATG GCTACACCAA CCGGACTGGT GCTGTGTACC TGTGCCCACT   360
CACTGCCCAC AAGGATGACT GTGAGCGGAT GAACATCACA GTGAAAAATG ACCCTGGCCA   420
TCACATTATT GAGGACATGT GGCTTGGAGT GACTGTGGCC AGCCAGGGCC CTGCAGGCAG   480
AGTTCTGGTC TGTGCCCACC GCTACACCCA GGTGCTGTGG TCAGGGTCAG AAGACCAGCG   540
GCGCATGGTG GGCAAGTGCT ACGTGCGAGG CAATGACCTA GAGCTGGACT CCAGTGATGA   600
CTGGCAGACC TACCACAACG AGATGTGCAA TAGCAACACA GACTACCTGG AGACGGGCAT   660
GTGCCAGCTG GGCACCAGCG GTGGCTTCAC CCAGAACACT GTGTACTTCG GCGCCCCCGG   720
TGCCTACAAC TGGAAAGGAA ACAGCTACAT GATTCAGCGC AAGGAGTGGG ACTTATCTGA   780
GTATAGTTAC AAGGACCCAG AGGACCAAGG AAACCTCTAT ATTGGGTACA CGATGCAGGT   840
AGGCAGCTTC ATCCTGCACC CCAAAAACAT CACCATTGTG ACAGGTGCCC CACGGCACCG   900
ACATATGGGC GCGGTGTTCT TGCTGAGCCA GGAGGCAGGC GGAGACCTGC GGAGGAGGCA   960
GGTGCTGGAG GGCTCGCAGG TGGGCGCCTA TTTTGGCAGC GCAATTGCCC TGGCAGACCT  1020
GAACAATGAT GGGTGGCAGG ACCTCCTGGT GGGCGCCCCC TACTACTTCG AGAGGAAAGA  1080
GGAAGTAGGG GGTGCCATCT ATGTCTTCAT GAACCAGGCG GGAACCTCCT TCCCTGCTCA  1140
CCCCTCACTC CTTCTTCATG GCCCCAGTGG CTCTGCCTTT GGTTTATCTG TGGCCAGCAT  1200
TGGTGACATC AACCAGGATG GATTTCAGGA TATTGCTGTG GGAGCTCCGT TTGAAGGCTT  1260
GGGCAAAGTG TACATCTATC ACAGTAGCTC TAAGGGGCTC CTTAGACAGC CCCAGCAGGT  1320
AATCCATGGA GAGAAGCTGG GACTGCCTGG GTTGGCCACC TTCGGCTATT CCCTCAGTGG  1380
GCAGATGGAT GTGGATGAGA ACTTCTACCC AGACCTTCTA GTGGGAAGCC TGTCAGACCA  1440
CATTGTGCTG CTGCGGGCCC GGCCAGTCAT CAACATCGTC CACAAGACCT TGGTGCCCAG  1500
GCCAGCTGTG CTGGACCCTG CACTTTGCAC GGCCACCTCT TGTGTGCAAG TGGAGCTGTG  1560
CTTTGCTTAC AACCAGAGTG CCGGGAACCC CAACTACAGG CGAAACATCA CCCTGGCCTA  1620
CACTCTGGAG GCTGACAGGG ACCGCCGGCC GCCCCGGCTC CGCTTTGCCG GCAGTGAGTC  1680
CGCTGTCTTC CACGGCTTCT TCTCCATGCC CGAGATGCGC TGCCAGAAGC TGGAGCTGCT  1740
CCTGATGGAC AACCTCCGTG ACAAACTCCG CCCCATCATC ATCTCCATGA ACTACTCTTT  1800
ACCTTTGCGG ATGCCCGATC GCCCCCGGCT GGGGCTGCGG TCCCTGGACG CCTACCCGAT  1860
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CCTCAACCAG GCACAGGCTC TGGAGAACCA CACTGAGGTC CAGTTCCAGA AGGAGTGCGG 1920
GCCTGACAAC AAGTGTGAGA GCAACTTGCA GATGCGGGCA GCCTTCGTGT CAGAGCAGCA 1980
GCAGAAGCTG AGCAGGCTCC AGTACAGCAG AGACGTCCGG AAATTGCTCC TGAGCATCAA 2040
CGTGACGAAC ACCCGGACCT CGGAGCGCTC CGGGGAGGAC GCCCACGAGG CGCTGCTCAC 2100
CCTGGTGGTG CCTCCCGCCC TGCTGCTGTC CTCAGTGCGC CCCCCCGGGG CCTGCCAAGC 2160
TAATGAGACC ATCTTTTGCG AGCTGGGGAA CCCCTTCAAA CGGAACCAGA GGATGGAGCT 2220
GCTCATCGCC TTTGAGGTCA TCGGGGTGAC CCTGCACACA AGGGACCTTC AGGTGCAGCT 2280
GCAGCTCTCC ACGTCGAGTC ACCAGGACAA CCTGTGGCCC ATGATCCTCA CTCTGCTGGT 2340
GGACTATACA CTCCAGACCT CGCTTAGCAT GGTAAATCAC CGGCTACAAA GCTTCTTTGG 2400
GGGGACAGTG ATGGGTGAGT CTGGCATGAA AACTGTGGAG GATGTAGGAA GCCCCCTCAA 2460
GTATGAATTC CAGGTGGGCC CAATGGGGGA GGGGCTGGTG GGCCTGGGGA CCCTGGTCCT 2520
AGGTCTGGAG TGGCCCTACG AAGTCAGCAA TGGCAAGTGG CTGCTGTATC CCACGGAGAT 2580
CACCGTCCAT GGCAATGGGT CCTGGCCCTG CCGACCACCT GGAGACCTTA TCAACCCTCT 2640
CAACCTCACT CTTTCTGACC CTGGGGACAG GCCATCATCC CCACAGCGCA GGCGCCGACA 2700
GCTGGATCCA GGGGGAGGCC AGGGCCCCCC ACCTGTCACT CTGGCTGCTG CCAAAAAAGC 2760
CAAGTCTGAG ACTGTGCTGA CCTGTGCCAC AGGGCGTGCC CACTGTGTGT GGCTAGAGTG 2820
CCCCATCCCT GATGCCCCCG TTGTCACCAA CGTGACTGTG AAGGCACGAG TGTGGAACAG 2880
CACCTTCATC GAGGATTACA GAGACTTTGA CCGAGTCCGG GTAAATGGCT GGGCTACCCT 2940
ATTCCTCCGA ACCAGCATCC CCACCATCAA CATGGAGAAC AAGACCACGT GGTTCTCTGT 3000
GGACATTGAC TCGGAGCTGG TGGAGGAGCT GCCGGCCGAA ATCGAGCTGT GGCTGGTGCT 3060
GGTGGCCGTG GGTGCAGGGC TGCTGCTGCT GGGGCTGATC ATCCTCCTGC TGTGGAAGTG 3120
CGGCTTCTTC AAGCGAGCCC GCACTCGCGC CCTGTATGAA GCTAAGAGGC AGAAGGCGGA 3180
GATGAAGAGC CAGCCGTCAG AGACAGAGAG GCTGACCGAC GACTACTGAG GGGGCAGCCC 3240
CCCGCCCCCG GCCCACCTGG TGTGACTTCT TTAAGCGGAC CCGCTATTAT CAGATCATGC 3300
CCAAGTACCA CGCAGTGCGG ATCCGGGAGG AGGAGCGCTA CCCACCTCCA GGGAGCACCC 3360
TGCCCACCAA GAAGCACTGG GTGACCAGCT GGCAGACTCG GGACCAATAC TACTGACGTC 3420
CTCCCTGATC CCACCCCCTC CTCCCCCAGT GTCCCCTTTC TTCCTATTTA TCATAAGTTA 3480
TGCCTCTGAC AGTCCACAGG GGCCACCACC TTTGGCTGGT AGCAGCAGGC TCAGGCACAT 3540
ACACCTCGTC AAGAGCATGC ACATGCTGTC TGGCCCTGGG GATCTTCCCA CAGGAGGGCC 3600
AGCGCTGTGG ACCTTACAAC GCCGAGTGCA CTGCATTCCT GTGCCCTAGA TGCACGTGGG 3660
GCCCACTGCT CGTGGACTGT GCTGGTGCAT CACGGATGGT GCATGGGCTC GCCGTGTCTC 3720
AGCCTCTGCC AGCGCCAGCG CCAAAACAAG CCAAAGAGCC TCCCACCAGA GCCGGGAGGA 3780
AAAGGCCCCT GCAATGTGGT GACACCTCCC CTTTCACACC TGGATCCATC TTGAGAGCCA 3840
CAGTCACTGG ATTGACTTTG CTGTCAAAAC TACTGACAGG GAGCAGCCCC CGGGCCGCTG 3900
GCTGGTGGGC CCCCAATTGA CACCCATGCC AGAGAGGTGG GGATCCTGCC TAAGGTTGTC 3960
TACGGGGGCA CTTGGAGGAC CTGGCGTGCT CAGACCCAAC AGCAAAGGAA CTAGAAAGAA 4020
GGACCCAGAA GGCTTGCTTT CCTGCATCTC TGTGAAGCCT CTCTCCTTGG CCACAGACTG 4080
AACTCGCAGG GAGTGCAGCA GGAAGGAACA AAGACAGGCA AACGGCAACG TAGCCTGGGC 4140
TCACTGTGCT GGGGCATGGC GGGATCCTCC ACAGAGAGGA GGGGACCAAT TCTGGACAGA 4200
CAGATGTTGG GAGGATACAG AGGAGATGCC ACTTCTCACT CACCACTACC AGCCAGCCTC 4260
CAGAAGGCCC CAGAGAGACC CTGCAAGACC ACGGAGGGAG CCGACACTTG AATGTAGTAA 4320
TAGGCAGGGG GCCCTGCCAC CCCATCCAGC CAGACCCCAG CTGAACCATG CGTCAGGGGC 4380
CTAGAGGTGG AGTTCTTAGC TATCCTTGGC TTTCTGTGCC AGCCTGGCTC TGCCCCTCCC 4440
CCATGGGCTG TGTCCTAAGG CCCATTTGAG AAGCTGAGGC TAGTTCCAAA AACCTCTCCT 4500
GACCCCTGCC TGTTGGCAGC CCACTCCCCA GCCCCAGCCC CTTCCATGGT ACTGTAGCAG 4560
GGGAATTCCC TCCCCCTCCT TGTGCCTTCT TTGTATATAG GCTTCTCACC GCGACCAATA 4620
AACAGCTCCC AGTTTGT

Seq ID NO: 146 Protein sequence
Protein Accession #: NP_002195.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGPGPSRAPR APRLMLCALA LMVAAGGCVV SAFNLDTRPL VVKEAGNPGS LFGYSVALHR    60
QTERQQRYLL LAGAPRELAV PDGYTNRTGA VYLCPLTAHK DDCERMNITV KNDPGHHIIE   120
DMWLGVTVAS QGPAGRVLVC AHRYTQVLWS GSEDQRRMVG KCYVRGNDLE LDSSDDWQTY   180
HNEMCNSNTD YLETGMCQLG TSGGFTQNTV YFGAPGAYNW KGNSYMIQRK EWDLSEYSYK   240
DPEDQGNLYI GYTMQVGSFI LHPKNITIVT GAPRHRHMGA VFLLSQEAGG DLRRRQVLEG   300
SQVGAYFGSA IALADLNNDG WQDLLVGAPY YFERKEEVGG AIYVFMNQAG TSFPAHPSLL   360
LHGPSGSAFG LSVASIGDIN QDGFQDIAVG APFEGLGKVY IYHSSSKGLL RQPQQVIHGE   420
KLGLPGLATF GYSLSGQMDV DENFYPDLLV GSLSDHIVLL RARPVINIVH KTLVPRPAVL   480
DPALCTATSC VQVELCFAYN QSAGNPNYRR NITLAYTLEA DRDRRPPRLR FAGSESAVFH   540
GFFSMPEMRC QKLELLLMDN LRDKLRPIII SMNYSLPLRM PDRPRLGLRS LDAYPILNQA   600
QALENHTEVQ FQKECGPDNK CESNLQMRAA FVSEQQQKLS RLQYSRDVRK LLLSINVTNT   660
RTSERSGEDA HEALLTLVVP PALLLSSVRP PGACQANETI FCELGNPFKR NQRMELLIAF   720
EVIGVTLHTR DLQVQLQLST SSHQDNLWPM ILTLLVDYTL QTSLSMVNHR LQSFFGGTVM   780
GESGMKTVED VGSPLKYEFQ VGPMGEGLVG LGTLVLGLEW PYEVSNGKWL LYPTEITVHG   840
NGSWPCRPPG DLINPLNLTL SDPGDRPSSP QRRRRQLDPG GGQGPPPVTL AAAKKAKSET   900
VLTCATGRAH CVWLECPIPD APVVTNVTVK ARVWNSTFIE DYRDFDRVRV NGWATLFLRT   960
SIPTINMENK TTWFSVDIDS ELVEELPAEI ELWLVLVAVG AGLLLLGLII LLLWKCGFFK  1020
RARTRALYEA KRQKAEMKSQ PSETERLTDD Y
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Seq ID NO: 147 DNA sequence
Nucleic Acid Accession #: NM_005501.1
Coding sequence: 74..3274

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1          11         21         31         41         51
|          |          |          |          |          |
AGGTGAACAG GTCCTCACGC CCAGCTCCGC CCCCTCACGC GCTCTCGCCG GGACCCCGCT    60
TCCGCTGGCA GCCATGGGCC CCGGCCCCAG CCGCGCGCCC CGCGCCCCAC GCCTGATGCT   120
CTGTGCGCTC GCCTTGATGG TGGCGGCCGG CGGCTGCGTC GTCTCCGCCT TCAACCTGGA   180
TACCCGATTC CTGGTAGTGA AGGAGGCCGG GAACCCGGGC AGCCTCTTCG GCTACTCGGT   240
CGCCCTCCAT CGGCAGACAG AGCGGCAGCA GCGCTACCTG CTCCTGGCTG GTGCCCCCCG   300
GGAGCTCGCT GTGCCCGATG GCTACACCAA CCGGACTGGT GCTGTGTACC TGTGCCCACT   360
CACTGCCCAC AAGGATGACT GTGAGCGGAT GAACATCACA GTGAAAAATG ACCCTGGCCA   420
TCACATTATT GAGGACATGT GGCTTGGAGT GACTGTGGCC AGCCAGGGCC CTGCAGGCAG   480
AGTTCTGGTC TGTGCCCACC GCTACACCCA GGTGCTGTGG TCAGGGTCAG AAGACCAGCG   540
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GCGCATGGTG GGCAAGTGCT ACGTGCGAGG CAATGACCTA GAGCTGGACT CCAGTGATGA   600
CTGGCAGACC TACCACAACG AGATGTGCAA TAGCAACACA GACTACCTGG AGACGGGCAT   660
GTGCCAGCTG GGCACCAGCG GTGGCTTCAC CCAGAACACT GTGTACTTCG GCGCCCCCGG   720
TGCCTACAAC TGGAAAGGAA ACAGCTACAT GATTCAGCGC AAGGAGTGGG ACTTATCTGA   780
GTATAGTTAC AAGGACCCAG AGGACCAAGG AAACCTCTAT ATTGGGTACA CGATGCAGGT   840
AGGCAGCTTC ATCCTGCACC CCAAAAACAT CACCATTGTG ACAGGTGCCC CACGGCACCG   900
ACATATGGGC GCGGTGTTCT TGCTGAGCCA GGAGGCAGGC GGAGACCTGC GGAGGAGGCA   960
GGTGCTGGAG GGCTCGCAGG TGGGCGCCTA TTTTGGCAGC GCAATTGCCC TGGCAGACCT  1020
GAACAATGAT GGGTGGCAGG ACCTCCTGGT GGGCGCCCCC TACTACTTCG AGAGGAAAGA  1080
GGAAGTAGGG GGTGCCATCT ATGTCTTCAT GAACCAGGCG GGAACCTCCT TCCCTGCTCA  1140
CCCCTCACTC CTTCTTCATG GCCCCAGTGG CTCTGCCTTT GGTTTATCTG TGGCCAGCAT  1200
TGGTGACATC AACCAGGATG GATTTCAGGA TATTGCTGTG GGAGCTCCGT TTGAAGGCTT  1260
GGGCAAAGTG TACATCTATC ACAGTAGCTC TAAGGGGCTC CTTAGACAGC CCCAGCAGGT  1320
AATCCATGGA GAGAAGCTGG GACTGCCTGG GTTGGCCACC TTCGGCTATT CCCTCAGTGG  1380
GCAGATGGAT GTGGATGAGA ACTTCTACCC AGACCTTCTA GTGGGAAGCC TGTCAGACCA  1440
CATTGTGCTG CTGCGGGCCC GGCCAGTCAT CAACATCGTC CACAAGACCT TGGTGCCCAG  1500
GCCAGCTGTG CTGGACCCTG CACTTTGCAC GGCCACCTCT TGTGTGCAAG TGGAGCTGTG  1560
CTTTGCTTAC AACCAGAGTG CCGGGAACCC CAACTACAGG CGAAACATCA CCCTGGCCTA  1620
CACTCTGGAG GCTGACAGGG ACCGCCGGCC GCCCCGGCTC CGCTTTGCCG GCAGTGAGTC  1680
CGCTGTCTTC CACGGCTTCT TCTCCATGCC CGAGATGCGC TGCCAGAAGC TGGAGCTGCT  1740
CCTGATGGAC AACCTCCGTG ACAAACTCCG CCCCATCATC ATCTCCATGA ACTACTCTTT  1800
ACCTTTGCGG ATGCCCGATC GCCCCCGGCT GGGGCTGCGG TCCCTGGACG CCTACCCGAT  1860
CCTCAACCAG GCACAGGCTC TGGAGAACCA CACTGAGGTC CAGTTCCAGA AGGAGTGCGG  1920
GCCTGACAAC AAGTGTGAGA GCAACTTGCA GATGCGGGCA GCCTTCGTGT CAGAGCAGCA  1980
GCAGAAGCTG AGCAGGCTCC AGTACAGCAG AGACGTCCGG AAATTGCTCC TGAGCATCAA  2040
CGTGACGAAC ACCCGGACCT CGGAGCGCTC CGGGGAGGAC GCCCACGAGG CGCTGCTCAC  2100
CCTGGTGGTG CCTCCCGCCC TGCTGCTGTC CTCAGTGCGC CCCCCCGGGG CCTGCCAAGC  2160
TAATGAGACC ATCTTTTGCG AGCTGGGGAA CCCCTTCAAA CGGAACCAGA GGATGGAGCT  2220
GCTCATCGCC TTTGAGGTCA TCGGGGTGAC CCTGCACACA AGGGACCTTC AGGTGCAGCT  2280
GCAGCTCTCC ACGTCGAGTC ACCAGGACAA CCTGTGGCCC ATGATCCTCA CTCTGCTGGT  2340
GGACTATACA CTCCAGACCT CGCTTAGCAT GGTAAATCAC CGGCTACAAA GCTTCTTTGG  2400
GGGGACAGTG ATGGGTGAGT CTGGCATGAA AACTGTGGAG GATGTAGGAA GCCCCCTCAA  2460
GTATGAATTC CAGGTGGGCC CAATGGGGGA GGGGCTGGTG GGCCTGGGGA CCCTGGTCCT  2520
AGGTCTGGAG TGGCCCTACG AAGTCAGCAA TGGCAAGTGG CTGCTGTATC CCACGGAGAT  2580
CACCGTCCAT GGCAATGGGT CCTGGCCCTG CCGACCACCT GGAGACCTTA TCAACCCTCT  2640
CAACCTCACT CTTTCTGACC CTGGGGACAG GCCATCATCC CCACAGCGCA GGCGCCGACA  2700
GCTGGATCCA GGGGGAGGCC AGGGCCCCCC ACCTGTCACT CTGGCTGCTG CCAAAAAAGC  2760
CAAGTCTGAG ACTGTGCTGA CCTGTGCCAC AGGGCGTGCC CACTGTGTGT GGCTAGAGTG  2820
CCCCATCCCT GATGCCCCCG TTGTCACCAA CGTGACTGTG AAGGCACGAG TGTGGAACAG  2880
CACCTTCATC GAGGATTACA GAGACTTTGA CCGAGTCCGG GTAAATGGCT GGGCTACCCT  2940
ATTCCTCCGA ACCAGCATCC CCACCATCAA CATGGAGAAC AAGACCACGT GGTTCTCTGT  3000
GGACATTGAC TCGGAGCTGG TGGAGGAGCT GCCGGCCGAA ATCGAGCTGT GGCTGGTGCT  3060
GGTGGCCGTG GGTGCAGGGC TGCTGCTGCT GGGGCTGATC ATCCTCCTGC TGTGGAAGTG  3120
TGACTTCTTT AAGCGGACCC GCTATTATCA GATCATGCCC AAGTACCACG CAGTGCGGAT  3180
CCGGGAGGAG GAGCGCTACC CACCTCCAGG GAGCACCCTG CCCACCAAGA AGCACTGGGT  3240
GACCAGCTGG CAGACTCGGG ACCAATACTA CTGACGTCCT CCCTGATCCC ACCCCCTCCT  3300
CCCCCAGTGT CCCCTTTCTT CCTATTTATC ATAAGTTATG CCTCTGACAG TCCACAGGGG  3360
CCACCACCTT TGGCTGGTAG CAGCAGGCTC AGGCACATAC ACCTCGTCAA GAGCATGCAC  3420
ATGCTGTCTG GCCCTGGGGA TCTTCCCACA GGAGGGCCAG CGCTGTGGAC CTTACAACGC  3480
CGAGTGCACT GCATTCCTGT GCCCTAGATG CACGTGGGGC CCACTGCTCG TGGACTGTGC  3540
TGGTGCATCA CGGATGGTGC ATGGGCTCGC CGTGTCTCAG CCTCTGCCAG CGCCAGCGCC  3600
AAAACAAGCC AAAGAGCCTC CCACCAGAGC CGGGAGGAAA AGGCCCCTGC AATGTGGTGA  3660
CACCTCCCCT TTCACACCTG GATCCATCTT GAGAGCCACA GTCACTGGAT TGACTTTGCT  3720
GTCAAAACTA CTGACAGGGA GCAGCCCCCG GGCCGCTGGC TGGTGGGCCC CCAATTGACA  3780
CCCATGCCAG AGAGGTGGGG ATCCTGCCTA AGGTTGTCTA CGGGGGCACT TGGAGGACCT  3840
GGCGTGCTCA GACCCAACAG CAAAGGAACT AGAAAGAAGG ACCCAGAAGG CTTGCTTTCC  3900
TGCATCTCTG TGAAGCCTCT CTCCTTGGCC ACAGACTGAA CTCGCAGGGA GTGCAGCAGG  3960
AAGGAACAAA GACAGGCAAA CGGCAACGTA GCCTGGGCTC ACTGTGCTGG GGCATGGCGG  4020
GATCCTCCAC AGAGAGGAGG GGACCAATTC TGGACAGACA GATGTTGGGA GGATACAGAG  4080
GAGATGCCAC TTCTCACTCA CCACTACCAG CCAGCCTCCA GAAGGCCCCA GAGAGACCCT  4140
GCAAGACCAC GGAGGGAGCC GACACTTGAA TGTAGTAATA GGCAGGGGGC CCTGCCACCC  4200
CATCCAGCCA GACCCCAGCT GAACCATGCG TCAGGGGCCT AGAGGTGGAG TTCTTAGCTA  4260
TCCTTGGCTT TCTGTGCCAG CCTGGCTCTG CCCCTCCCCC ATGGGCTGTG TCCTAAGGCC  4320
CATTTGAGAA GCTGAGGCTA GTTCCAAAAA CCTCTCCTGA CCCCTGCCTG TTGGCAGCCC  4380
ACTCCCCAGC CCCAGCCCCT TCCATGGTAC TGTAGCAGGG GAATTCCCTC CCCCTCCTTG  4440
TGCCTTCTTT GTATATAGGC TTCTCACCGC GACCAATAAA CAGCTCCCAG TTTGT
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Seq ID NO: 148 Protein sequence
Protein Accession #: NP_005492.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGPGPSRAPR APRLMLCALA LMVAAGGCVV SAFNLDTRFL VVKEAGNPGS LFGYSVALHR    60
QTERQQRYLL LAGAPRELAV PDGYTNRTGA VYLCPLTAHK DDCERMNITV KNDPGHHIIE   120
DMWLGVTVAS QGPAGRVLVC AHRYTQVLWS GSEDQRRMVG KCYVRGNDLE LDSSDDWQTY   180
HNEMCNSNTD YLETGMCQLG TSGGFTQNTV YFGAPGAYNW KGNSYMIQRK EWDLSEYSYK   240
DPEDQGNLYI GYTMQVGSFI LHPKNITIVT GAPRHRHMGA VFLLSQEAGG DLRRRQVLEG   300
SQVGAYFGSA IALADLNNDG WQDLLVGAPY YFERKEEVGG AIYVFMNQAG TSFPAHPSLL   360
LHGPSGSAFG LSVASIGDIN QDGFQDIAVG APFEGLGKVY IYHSSSKGLL RQPQQVIHGE   420
KLGLPGLATF GYSLSGQMDV DENFYPDLLV GSLSDHIVLL RARPVINIVH KTLVPRPAVL   480
DPALCTATSC VQVELCFAYN QSAGNPNYRR NITLAYTLEA DRDRRPPRLR FAGSESAVFH   540
GFFSMPEMRC QKLELLLMDN LRDKLRPIII SMNYSLPLRM PDRPRLGLRS LDAYPILNQA   600
QALENHTEVQ FQKECGPDNK CESNLQMRAA FVSEQQQKLS RLQYSRDVRK LLLSINVTNT   660
RTSERSGEDA HEALLTLVVP PALLLSSVRP PGACQANETI FCELGNPFKR NQRMELLIAP   720
EVIGVTLHTR DLQVQLQLST SSHQDNLWPM ILTLLVDYTL QTSLSMVNHR LQSFFGGTVM   780
GESGMKTVED VGSPLKYEFQ VGPMGEGLVG LGTLVLGLEW PYEVSNGKWL LYPTEITVHG   840
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NGSWPCRPPG DLINPLNLTL SDPGDRPSSP QRRRRQLDPG GGQGPPPVTL AAAKKAKSET    900
VLTCATGRAH CVWLECPIPD APVVTNVTVK ARVWNSTFIE DYRDFDRVRV NGWATLFLRT    960
SIPTINMENK TTWFSVDIDS ELVEELPAEI ELWLVLVAVG AGLLLLGLII LLLWKCDFFK   1020
RTRYYQIMPK YHAVRIREEE RYPPPGSTLP TKKHWVTSWQ TRDQYY
```

Seq ID NO: 149 DNA sequence
Nucleic Acid Accession #: NM_006424.1
Coding sequence:

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1          11         21         31         41         51
|          |          |          |          |          |
CGGGCCAGGT TTCCAGGCTC GGCCGCCGCC TCCATCCCAG CACCTGCGGA GGGAGCGCTG     60
ACCATGGCTC CCTGGCCTGA ATTGGGAGAT GCCCAGCCCA ACCCCGATAA GTACCTCGAA    120
GGGGCCGCAG GTCAGCAGCC CACTGCCCCT GATAAAAGCA AAGAGACCAA CAAAACAGAT    180
AACACTGAGG CACCTGTAAC CAAGATTGAA CTTCTGCCGT CCTACTCCAC GGCTACACTG    240
ATAGATGAGC CCACTGAGGT GGATGACCCC TGGAACCTAC CCACTCTTCA GGACTCGGGG    300
ATCAAGTGGT CAGAGAGAGA CACCAAAGGG AAGATTCTCT GTTTCTTCCA AGGGATTGGG    360
AGATTGATTT TACTTCTCGG ATTTCTCTAC TTTTTCGTGT GCTCCCTGGA TATTCTTAGT    420
AGCGCCTTCC AGCTGGTTGG AGGAAAAATG GCAGGACAGT TCTTCAGCAA CAGCTCTATT    480
ATGTCCAACC CTTTGTTGGG GCTGGTGATC GGGGTGCTGG TGACCGTCTT GGTGCAGAGC    540
TCCAGCACCT CAACGTCCAT CGTTGTCAGC ATGGTGTCCT CTTCATTGCT CACTGTTCGG    600
GCTGCCATCC CCATTATCAT GGGGGCCAAC ATTGGAACGT CAATCACCAA CACTATTGTT    660
GCGCTCATGC AGGTGGGAGA TCGGAGTGAG TTCAGAAGAG CTTTTGCAGG AGCCACTGTC    720
CATGACTTCT TCAACTGGCT GTCCGTGTTG GTGCTCTTGC CCGTGGAGGT GGCCACCCAT    780
TACCTCGAGA TCATAACCCA GCTTATAGTG GAGAGCTTCC ACTTCAAGAA TGGAGAAGAT    840
GCCCCAGATC TTCTGAAAGT CATCACTAAG CCCTTCACAA AGCTCATTGT CCAGCTGGAT    900
AAAAAAGTTA TCAGCCAAAT TGCAATGAAC GATGAAAAAG CGAAAAACAA GAGTCTTGTC    960
AAGATTTGGT GCAAAACTTT TACCAACAAG ACCCAGATTA ACGTCACTGT TCCCTCGACT   1020
GCTAACTGCA CCTCCCCTTC CCTCTGTTGG ACGGATGGCA TCCAAAACTG GACCATGAAG   1080
AATGTGACCT ACAAGGAGAA CATCGCCAAA TGCCAGCATA TCTTTGTGAA TTTCCACCTC   1140
CCGGATCTTG CTGTGGGCAC CATCTTGCTC ATACTCTCCC TGCTGGTCCT CTGTGGTTGC   1200
CTGATCATGA TTGTCAAGAT CCTGGGCTCT GTGCTCAAGG GGCAGGTCGC CACTGTCATC   1260
AAGAAGACCA TCAACACTGA TTTCCCCTTT CCCTTTGCAT GGTTGACTGG CTACCTGGCC   1320
ATCCTCGTCG GGGCAGGCAT GACCTTCATC GTACAGAGCA GCTCTGTGTT CACGTCGGCC   1380
TTGACCCCCC TGATTGGAAT CGGCGTGATA ACCATTGAGA GGGCTTATCC ACTCACGCTG   1440
GGCTCCAACA TCGGCACCAC CACCACCGCC ATCCTGGCCG CCTTAGCCAG CCCTGGCAAT   1500
GCATTGAGGA GTTCACTCCA GATCGCCCTG TGCCACTTTT TCTTCAACAT CTCCGGCATC   1560
TTGCTGTGGT ACCCGATCCC GTTCACTCGC CTGCCCATCC GCATGGCCAA GGGGCTGGGC   1620
AACATCTCTG CCAAGTATCG CTGGTTCGCC GTCTTCTACC TGATCATCTT CTTCTTCCTG   1680
ATCCCGCTGA CGGTGTTTGG CCTCTCGCTG GCCGGCTGGC GGGTGCTGGT TGGTGTCGGG   1740
GTTCCCGTCG TCTTCATCAT CATCCTGGTA CTGTGCCTCC GACTCCTGCA GTCTCGCTGC   1800
CCACGCGTCC TGCCGAAGAA ACTCCAGAAC TGGAACTTCC TGCCGCTGTG GATGCGCTCG   1860
CTGAAGCCCT GGGATGCCGT CGTCTCCAAG TTCACCGGCT GCTTCCAGAT GCGCTGCTGC   1920
TACTGCTGCC GCGTGTGCTG CCGCGCGTGC TGCTTGCTGT GTGGCTGCCC CAAGTGCTGC   1980
CGCTGCAGCA AGTGCTGCGA GGACTTGGAG GAGGCGCAGG AGGGGCAGGA TGTCCCTGTC   2040
AAGGCTCCTG AGACCTTTGA TAACATAACC ATTAGCAGAG AGGCTCAGGG TGAGGTCCCT   2100
GCCTCGGACT CAAAGACCGA ATGCACGGCC TTGTAGGGGA CGCCCCAGAT TGTCAGGGAT   2160
GGGGGGATGG TCCTTGAGTT TTGCATGCTC TCCTCCCTCC CACTTCTGCA CCCTTTCACC   2220
ACCTCGAGGA GATTTGCTCC CCATTAGCGA ATGAAATTGA TGCAGTCCTA AAAAAAAAAA
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Seq ID NO: 150 Protein sequence:
Protein Accession #: NP_006415.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAPWPELGDA QPNPDKYLEG AAGQQPTAPD KSKETNKTDN TEAPVTKIEL LPSYSTATLI     60
DEPTEVDDPW NLPTLQDSGI KWSERDTKGK ILCFFQGIGR LILLLGFLYF FVCSLDILSS    120
AFQLVGGKMA GQFFSNSSIM SNPLLGLVIG VLVTVLVQSS STSTSIVVSM VSSSLLTVRA    180
AIPIIMGANI GTSITNTIVA LMQVGDRSEF RRAFAGATVH DFFNWLSVLV LLPVEVATHY    240
LEIITQLIVE SFHFKNGEDA PDLLKVITKP FTKLIVQLDK KVISQIAMND EKAKNKSLVK    300
IWCKTFTNKT QINVTVPSTA NCTSPSLCWT DGIQNWTMKN VTYKENIAKC QHIFVNFHLP    360
DLAVGTILLI LSLLVLCGCL IMIVKILGSV LKGQVATVIK KTINTDFPFP FAWLTGYLAI    420
LVGAGMTFIV QSSSVFTSAL TPLIGIGVIT IERAYPLTLG SNIGTTTTAI LAALASPGNA    480
LRSSLQIALC HFFFNISGIL LWYPIPFTRL PIRMAKGLGN ISAKYRWFAV FYLIIFFFLI    540
PLTVFGLSLA GWRVLVGVGV PVVFIIILVL CLRLLQSRCP RVLPKKLQNW NFLPLWMRSL    600
KPWDAVVSKF TGCFQMRCCY CCRVCCRACC LLCGCPKCCR CSKCCEDLEE AQEGQDVPVK    660
APETFDNITI SREAQGEVPA SDSKTECTAL
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Seq ID NO: 151 DNA sequence
Nucleic Acid Accession #:
Coding sequence: 1..1119

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAACCGCA GCCACCGGCA CGGGGCGGGC AGCGGCTGCC TGGGCACTAT GGAGGTGAAG     60
AGCAAGTTTG GAGCTGAATT TCGTCGGTTT TCGCTGGAAA GATCAAAACC TGGAAAATTT    120
GAGGAGTTTT ATGGATTACT ACAACATGTT CATAAGATCC CCAATGTTGA CGTTTTGGTA    180
GGCTATGCAG ACATCCATGG AGACTTACTA CCTATAAATA ATGATGATAA TTATCACAAA    240
GCTGTTTCAA CGGCCAATCC ACTGCTTAGG ATATTTATAC AAAAGAAGGA AGAAGCAGAC    300
TACAGTGCCT TTGGTACAGA CACGCTAATA AAGAAGAAGA ATGTTTTAAC CAACGTATTG    360
CGTCCTGACA ACCATAGAAA AAAGCCACAT ATAGTCATTA GTATGCCCCA AGACTTTAGA    420
CCTGTGTCTT CTATTATAGA CGTGGATATT CTCCCAGAAA CGCATCGTAG GGTACGTCTT    480
TACAAATACG GCACGGAGAA ACCCCTAGGA TTCTACATCC GGGATGGCTC CAGTGTCAGG    540
GTAACACCAC ATGGCTTAGA AAAGGTTCCA GGGATCTTTA TATCCAGGCT TGTCCCAGGA    600
GGTCTGGCTC AAAGTACAGG ACTATTAGCT GTTAATGATG AAGTTTTAGA AGTTAATGGC    660
ATAGAAGTTT CAGGGAAGAG CCTTGATCAA GTAACAGACA TGATGATTGC AAATAGCCGT    720
AACCTCATCA TAACAGTGAG ACCGGCAAAC CAGAGGAATA ATGTTGTGAG GAACAGTCGG    780
ACTTCTGGCA GTTCCGGTCA GTCTACTGAT AACAGCCTTC TTGGCTACCC ACAGCAGATT    840
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GAACCAAGCT TTGAGCCAGA GGATGAAGAC AGCGAAGAAG ATGACATTAT CATTGAAGAC   900
AATGGAGTGC CACAGCAGAT TCCAAAAGCT GTTCCTAATA CTGAGAGCCT GGAGTCATTA   960
ACACAGATAG AGCTAAGCTT TGAGTCTGGA CAGAATGGCT TTATTCCCTC TAATGAAGTG  1020
AGCTTAGCAG CCATAGCAAG CAGCTCAAAC ACGGAATTTG AAACACATGC TCCAGATCAA  1080
AAACTCTTAG AAGAAGATGG AACAATCATA ACATTATGA
```

Seq ID NO: 152 Protein sequence
Protein Accession #: XP_030559

```
1          11         21         31         41         51
|          |          |          |          |          |
MNRSHRHGAG SGCLGTMEVK SKFGAEFRRF SLERSKPGKP EEFYGLLQHV HKIPNVDVLV    60
GYADIHGDLL PINNDDNYHK AVSTANPLLR IFIQKKEEAD YSAFGTDTLI KKKNVLTNVL   120
RPDNHRKKPH IVISMPQDFR PVSSIIDVDI LPETHRRVRL YKYGTEKPLG FYIRDGSSVR   180
VTPHGLEKVP GIFISRLVPG GLAQSTGLLA VNDEVLEVNG IEVSGKSLDQ VTDMMIANSR   240
NLIITVRPAN QRNNVVRNSR TSGSSGQSTD NSLLGYPQQI EPSFEPEDED SEEDDIIIED   300
NGVPQQIPKA VPNTESLESL TQIELSFESG QNGFIPSNEV SLAAIASSSN TEFETHAPDQ   360
KLLEEDGTII TL
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Seq ID NO: 153 DNA sequence
Nucleic Acid Accession #: NM_003064.2
Coding sequence: 23..421

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1          11         21         31         41         51
|          |          |          |          |          |
CAGAGTCACT CCTGCCTTCA CCATGAAGTC CAGCGGCCTC TTCCCCTTCC TGGTGCTGCT    60
TGCCCTGGGA ACTCTGGCAC CTTGGGCTGT GGAAGGCTCT GGAAAGTCCT TCAAAGCTGG   120
AGTCTGTCCT CCTAAGAAAT CTGCCCAGTG CCTTAGATAC AAGAAACCTG AGTGCCAGAG   180
TGACTGGCAG TGTCCAGGGA AGAAGAGATG TTGTCCTGAC ACTTGTGGCA TCAAATGCCT   240
GGATCCTGTT GACACCCCAA ACCCAACAAG GAGGAAGCCT GGGAAGTGCC CAGTGACTTA   300
TGGCCAATGT TTGATGCTTA ACCCCCCCAA TTTCTGTGAG ATGGATGGCC AGTGCAAGCG   360
TGACTTGAAG TGTTGCATGG GCATGTGTGG GAAATCCTGC GTTTCCCCTG TGAAAGCTTG   420
ATTCCTGCCA TATGGAGGAG GCTCTGGAGT CCTGCTCTGT GTGGTCCAGG TCCTTTCCAC   480
CCTGAGACTT GGCTCCACCA CTGATATCCT CCTTTGGGGA AAGGCTTGGC ACACAGCAGG   540
CTTTCAAGAA GTGCCAGTTG ATCAATGAAT AAATAAACGA GCCTATTTCT CTTTGCAC
```

Seq ID NO: 154 Protein sequence
Protein Accession #: NP_003055.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKSSGLFPFL VLLALGTLAP WAVEGSGKSF KAGVCPPKKS AQCLRYKKPE CQSDWQCPGK    60
KRCCPDTCGI KCLDPVDTPN PTRRKPGKCP VTYGQCLMLN PPNFCEMDGQ CKRDLKCCMG   120
MCGKSCVSPV KA
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Seq ID NO: 155 DNA sequence
Nucleic Acid Accession #: NM_001306.1
Coding sequence: 199..861

```
1          11         21         31         41         51
|          |          |          |          |          |
AATTCGGCAC GAGGGCAGGT GCAGGCGCAC GCGGCGAGAG CGTATGGAGC CGAGCCGTTA    60
GCGCGCGCCG TCGGTGAGTC AGTCCGTCCG TCCGTCCGTC CGTCGGGGCG CCGCAGCTCC   120
CGCCAGGCCC AGCGGCCCCG GCCCCTCGTC TCCCCGCACC CGGAGCCACC CGGTGGAGCG   180
GGCCTTGCCG CGGCAGCCAT GTCCATGGGC CTGGAGATCA CGGGCACCGC GCTGGCCGTG   240
CTGGGCTGGC TGGGCACCAT CGTGTGCTGC GCGTTGCCCA TGTGGCGCGT GTCGGCCTTC   300
ATCGGCAGCA ACATCATCAC GTCGCAGAAC ATCTGGGAGG GCCTGTGGAT GAACTGCGTG   360
GTGCAGAGCA CCGGCCAGAT GCAGTGCAAG GTGTACGACT CGCTGCTGGC ACTGCCACAG   420
GACCTTCAGG CGGCCCGCGC CCTCATCGTG GTGGCCATCC TGCTGGCCGC CTTCGGGCTG   480
CTAGTGGCGC TGGTGGGCGC CCAGTGCACC AACTGCGTGC AGGACGACAC GGCCAAGGCC   540
AAGATCACCA TCGTGGCAGG CGTGCTGTTC CTTCTCGCCG CCCTGCTCAC CCTCGTGCCG   600
GTGTCCTGGT CGGCCAACAC CATTATCCGG GACTTCTACA ACCCCGTGGT GCCCGAGGCG   660
CAGAAGCGCG AGATGGGCGC GGGCCTGTAC GTGGGCTGGG CGGCCGCGGC GCTGCAGCTG   720
CTGGGGGGCG CGCTGCTCTG CTGCTCGTGT CCCCCACGCG AGAAGAAGTA CACGGCCACC   780
AAGGTCGTCT ACTCCGCGCC GCGCTCCACC GGCCCGGGAG CCAGCCTGGG CACAGGCTAC   840
GACCGCAAGG ACTACGTCTA AGGGACAGAC GCAGGGAGAC CCCACCACCA CCACCACCAC   900
CAACACCACC ACCACCACCG CGAGCTGGAG CGCGCACCAG GCCATCCAGC GTGCAGCCTT   960
GCCTCGGAGG CCAGCCCACC CCCAGAAGCC AGGAAGCCCC CGCGCTGGAC TGGGGCAGCT  1020
TCCCCAGCAG CCACGGCTTT GCGGGCCGGG CAGTCGACTT CGGGGCCCAG GGACCAACCT  1080
GCATGGACTG TGAAACCTCA CCCTTCTGGA GCACGGGGCC TGGGTGACCG CCAATACTTG  1140
ACCACCCCGT CGAGCCCCAT CGGGCCGCTG CCCCCATGTC GCGCTGGGCA GGGACCGGCA  1200
GCCCTGGAAG GGGCACTTGA TATTTTTCAA TAAAAGCCTC TCGTTTTAGC
```

Seq ID NO: 156 Protein sequence
Protein Accession #: NP_001297.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSMGLEITGT ALAVLGWLGT IVCCALPMWR VSAFIGSNII TSQNIWEGLW MNCVVQSTGQ    60
MQCKVYDSLL ALPQDLQAAR ALIVVAILLA AFGLLVALVG AQCTNCVQDD TAKAKITIVA   120
GVLFLLAALL TLVPVSWSAN TIIRDFYNPV VPEAQKREMG AGLYVGWAAA ALQLLGGALL   180
CCSCPPREKK YTATKVVYSA PRSTGPGASL GTGYDRKDYV
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Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: NM_005564
Coding sequence: 1..597

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCCCTAG GTCTCCTGTG GCTGGGCCTA GCCCTGTTGG GGGCTCTGCA TGCCCAGGCC    60
CAGGACTCCA CCTCAGACCT GATCCCAGCC CCACCTCTGA GCAAGGTCCC TCTGCAGCAG   120
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AACTTCCAGG ACAACCAATT CCAGGGGAAG TGGTATGTGG TAGGCCTGGC AGGGAATGCA   180
ATTCTCAGAG AAGACAAAGA CCCGCAAAAG ATGTATGCCA CCATCTATGA GCTGAAAGAA   240
GACAAGAGCT ACAATGTCAC CTCCGTCCTG TTTAGGAAAA AGAAGTGTGA CTACTGGATC   300
AGGACTTTTG TTCCAGGTTG CCAGCCCGGC GAGTTCACGC TGGGCAACAT TAAGAGTTAC   360
CCTGGATTAA CGAGTTACCT CGTCCGAGTG GTGAGCACCA ACTACAACCA GCATGCTATG   420
GTGTTCTTCA AGAAAGTTTC TCAAAACAGG GAGTACTTCA AGATCACCCT CTACGGGAGA   480
ACCAAGGAGC TGACTTCGGA ACTAAAGGAG AACTTCATCC GCTTCTCCAA ATATCTGGGC   540
CTCCCTGAAA ACCACATCGT CTTCCCTGTC CCAATCGACC AGTGTATCGA CGGCTGA

Seq ID NO: 158 Protein sequence
Protein Accession #: NP_005555
1          11         21         31         41         51
|          |          |          |          |          |
MPLGLLWLGL ALLGALHAQA QDSTSDLIPA PPLSKVPLQQ NFQDNQFQGK WYVVGLAGNA    60
ILREDKDPQK MYATIYELKE DKSYNVTSVL FRKKKCDYWI RTFVPGCQPG EFTLGNIKSY   120
PGLTSYLVRV VSTNYNQHAM VFFKKVSQNR EYFKITLYGR TKELTSELKE NFIRFSKYLG   180
LPENHIVFPV PIDQCIDG

Seq ID NO: 159 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874
1          11         21         31         41         51
|          |          |          |          |          |
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC    60
ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCCTCCAGGC   120
CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC   180
CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCCAG CCCTGGCAGG CAGCCCTGTT   240
CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC   300
AGCCCACTGC CTCAAGCCCC GCTACATAGT TCACCTGGGG CAGCACAACC TCCAGAAGGA   360
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCCG GCTTCAACAA   420
CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT   480
CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC   540
CAGCTGCCTC ATTTCCGGCT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCCTCACAC   600
CTTGCGATGC GCCAACATCA CCATCATTGA GCACCAGAAG TGTGAGAACG CCTACCCCGG   660
CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAGGAA GGGGGCAAGG ACTCCTGCCA   720
GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCCTGGGG   780
CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAATATGT   840
GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC   900
ACCCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCACTCT GTTAATAAGA AACCCTAAGC   960
CAAGACCCTC TACGAACATT CTTTGGGCCT CCTGGACTAC AGGAGATGCT GTCACTTAAT  1020
AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT  1080
GACTCTGGGA ATGACAACAC CTGGTTTGTT CTCTGTTGTA TCCCCAGCCC CAAAGACAGC  1140
TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

Seq ID NO: 160 Protein sequence
Protein Accession #: NP_006844.1
1          11         21         31         41         51
|          |          |          |          |          |
MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA    60
AHCLKPRYIV HLGQHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV   120
SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIIE HQKCENAYPG   180
NITDTMVCAS VQEGGKDSCQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVYTKVCKYV   240
DWIQETMKNN
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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

2. The method of claim 1, wherein the biological sample comprises isolated nucleic acids.

3. The method of claim 2, wherein the nucleic acids are mRNA.

4. The method of claim 2, further comprising the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

5. The method of claim 1, wherein the polynucleotide comprises a sequence as shown in Tables 1-26.

6. The method of claim 1, wherein the polynucleotide is immobilized on a solid surface.

7. The method of claim 1, wherein the patient is undergoing a therapeutic regimen to treat ovarian cancer.

8. The method of claim 1, wherein the patient is suspected of having ovarian cancer.

9. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

10. The nucleic acid molecule of claim 9, which is labeled.

11. An expression vector comprising the nucleic acid of claim 9.

12. A host cell comprising the expression vector of claim 11.

13. An isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

14. An antibody that specifically binds a polypeptide of claim 13.

15. The antibody of claim 14, further conjugated to an effector component.

16. The antibody of claim 15, wherein the effector component is a fluorescent label.

17. The antibody of claim 15, wherein the effector component is a radioisotope or a cytotoxic chemical.

18. The antibody of claim 15, which is an antibody fragment.

19. The antibody of claim 15, which is a humanized antibody

20. A method of detecting an ovarian cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody of claim 14.

21. The method of claim 20, wherein the antibody is further conjugated to an effector component.

22. The method of claim 21, wherein the effector component is a fluorescent label.

23. A method for identifying a compound that modulates an ovarian cancer-associated polypeptide, the method comprising the steps of:

(i) contacting the compound with an ovarian cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26; and

(ii) determining the functional effect of the compound upon the polypeptide.

24. A drug screening assay comprising the steps of

(i) administering a test compound to a mammal having ovarian cancer or a cell isolated therefrom;

(ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a

treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of ovarian cancer.